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OM protein - protein search, using sw model

Run on: March 11, 2004, 17:50:06 ; Search time 5.32258 Seconds

(without alignments)  
145,491 Million cell updates/sec

Title: US-09-977-406A-5

Perfect score: 1 EMQDNCETCTCYET 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A COMB pepi:\*  
2: /cgn2\_6/ptodata/2/1aa/5B COMB pepi:\*  
3: /cgn2\_6/ptodata/2/1aa/6A COMB pepi:\*  
4: /cgn2\_6/ptodata/2/1aa/6B COMB pepi:\*  
5: /cgn2\_6/ptodata/2/1aa/PTCUS COMB pepi:\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1 pepi:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	94	1	US-07-899-535A-1 Sequence 1, Appl
2	52	53.6	1172	1	US-08-313-288B-19 Sequence 19, Appl
3	50	51.5	466	4	US-09-724-864-44 Sequence 44, Appl
4	47	48.5	164	4	US-09-907-794A-12 Sequence 12, Appl
5	47	48.5	164	4	US-09-905-125A-12 Sequence 12, Appl
6	47	48.5	164	4	US-09-903-775A-12 Sequence 12, Appl
7	46	47.4	9	4	US-08-481-968A-24 Sequence 24, Appl
8	46	47.4	9	4	US-08-154-712B-24 Sequence 24, Appl
9	46	47.4	218	3	US-08-985-526-1 Sequence 1, Appl
10	45	46.4	239	5	PCT-US93-01652-1 Sequence 1, Appl
11	45	46.4	306	4	US-09-489-039A-11260 Sequence 11260, A
12	45	46.4	441	1	US-08-985-526-3 Sequence 3, Appl
13	45	46.4	1170	1	US-08-313-288B-20 Sequence 20, Appl
14	45	45.9	1290	4	US-09-543-681A-6461 Sequence 6461, Ap
15	44.5	45.9	1052	2	US-08-852-806-2 Sequence 2, Appl
16	44.5	45.9	1052	2	US-09-163-869-2 Sequence 2, Appl
17	43	44.3	376	4	US-09-496-005-1 Sequence 1, Appl
18	42.5	43.8	273	1	US-08-152-019A-30 Sequence 30, Appl
19	42	43.3	459	3	US-09-118-319-6 Sequence 6, Appl
20	42	43.3	459	3	US-09-286-691-2 Sequence 2, Appl
21	42	43.3	459	3	US-09-687-147-2 Sequence 2, Appl
22	42	43.3	493	6	US-9633334 Patent No. 5196333
23	42	43.3	753	3	US-07-861-458C-98 Sequence 98, Appl
24	42	43.3	755	4	US-07-861-458C-99 Sequence 99, Appl
25	42	43.3	1199	4	US-09-134-000C-5542 Sequence 5542, Ap
26	41.5	42.8	320	4	US-09-183-861-22 Sequence 22, Appl
27	41.5	42.8	320	4	US-09-183-861-55 Sequence 55, Appl

28	41.5	42.8	320	4	US-09-022-765-22 Sequence 22, Appl
29	41.5	42.8	320	4	US-09-022-765-55 Sequence 55, Appl
30	41.5	42.8	320	4	US-09-551-974A-22 Sequence 22, Appl
31	41.5	42.8	320	4	US-09-551-974A-55 Sequence 55, Appl
32	41.5	42.8	320	4	US-09-565-501A-22 Sequence 22, Appl
33	41.5	42.8	320	4	US-09-565-501A-55 Sequence 55, Appl
34	41.5	42.8	320	4	US-09-639-206A-22 Sequence 22, Appl
35	41.5	42.8	320	4	US-09-639-206A-55 Sequence 55, Appl
36	41.5	42.8	320	4	US-09-874-923-22 Sequence 22, Appl
37	41.5	42.8	320	4	US-09-874-923-55 Sequence 55, Appl
38	41.5	42.8	709	4	US-09-874-923-121 Sequence 121, App
39	41	42.3	313	4	US-09-328-352-4280 Sequence 4280, Ap
40	41	42.3	437	3	US-09-073-569-2 Sequence 2, Appl
41	41	42.3	437	4	US-09-830-189C-2 Sequence 2, Appl
42	41	42.3	1276	3	US-08-937-236-3 Sequence 3, Appl
43	41	42.3	1277	3	US-08-937-236-6 Sequence 6, Appl
44	41	42.3	1291	3	US-08-569-214-3 Sequence 3, Appl
45	41	42.3	1291	3	US-08-937-236-2 Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
US-07-899-535A-1  
Sequence 1, Application US/07899535A  
Patent No. 542A011  
GENERAL INFORMATION:  
APPLICANT: Smith, Anil R.  
APPLICANT: Gardel, Seema  
TITLE OF INVENTION: Pharmaceutical Preparations For  
TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate  
TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Mr. George Loud  
STREET: 2001 Jefferson Davis Highway, Suite 306  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/899,535A  
FILING DATE: 16-JUN-1992  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Loud, George A.  
REGISTRATION NUMBER: 25,814  
REFERENCE/DOCKET NUMBER: S&B-A835  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-415-0960  
TELEFAX: 703-415-0962  
TELEX: 24 8614  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 94 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
US-07-899-535A-1

Query Match 100.0%; Score 97; DB 1; Length 94;  
Best Local Similarity 100.0%; Pred. No. 3.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWOTDNCETCTCCT 15  
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Db 31 EWOTDNCETCTCCT 45

RESULT 2  
US-08-313-288B-19  
; Sequence 19, Application US/08313288B  
; Patent No. 5750502  
; GENERAL INFORMATION:  
; APPLICANT: Jessell, Thomas M. and Avihu Klar  
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A  
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/313,288B  
; FILING DATE: January 5, 1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 40028-A-PCT-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0526  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1172 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-313-288B-19  
Query Match 53.6% Score 52; DB 1; Length 1172;  
Best Local Similarity 63.6%; Pred. No. 30;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2 WOTDNCETCTC 12  
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Db 333 WVDSCCTCTC 343  
RESULT 3  
US-09-724-864-44  
; Sequence 44, Application US/09724864  
; Patent No. 6380362  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D  
; APPLICANT: Murison, James G.  
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
; TITLE OF INVENTION: by the polynucleotides and methods for their use.  
; FILE REFERENCE: 11000.105001  
; CURRENT APPLICATION NUMBER: US/09/724,864  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 44

LENGTH: 466  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-724-864-44

Query Match 51.5% Score 50; DB 4; Length 466;  
Best Local Similarity 70.0%; Pred. No. 23;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 DNCETCTC 14  
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Db 119 DNCRCCTCH 128

RESULT 4  
US-09-907-794A-12  
; Sequence 12, Application US/09907794A  
; Patent No. 6635468  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Flivaioff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gunney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kjaer, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/907,794A  
; PRIOR FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02

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; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 12
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-12

Query Match      48.5%; Score 47; DB 4; Length 164;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 DNCERTCTCYE 14
Db      120 DMCNRCCTCQE 129

RESULT 5
US-09-905-125A-12
; Sequence 12, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsens, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/00414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
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; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 12
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-12

Query Match      48.5%; Score 47; DB 4; Length 164;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 DNCERTCTCYE 14
Db      120 DMCNRCCTCQE 129

RESULT 6
US-09-902-775A-12
; Sequence 12, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsens, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; PRIOR FILING DATE: 2001-07-10
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PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO: 12  
LENGTH: 164  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-902-775A-12

Query Match 48.5%; Score 47; DB 4; Length 164;  
Best Local Similarity 70.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 NCERTCTCY 14  
Db 120 DNCNCTCCE 129

RESULT 7  
US-08-481-968A-24  
Sequence 24, Application US/08481968A  
Patent No. 6300490  
GENERAL INFORMATION:  
APPLICANT: Huber, Brian  
TITLE OF INVENTION: Molecular Constructs Comprising a Carcinoembryonic Antigen (CEA)  
TITLE OF INVENTION: Transcriptional Regulatory Region  
FILE REFERENCE: PB1087US4  
CURRENT APPLICATION NUMBER: US/08/481,968A  
CURRENT FILING DATE: 1998-06-07  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 24  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Consensus sequence  
FEATURE:  
NAME/KEY: misc. feature  
OTHER INFORMATION: Consensus sequence B18 from transcriptional dictionary of Locker  
OTHER INFORMATION: and Buzard (1990).  
US-08-481-968A-24

Query Match 47.4%; Score 46; DB 4; Length 9;  
Best Local Similarity 87.5%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 NCERTCTCY 13  
Db 2 NCCTCTCY 9  
RESULT 8  
US-08-154-712B-24  
Sequence 24, Application US/08154712B  
Patent No. 6337209  
GENERAL INFORMATION:  
APPLICANT: Huber, Brian  
TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic Antigen Reg  
TITLE OF INVENTION: Sequence  
FILE REFERENCE: PB1087US3  
CURRENT APPLICATION NUMBER: US/08/154,712B  
CURRENT FILING DATE: 1993-11-19  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 24  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Consensus sequence  
FEATURE:  
NAME/KEY: misc. feature  
OTHER INFORMATION: Consensus sequence B18 from transcriptional dictionary of Locker  
OTHER INFORMATION: and Buzard (1990).  
US-08-154-712B-24

Query Match 47.4%; Score 46; DB 4; Length 9;  
Best Local Similarity 87.5%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 NCERTCTCY 13  
Db 2 NCCTCTCY 9

RESULT 9  
US-08-985-526-1  
Sequence 1, Application US/08985526  
Patent No. 6080728  
GENERAL INFORMATION:  
APPLICANT: Mixson, James A  
TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA  
TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE  
TITLE OF INVENTION: THERAPY  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Connolly, Bove, Lodge, & Hutz  
STREET: 1220 Market Street, P.O. Box 2207  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: U.S.A.  
ZIP: 19899  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,526  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/608,845  
FILING DATE: 16-JUL-1996  
ATTORNEY/AGENT INFORMATION:



NAME: McMorrow Jr., Robert G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 658-9141  
TELEFAX: (302) 658-5613  
INFORMATION FOR SEQ ID NO.: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-985-526-1

Query Match 46.4%; Score 45; DB 3; Length 218;  
Best Local Similarity 50.0%; Pred. No. 52;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EMQDNCETCTC 12  
DB 30 EMTVDSCTECHC 41

RESULT 10  
PCT-US93-01652-1  
Sequence 1, Application PC/TUS9301652  
GENERAL INFORMATION:  
APPLICANT: Bouck, Noel P.  
APPLICANT: Polverini, Peter J.  
APPLICANT: Good, Deborah J.  
APPLICANT: Frazier, William A.  
TITLE OF INVENTION: Method and Composition for  
NUMBER OF INVENTION: Inhibiting Angiogenesis  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut  
STREET: 100 South Wacker Drive, Suite 960  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-4002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/01652  
FILING DATE: 19930222  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/841,656  
FILING DATE: 24-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/464,369  
FILING DATE: 12-JAN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Fentress, Susan B.  
REGISTRATION NUMBER: 31,327  
REFERENCE/DOCKET NUMBER: 92005-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)-456-8000  
TELEFAX: (312)-456-7776  
INFORMATION FOR SEQ ID NO.: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
PCT-US93-01652-1

Query Match 46.4%; Score 45; DB 5; Length 239;  
Best Local Similarity 50.0%; Pred. No. 57;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EMQDNCETCTC 12  
DB 19 EMTVDSCTECHC 30

RESULT 11  
US-09-489-039A-11260  
Sequence 11260, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2004001  
CURRENT FILING DATE: US/09/489,039A  
PRIOR FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 11260  
LENGTH: 306  
TYPE: PRT  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-11260

Query Match 46.4%; Score 45; DB 4; Length 306;  
Best Local Similarity 53.3%; Pred. No. 72;  
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYET 15  
DB 208 QMLTDGSAVAYET 222

RESULT 12  
US-08-985-526-3  
Sequence 3, Application US/08985526  
Patent No. 6080728  
GENERAL INFORMATION:  
APPLICANT: Mixson, James A.  
TITLE OF INVENTION: CARRIER-DNA COMPLEXES CONTAINING DNA  
TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE  
TITLE OF INVENTION: THERAPY  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Connolly, Bove, Lodge, & Hutz  
STREET: 1220 Market Street, P.O. Box 2207  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: U.S.A.  
ZIP: 19899  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,526  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/608,845  
FILING DATE: 16-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: McMorrow Jr., Robert G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 658-9141  
TELEFAX: (302) 658-5613  
INFORMATION FOR SEQ ID NO.: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

US-08-985-526-3

Query Match 46.4%; Score 45; DB 3; Length 441;  
Best Local Similarity 50.0%; Pred. No. 1e+02;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EWQDNCETCTC 12  
DB 253 EWTVDSCTECHC 264

RESULT 13

US-08-313-288B-20  
Sequence 20, Application US/08313288B

Patent No. 5750502

GENERAL INFORMATION:

APPLICANT: Jessell, Thomas M. and Avihu Klar

TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A

TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper &amp; Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/313,288B

FILING DATE: January 5, 1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 40028-A-PCT-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0526

TELEX:

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 1170 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-313-288B-20

Query Match 46.4%; Score 45; DB 1; Length 1170;

Best Local Similarity 50.0%; Pred. No. 2.5e+02;

Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 EWQDNCETCTC 12

DB 330 EWTVDSCTECHC 341

RESULT 14

US-09-543-681A-6461

Sequence 6461, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: NOCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 6461

LENGTH: 290

TYPE: PRT

ORGANISM: Proteus mirabilis

US-09-543-681A-6461

Query Match 45.9%; Score 44.5; DB 4; Length 290;

Best Local Similarity 50.0%; Pred. No. 79;

Matches 7; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 2 WQDNCETC-TCTE 14

DB 73 WNAQSCQCDCTCQ 86

RESULT 15

US-08-852-806-2

Sequence 2, Application US/08852806

Patent No. 5874245

GENERAL INFORMATION:

APPLICANT: Shoji Fukusumi

TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/852,806

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/017,915

FILING DATE: 16 MAY 1996

ATTORNEY/AGENT INFORMATION:

NAME: Han, William T

REGISTRATION NUMBER: 34,344

REFERENCE/DOCKET NUMBER: TAKS0002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5219

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1052 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

US-08-852-806-2

Query Match 45.9%; Score 44.5; DB 2; Length 1052;

Best Local Similarity 33.3%; Pred. No. 2.7e+02;

Matches 7; Conservative 3; Mismatches 2; Indels 9; Gaps 1;

QY 1 EWQDNCETCTCCTC 12

Fri Mar 12 09:42:16 2004

us-09-977-406a-5.rai

Db 388 DWDENCQTLTQAAHTRQC 408

Search completed: March 11, 2004, 17:56:55  
Job time : 6.32258 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2004, 17:49:21 ; Search time 4.2387 Seconds

(without alignments)  
340.793 Million cell updates/sec

Title: US-09-977-406a-5

Perfect score: 97

Sequence: 1 EMQDNCETCTCYET 15

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	97	100.0	114 2 A34567	beta-microseminopr
2	79	81.4	114 2 A54653	seminal plasma pro
3	57	58.8	884 2 T18649	hypothetical prote
4	54	55.7	863986	collagen alpha 5 c
5	53	54.6	91 2 S41663	beta-microseminopr
6	52	53.6	1172 1 TSHUP2	thrombospondin 2 p
7	52	53.6	1172 1 A2587	thrombospondin 2 p
8	51	52.6	835 2 UP0076	nei protein - chic
9	50	51.5	429 2 T11133	hypothetical prote
10	50	51.5	665 2 T44793	beta-galactosidase
11	47	48.5	330 2 T41967	hypothetical prote
12	47	48.5	347 2 A28453	anaerobic sulfite
13	47	48.5	347 2 AC0825	thrombospondin pre
14	47	48.5	1178 1 A39804	collagen alpha 2 c
15	47	48.5	1822 2 A35985	integrin alpha 2 c
16	45.5	46.9	398 2 A35281	hypothetical prote
17	45	46.4	205 2 T25986	hypothetical prote
18	45	46.4	912 2 G96830	thrombospondin 1 p
19	45	46.4	1170 1 TSHUP1	thrombospondin 1 p
20	44.5	45.9	1572 2 A40558	brain-specific ang
21	44.5	45.4	1572 2 T00027	hypothetical prote
22	44	45.4	491 2 T21421	probable peroxidase
23	44	45.4	724 2 T37858	mucin, submaxillar
24	43.5	44.8	13288 2 T03099	trypsin inhibitor
25	43	44.3	66 1 T1AC	hypothetical prote
26	43	44.3	218 2 B96938	nine-heme cytochrom
27	43	44.3	326 2 JC7094	probable cytochrom
28	43	44.3	372 2 G71074	tubulin beta-2 cha
29	43	44.3	446 2 A27810	

30	43	44.3	977 2 T16232	hypothetical prote
31	43	44.3	1444 2 T18856	angiogenesis inhib
32	43	44.3	3198 2 A43426	collagen alpha 2 f
33	42.5	43.8	1790 1 MFFB1	lamnin beta-1 cha
34	42.5	43.8	5376 2 T42215	zonadhesin - mouse
35	42	43.3	88 2 S16588	hypothetical prote
36	42	43.3	220 2 G84188	hypothetical prote
37	42	43.3	334 2 G75069	cytochrome-c3 hydr
38	42	43.3	367 2 E75133	cytochrome-c3 hydr
39	42	43.3	367 2 S48833	unknown protein 11
40	42	43.3	601 2 B96744	lysine decarboxyla
41	42	43.3	733 2 E82342	mechanosensory pro
42	42	43.3	749 2 T29859	Nei-homolog protei
43	42	43.3	810 2 T10756	mucin SAC (clone L
44	42	43.3	1042 2 A57534	mucin MUC5B, trach
45	42	43.3	1056 2 A53767	

## ALIGNMENTS

RESULT 1  
A34567  
beta-microseminoprotein precursor - human  
N/Alternate names: beta-inhibin; prostatic secretory protein; PSP-94; seminal plasma pr  
C/Species: Homo sapiens (man)  
C/Date: 13-Jul-1990 #sequence revision 13-Jul-1990 #ext change 20-Aug-1999  
C/Accession: A34567, A26451, A29777, A30984, A60673, S16238, I52682  
R/Green, C.B.; Liu, W.Y.; Kwok, S.C.M.  
Biochem. Biophys. Res. Commun. 167, 1184-1190, 1990  
A/Title: Cloning and nucleotide sequence analysis of the human beta-microseminoprotein  
A/Reference number: A34567, PMID:90211299, PMID:2322265  
A/Accession: A34567  
A/Status: not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-114 <GRE>  
A/Cross-references: GB:M34376, NID:G514370, PIDN:AAA59871.1; PID:G514372  
R/Mikay, M.; Nolet, S.; Fournier, S.; Benjannet, S.; Chapdelaine, P.; Paradis, G.; Dub  
DNA 6, 23-29, 1987  
A/Title: Molecular cloning and sequence of the cDNA for a 94-amino-acid seminal plasma  
A/Reference number: A26451, PMID:87161231, PMID:3829888  
A/Accession: A26451  
A/Molecule type: mRNA  
A/Residues: 1-114 <MBI>  
A/Cross-references: GB:M15885, NID:G338414, PIDN:AAA6635.1; PID:G338415  
R/Akiyama, K.; Yoshitaka, Y.; Schmidt, K.; Offner, G.D.; Troxler, R.F.; Tsuda, R.; Hara,  
Biochim. Biophys. Acta 829, 288-294, 1995  
A/Title: The amino acid sequence of human beta-microseminoprotein.  
A/Reference number: A29777, PMID:8519974, PMID:395056  
A/Accession: A29777  
A/Molecule type: protein  
A/Residues: 21-58, 'PT', 61-113 <AXI>  
R/Seidah, N.G.; Arbatli, N.J.; Rochemont, J.; Sheeh, A.R.; Christien, M.  
FEBS Lett. 175, 349-355, 1984  
A/Title: Complete amino acid sequence of human seminal plasma beta-inhibin. Prediction  
A/Reference number: A30984, PMID:85004133, PMID:643450  
A/Accession: A30984  
A/Molecule type: protein  
A/Residues: 21-112, 'G', 114 <SEI>  
R/Meibier, H.; Andersson, C.; Murre, A.; Rannevik, G.; Lindstroem, C.; Lilja, H.; Fernu  
Am. J. Pathol. 137, 593-604, 1990  
A/Title: Beta microseminoprotein is not a prostate-specific protein.  
A/Reference number: A60673, PMID:90379237, PMID:2205099  
A/Accession: A60673  
A/Molecule type: protein  
A/Residues: 21, 'X', 23-34 <WEI>  
R/Nolet, S.; Mikay, M.; Christien, M.  
Biochim. Biophys. Acta 1089, 247-249, 1991  
A/Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence i  
A/Reference number: S16237, PMID:91274357, PMID:2054385  
A/Accession: S16238  
A/Molecule type: DNA

A:Residues: 1-114 <NO>  
 A:Cross-references: EMBL:X57928; NID:G35760; PIDN:CAA41002.1; PID:G6825707  
 A>Note: the authors translated the codon ACT for residue 54 as Trp  
 R:Linu, A.Y.; Bradner, R.C.; Vessella, R.L.  
 A:Title: Decreased expression of prostatic secretory protein PSP94 in prostate cancer.  
 A:Reference number: 152682; PMID:94115955; PMID:7506990  
 A:Accession: 152692  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-114 <RES>  
 A:Cross-references: GB:S67815; NID:G460566; PIDN:AA529732.1; PID:G460569  
 C:Comment: This protein is a component of seminal plasma as well as secretory fluids from  
 C:Genetics:  
 A:Gene: GDB:MSMB  
 A:Cross-references: GDB:128042; OMTN:157145  
 A:Map position: 10q11.2-10q11.2  
 A:Introns: 1/3; 37/1; 72/2  
 C:Superfamily: seminal plasma protein  
 C:Keywords: semen  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-114/Product: seminal plasma protein #status experimental <MAT>

Query Match 100.0%; Score 97; DB 2; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCCTCTCYET 15  
 |||||  
 Db 51 EMQDNCCTCTCYET 65

RESULT 2  
 A54663  
 seminal plasma protein PSP-94 precursor - rhesus macaque  
 N:Alternate names: prostatic secretory protein PSP94  
 C:Species: Macaca mulatta (rhesus macaque)  
 C:Date: 02-Jun-1995 #sequence\_revision 02-Jun-1995 #text\_change 20-Aug-1999  
 C:Accession: S16237; A54663  
 R:Nolet, S.; Mbikay, M.; Chretien, M.  
 Biochim. Biophys. Acta 1089, 247-249, 1991  
 A:Title: Prostatic secretory protein PSP(94): Gene organization and promoter sequence in  
 A:Reference number: S16237; PMID:91274357; PMID:2054385  
 A:Accession: S16237  
 A:Molecule type: DNA  
 A:Residues: 1-114 <NO>  
 A:Cross-references: EMBL:X57932; NID:G38094; PIDN:CAA41003.1; PID:G629152  
 A>Note: the authors translated the codon ACT for residue 54 as Trp  
 R:Nolet, S.; St-Louis, D.; Mbikay, M.; Chretien, M.  
 Genomics 9, 775-777, 1991  
 A:Title: Rapid evolution of prostatic protein PSP-94 suggested by sequence divergence be  
 A:Reference number: A54663; PMID:91244325; PMID:2037304  
 A:Accession: A54663  
 A:Molecule type: mRNA  
 A:Residues: 1-114 <NO>  
 A:Cross-references: EMBL:M92161; NID:G342280; PIDN:AAA36903.1; PID:G342281  
 C:Genetics:  
 A:Introns: 1/3; 37/1; 72/2  
 C:Superfamily: seminal plasma protein  
 F:1-20/Domain: signal sequence #status predicted <SIG>

Query Match 81.4%; Score 79; DB 2; Length 114;  
 Best Local Similarity 73.3%; Pred. No. 0.00066;  
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EMQDNCCTCTCYET 15  
 |||||  
 Db 51 KWKDNCCTCTCYET 65

RESULT 3  
 T18649  
 hypothetical protein B0024.14 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T18649  
 R:McMurry, A.  
 submitted to the EMBL Data Library, April 1996  
 A:Reference number: Z19001  
 A:Accession: T18649  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-884 <WIL>  
 A:Cross-references: EMBL:Z71178; PIDN:CAA94886.1; GSPDB:GN00023; CESP:B0024.14  
 A:Experimental source: clone B0024  
 C:Genetics:  
 A:Gene: CESP:B0024.14  
 A:Map position: 5  
 A:Introns: 46/3; 84/1; 212/1; 307/2; 345/2; 394/1; 424/2; 481/1; 596/1; 702/1; 765/3; 8

Query Match 58.8%; Score 57; DB 2; Length 884;  
 Best Local Similarity 61.5%; Pred. No. 2.7;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WQDNCCTCTCYE 14  
 |||||  
 Db 245 WQDNCCTCTCSE 257

RESULT 4  
 S63986  
 collagen alpha 5 chain - sea urchin (Strongylocentrotus purpuratus) (fragment)  
 C:Species: Strongylocentrotus purpuratus (purple urchin)  
 C:Date: 20-Jul-1996 #sequence\_revision 08-Nov-1996 #text\_change 25-Apr-1997  
 C:Accession: S63986; S64638  
 R:Exposito, J.Y.; Boule, N.; Delage, G.; Garrone, R.  
 Eur. J. Biochem. 234, 59-65, 1995  
 A:Title: Characterization of two genes coding for a similar four-cysteine motif of the  
 A:Reference number: S63985; PMID:96096722; PMID:8529659  
 A:Accession: S63986  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1376 <EXP>  
 A:Cross-references: EMBL:X89804  
 R:Exposito, J.Y.  
 submitted to the EMBL Data Library, July 1995  
 A:Reference number: S64637  
 A:Accession: S64638  
 A:Molecule type: DNA  
 A:Residues: 1-658; G', 660-870, G', 872-901, H', 903-1185, T', 1187-1214, Y', 1216-1376 <EXM>  
 A:Cross-references: EMBL:X89804  
 C:Genetics:  
 A:Gene: COL5A3A  
 A:Introns: 73/1; 136/2; 221/1; 369/1; 517/1; 659/1; 799/1; 946/1; 1093/1; 1236/1  
 C:Superfamily: von Willebrand factor type C repeat homology  
 C:Keywords: extracellular matrix  
 F:15-73/Domain: von Willebrand factor type C repeat homology <VWC>

Query Match 55.7%; Score 54; DB 2; Length 1376;  
 Best Local Similarity 58.3%; Pred. No. 9.6;  
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EMQDNCCTCTC 12  
 |||||  
 Db 28 EWKVDCTCTCAC 39

RESULT 5  
 S41663  
 beta-microseminoprotein - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
 C:Accession: S41663  
 R:Ferlund, P.; Granberg, L.B.; Roepstorff, P.  
 Arch. Biochem. Biophys. 309, 70-76, 1994  
 A:Title: Amino acid sequence of beta-microseminoprotein from porcine seminal plasma.

A:Reference number: S41663; MUID:94161559; PMID:8117114  
 A:Accession: S41663  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-91 <PER>  
 C:Superfamily: seminal plasma protein

Query Match 54.6%; Score 53; DB 2; Length 91;  
 Best Local Similarity 63.6%; Pred. No. 1.7;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 WQDNCETCTC 12  
 DB 29 WKTXDCECTC 39

## RESULT 6

TSHUP2  
 Thrombospondin 2 precursor - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1995 #sequence\_revision 03-Aug-1995 #text\_change 13-Aug-1999

C:Accession: A47379; A42173

R:Label: T.L.; Byers, P.H.

A:Title: Sequence and characterization of the complete human thrombospondin 2 cDNA: pote

A:Reference number: A47379; MUID:94010892; PMID:8406456

A:Accession: A47379

A:Molecule type: mRNA

A:Residues: 1-1172 <LAA>

A:Cross-references: GB:L12350; NID:G307505; PIDN:AAA03703.1; PID:G307506

R:Label: T.L.; Milewicz, D.J.; Distche, C.M.; Byers, P.H.

Genomics 12, 421-429, 1992

A:Title: Thrombospondin II: partial cDNA sequence, chromosome location, and expression c

A:Reference number: A42173; MUID:92217961; PMID:1559694

A:Accession: A42173

A:Molecule type: mRNA

A:Residues: 560-1172 <LAA>

A:Cross-references: GB:M81339

A:Experimental source: fibroblast

A>Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBI:95096)

C:Genetics:

A:Gene: GDB:THBS2; TSP2

A:Cross-references: GB:128789; OMIM:188061

A:Map position: 6q27-6q27

C:Complex: homotrimer, disulfide linked

C:Function:

A:Description: participates in cell migration and adhesion, and in platelet aggregation

C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; VC

C:Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-1172/Product: thrombospondin 2 #status predicted <MAT>

F:319-377/Domain: von Willebrand factor type C repeat homology <WVC>

F:380-431/Domain: thrombospondin type 1 repeat homology <THR1>

F:436-492/Domain: thrombospondin type 1 repeat homology <THR2>

F:493-549/Domain: thrombospondin type 1 repeat homology <THR3>

F:553-588/Domain: EGF homology <EGF1>

F:652-691/Domain: EGF homology <EGF2>

F:928-930/Region: cell attachment (R-G-D) motif

F:151,318,330,457,584,710,1069/Binding site: carbohydrate (Asn) (covalent) #status predi

F:167-226/Disulfide bonds: #status predicted

F:166-270/Disulfide bonds: interchain #status predicted

F:612/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 53.6%; Score 52; DB 1; Length 1172;

Best Local Similarity 63.6%; Pred. No. 16;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 WQDNCETCTC 12

DB 333 WVDSCCTCTC 343

## RESULT 7

A42587  
 Thrombospondin 2 precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Aug-1999  
 C:Accession: A42587; A39851  
 R:Label: C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seidlin, M.F.; Dixit, V.M.

U. Biol. Chem. 267, 3274-3281, 1992  
 A:Title: Characterization of mouse thrombospondin 2 sequence and expression during cell

A:Reference number: A42587; MUID:92147683; PMID:1371115

A:Accession: A42587

A:Molecule type: nucleic acid

A:Status: preliminary; not compared with conceptual translation

A:Residues: 1-1172 <LAA>

A:Cross-references: GB:L07803; GB:M87275; NID:G340421; PIDN:AAA53064.1; PID:G567241

A>Note: sequence extracted from NCBI backbone (NCBI:81502)

R:Bornstein, P.; O'Rourke, K.; Wikstrom, K.; Wolf, F.W.; Katz, R.; Li, P.; Dixit, V.M.

J. Biol. Chem. 266, 12821-12824, 1991

A:Title: A second, expressed thrombospondin gene (Thbs2) exists in the mouse genome.

A:Reference number: A39851; MUID:91302287; PMID:1712771

A:Accession: A39851

A:Molecule type: mRNA

A:Status: preliminary

A:Residues: 1-873 <BOR>

A:Cross-references: GB:M64866; NID:G201994; PIDN:AAA40432.1; PID:G201995

C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; v

C:Keywords: calcium binding; glycoprotein

F:319-377/Domain: von Willebrand factor type C repeat homology <WVC>

F:380-431/Domain: thrombospondin type 1 repeat homology <THR1>

F:436-492/Domain: thrombospondin type 1 repeat homology <THR2>

F:493-549/Domain: thrombospondin type 1 repeat homology <THR3>

F:553-588/Domain: EGF homology <EGF1>

F:652-691/Domain: EGF homology <EGF2>

Query Match 53.6%; Score 52; DB 2; Length 1172;

Best Local Similarity 63.6%; Pred. No. 16;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 WQDNCETCTC 12

DB 333 WVDSCCTCTC 343

## RESULT 8

JP0076  
 nel protein - chicken

C:Species: Gallus gallus (chicken)

C:Date: 24-Feb-1995 #sequence\_revision 24-Feb-1995 #text\_change 13-Aug-1999

C:Accession: A38963; JP0076

R:Matsumashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Horii, K.

Dev. Dyn. 203, 212-222, 1995

A:Title: New gene, nel, encoding a Mr 93K protein with EGF-like repeats is strongly exp

A:Reference number: A38963; MUID:95383734; PMID:7655083

A:Accession: A38963

A:Molecule type: mRNA

A:Residues: 1-835 <MAT>

A:Cross-references: DDBJ:D45365

A:Experimental source: 9-day embryo

R:Matsumashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Horii, K.

submitted to JIPID, January 1995

A:Description: A new gene, nel, encoding a Mr 93K protein with EGF-like repeats is strc

A:Reference number: JP0076

A:Accession: JP0076

A:Molecule type: mRNA

A:Residues: 1-835 <MA2>

A:Cross-references: DDBJ:D45365

A:Experimental source: 9-day embryo

C:Superfamily: von Willebrand factor type C repeat homology; EGF homology

F:273-333/Domain: von Willebrand factor type C repeat homology <WVC>

F:335-592/Region: EGF-like repeats

F:444-480/Domain: EGF homology <EGF1>

F:486-521/Domain: EGF homology <EGF2>

F:525-552/Domain: EGF homology <EGF2>

Query Match 52.6%; Score 51; DB 2; Length 835;  
 Best Local Similarity 54.5%; Pred. No. 17;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WOTDNCETCTC 12  
 |||||  
 DB 655 WRIDRCVSCC 665

## RESULT 9

T2113  
 hypothetical protein F19C6.3 - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
 C/Accession: T2113

R/Harris, B.

Submitted to the EMBL Data Library, January 1995

A/Reference number: Z19376

A/Accession: T2113

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-429 <MIL>

A/Cross-references: EMBL:Z48006; PIRN:CA88048.1; GSPDB:GN00028; CESP:F19C6.3

A/Experimental source: clone F19C6

C/Genetics:

A/Map position: X

A/Introns: 71/3; 137/2; 192/3; 217/3; 273/3; 309/2; 366/3; 390/3

Query Match 51.5%; Score 50; DB 2; Length 429;  
 Best Local Similarity 57.1%; Pred. No. 14;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYE 14  
 |||||  
 DB 227 ERTVNCVCTCTCD 240

## RESULT 10

T44793  
 beta-galactosidase (EC 3.2.1.23) [validated] - *Haloflex alicantel*

C/Species: *Haloflex alicantel*  
 C/Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 18-Feb-2000  
 C/Accession: T44793

R/Holmes, M.L.; Dyal, Smith, M.L.

Submitted to the EMBL Data Library, May 1999

A/Reference number: Z22843

A/Accession: T44793

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-665 <HOL>

A/Cross-references: EMBL:U70664; PIRN:AA840123.1

A/Experimental source: strain SBI

C/Genetics:

A/Genes: dgah

C/Complex: homodimer [validated, PMID:97201076]

C/Function:

A/Description: EC 3.2.1.23 [validated, PMID:97201076]

A/Note: Cleaves several different beta-galactoside substrates such as ONP-Gal, X-Gal and

C/Suprafamily: *Bacillus beta-galactosidase*

C/Keywords: glycosidase; homodimer; hydrolase

Query Match 51.5%; Score 50; DB 1; Length 665;  
 Best Local Similarity 68.8%; Pred. No. 19;  
 Matches 11; Conservative 0; Mismatches 1; Indels 4; Gaps 2;

QY 2 WOTDNCETCTCY 13  
 |||||  
 DB 137 WOTDNCETCTCY 152

## RESULT 11

T41967

hypothetical protein U65 - human herpesvirus 7 (strain J1)

C/Species: human herpesvirus 7

A/Variety: strain J1

C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000

C/Accession: T41967

R/Nicholas, J.

Submitted to the EMBL Data Library, December 1995

A/Description: Determination and analysis of the complete nucleotide sequence of human

A/Reference number: Z22022

A/Accession: T41967

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-330 <NIC>

A/Cross-references: EMBL:U43400; PIRN:AA054727.1

A/Experimental source: strain J1

C/Genetics:

A/Note: U65

C/Suprafamily: Epstein-Barr virus BGLF2 protein

Query Match 48.5%; Score 47; DB 2; Length 330;  
 Best Local Similarity 80.0%; Pred. No. 28;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TDNCETCTCY 13  
 |||||  
 DB 233 TDNCETCTCY 242

## RESULT 12

A38453

anaerobic sulfite reduction protein A - *Salmonella typhimurium*

C/Species: *Salmonella typhimurium*

C/Date: 12-Jul-1991 #sequence\_revision 12-Jul-1991 #text\_change 08-Oct-1999

C/Accession: A38453

R/Huang, C.J.; Barrett, E.L.

J. Bacteriol. 173, 1544-1553, 1991

A/Title: Sequence analysis and expression of the *Salmonella typhimurium* asr operon enco

A/Reference number: A38453; PMID:91139599; PMID:170486

A/Accession: A38453

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-347 <HUA>

A/Cross-references: GB:M57706; NID:G153881; PIRN:AAA9275.1; PID:G153882

Query Match 48.5%; Score 47; DB 2; Length 347;  
 Best Local Similarity 70.0%; Pred. No. 29;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TDNCETCTCY 13  
 |||||  
 DB 237 TDNCETCTCY 246

## RESULT 13

AC0825

anaerobic sulfite reductase chain A (EC 1.8.2.-) [imported] - *Salmonella enterica* subsp

C/Species: *Salmonella enterica* subsp. *enterica* serovar Typh

A/Note: this species has also been called *Salmonella typhi*

C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002

C/Accession: AC0825

R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher

th, T.; Conerton, F.; Cronin, A.; Davis, F.; Davies, R.M.; Dowd, L.; White, N.; Farrar

S.; Moule, S.; O'Garra, P.

Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A/Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* sero

A/Reference number: AB0502; PMID:21534947; PMID:11677608

A/Accession: AC0825

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-347 <PAR>

A/Cross-references: GB:AL513382; PIRN:CAD02751.1; PID:G16503762; GSPDB:GN00176

C/Genetics:



A:Gene: asrA  
C:Keywords: oxidoreductase

Query Match 48.5%; Score 47; DB 2; Length 347;  
Best Local Similarity 70.0%; Pred. No. 29;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TDNCCTCTCY 13  
DB 237 TTGCTCTCY 246

## RESULT 14

A39804  
thrombospondin precursor - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A39804  
R:Lawler, J.; Duquette, M.; Ferro, P.  
J. Biol. Chem. 266, 8039-8043, 1991  
A:Title: Cloning and sequencing of chicken thrombospondin.  
A:Reference number: A39804; MUID:9.1217026; PMID:2022631  
A:Accession: A39804  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1178 <LAW>  
A:Cross-references: GB:M60853; NID:G212763; PID:AAA51437.1; PID:G212764  
C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vd  
F:325-353/Domain: von Willebrand factor type C repeat homology <VWC>  
F:386-437/Domain: thrombospondin type 1 repeat homology <THR1>  
F:442-498/Domain: thrombospondin type 1 repeat homology <THR2>  
F:499-555/Domain: thrombospondin type 1 repeat homology <THR3>  
F:658-697/Domain: EGF homology <EGF>

Query Match 48.5%; Score 47; DB 1; Length 1178;  
Best Local Similarity 42.9%; Pred. No. 74;  
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 WQDNCCTCTCY 15  
DB 339 WVDSCCTCTCQDS 352

## RESULT 15

S63985  
collagen alpha 2 chain precursor - sea urchin (Strongylocentrotus purpuratus) (fragment)  
C:Species: Strongylocentrotus purpuratus (purple urchin)  
C:Date: 20-Jul-1986 #sequence\_revision 01-Nov-1996 #text\_change 15-Sep-2003  
C:Accession: S63985; S64637  
R:Exposito, J.Y.; Boule, N.; Deleage, G.; Garrone, R.  
Eur. J. Biochem. 234, 59-65, 1995  
A:Title: Characterization of two genes coding for a similar four-cysteine motif of the a  
A:Reference number: S63985; MUID:96096722; PMID:8529669  
A:Accession: S63985  
A:Status: nucleic acid sequence not shown

A:Molecule type: DNA  
A:Residues: 1-1822 <EXP>  
A:Cross-references: EMBL:X89806  
R:Exposito, J.Y.  
submitted to the EMBL Data Library, July 1995  
A:Reference number: S64637  
A:Accession: S64637

A:Molecule type: DNA  
A:Residues: 1381,'DT',384-677,'N',679-1010,'L',1012-1822 <EXW>  
A:Cross-references: EMBL:X89806  
C:Genetics:

A:Gene: COL12A1pna  
A:Introns: 33/1; 106/1; 169/2; 254/1; 395/1; 460/3; 534/1; 678/1; 743/3 817/1; 965/1; 11  
F:48-106/Domain: von Willebrand factor type C repeat homology <VWC>

Query Match 48.5%; Score 47; DB 2; Length 1822;  
Best Local Similarity 54.5%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 WQDNCCTCTC 12  
DB 62 WSVDECTTCEC 72

Search completed: March 11, 2004, 17:55:59  
Job time: 6.23387 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2004, 17:57:02 ; Search time 2.78226 Seconds

(Without alignments)  
280.726 Million cell updates/sec

Title: US-09-977-406a-5  
Perfect score: 15  
Sequence: 1 EMQDNCECTCYET 15

Scoring table: OLIGO

Gapop 60.0 , Gapept 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	114	1 MSMB_HUMAN	P08118 homo sapien
2	7	46.7	114	1 MSMB_PAPAN	Q28767 papio anibi
3	6	40.0	326	1 CYC9_DESD	Q9rm68 desulfocylb
4	6	40.0	459	1 MURD_LACP	Q88v80 laccobacilli
5	6	40.0	3110	1 LMA2_HUMAN	P24043 homo sapien
6	5	33.3	37	1 DEF4_ANDAU	P56686 androctonus
7	5	33.3	38	1 DEF4_LEIOH	P41965 leiturus qui
8	5	33.3	38	1 DEF1_AESCY	P80154 aescuna cya
9	5	33.3	74	1 DEF1_DERVA	Q86415 dermacentor
10	5	33.3	114	1 MSMB_MACMU	P25142 macaca mula
11	5	33.3	119	1 ACPS_MYCPN	F75480 mycoplasma
12	5	33.3	130	1 YFQ2_ECOLI	P76548 escherichia
13	5	33.3	235	1 PUR7_CHLTE	Q8kdt4 chlorobium
14	5	33.3	295	1 YF63_SMY3	P74594 synchocyst
15	5	33.3	319	1 ISL2_CHICK	P53410 gallus gall
16	5	33.3	340	1 IS2B_ONCTS	P50212 oncorhynch
17	5	33.3	347	1 ASRA_SALTY	P26474 salinonella
18	5	33.3	349	1 ISL1_CHICK	P50211 gallus gall
19	5	33.3	354	1 NOV_MOUSE	Q64299 mus musculu
20	5	33.3	358	1 IS2A_ONCTS	P53408 oncorhynch
21	5	33.3	358	1 ISL3_BRARE	P53407 brachydanio
22	5	33.3	359	1 ISL2_BRARE	P53406 brachydanio
23	5	33.3	359	1 ISL2_HUMAN	Q96447 homo sapien
24	5	33.3	359	1 ISL2_MOUSE	Q96440 mus musculu
25	5	33.3	359	1 WNT8_BRARE	P51028 brachydanio
26	5	33.3	360	1 ISL2_RAT	P50480 rattus norv
27	5	33.3	360	1 MEIM_ACTCH	P50303 actinidia c
28	5	33.3	363	1 ISL3_ONCTS	P53409 oncorhynch
29	5	33.3	363	1 METX_PEA	P49612 pisum sativ
30	5	33.3	374	1 DNAT_CIOAB	P30725 clostridium
31	5	33.3	374	1 METL_PEA	P49613 pisum sativ
32	5	33.3	390	1 METX_PETHY	P48498 petunia hybr
33	5	33.3	390	1 METL_ACTCH	P50302 actinidia c

## ALIGNMENTS

34	5	33.3	390	1	METM_CATRO	Q96553 catharanthu
35	5	33.3	390	1	METM_LYCES	P43282 lycopersico
36	5	33.3	392	1	METK_MESCR	P93284 mesembryant
37	5	33.3	393	1	METK_ARATH	P23686 arabidopsis
38	5	33.3	393	1	METK_BRATU	P49611 brassica ju
39	5	33.3	393	1	METK_CATRO	Q96551 catharanthu
40	5	33.3	393	1	METK_LYCES	P43280 lycopersico
41	5	33.3	393	1	METK_MUSAC	O22338 musa acumin
42	5	33.3	393	1	METK_PININ	P50300 pinus banks
43	5	33.3	393	1	METL_ARATH	P17562 arabidopsis
44	5	33.3	393	1	METL_CATRO	Q96552 catharanthu
45	5	33.3	393	1	METL_LYCES	P43281 lycopersico

## RESULT 1

MSMB_HUMAN	STANDARD;	PRT;	114 AA.
ID	MSMB_HUMAN	Q13125; Q9UC59;	
AC	P08118; P11999; Q13125; Q9UC59;		
DT	01-AUG-1988 (Rel. 08, Created)		
DT	01-AUG-1988 (Rel. 08, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94) (Seminal plasma beta-inhibin) (Immunoglobulin binding factor) (IGBF) (PNA4).		
GN	MSMB OR PRSP.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OX	NCBI_Taxid:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=87161231; PubMed=3829888;		
RA	Paradis G., Nole S., Fournier S., Benjannet S., Chapdelaine P.,		
RA	Chretien M., Dube D.Y., Tremblay R., Lazare C., Seidah N.G.,		
RT	"Molecular cloning and sequence of the cDNA for a 94-amino-acid		
RL	seminal plasma protein secreted by the human prostate.";		
RL	DNA 6:23-29 (1987).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=91274357; PubMed=2054385;		
RA	Nole S., Mlikay M., Chretien M.,		
RT	"Prostatic secretory protein PSP94: gene organization and promoter		
RL	sequence in rhesus monkey and human.";		
RL	Biochim. Biophys. Res. Commun. 1089:247-249 (1991).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=90211299; PubMed=2322265;		
RA	Green C.B., Liu W.Y., Kwok S.C.M.,		
RT	"Cloning and nucleotide sequence analysis of the human beta-		
RL	microseminoprotein gene.";		
RL	Biochem. Biophys. Res. Commun. 167:1184-1190 (1990).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=90073664; PubMed=2590204;		
RA	Ulvhaek M., Lindstrom C., Weiber H., Abrahamsson P.-A., Lilja H.,		
RT	Lundwall A.;		
RT	"Molecular cloning of a small prostate protein, known as beta-		
RL	microseminoprotein, PSP94 or beta-inhibin, and demonstration of		
RL	transcripts in non-genital tissues.";		
RL	Biochem. Biophys. Res. Commun. 164:1310-1315 (1989).		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Prostate;		
RX	MEDLINE=94115955; PubMed=7506990;		
RA	Liu A.Y., Bradner R.C., Vessella R.L.;		
RT	"Decreased expression of prostatic secretory protein PSP94 in		
RL	prostate cancer.";		
RL	Cancer Lett. 74:91-99 (1993).		
RN	[6]		



Query Match 100.0%; Score 15; DB 1; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-12;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMOTNCECTCYET 15  
 |||||  
 51 EMOTNCECTCYET 65

Db 51 EMOTNCECTCYET 65

RESULT 2  
 MSMB PAPAN STANDARD; PRT; 114 AA.

AC Q28767;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94).  
 GN MSMB OR PSP94.  
 OS Papio anubis (Olive baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Papio.  
 OX NCBI\_TaxID=9555;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RX MEDLINE=97316893; PubMed=9174167;  
 RA Xuan J.W., Wu D., Guo Y., Garde S., Shum D.T., Mikiy M., Zhong R., Chin J.L.;  
 RT "Molecular cloning and gene expression analysis of PSP94 (prostate secretory protein of 94 amino acids) in primates."  
 RL DNA Cell Biol. 16:627-638(1997).  
 CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).  
 CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC DR EMBL; U49786; AAB62726.1; -  
 DR InterPro; IPR008735; PSP94.  
 DR Pfam; PF05825; PSP94; 1.  
 KM Signal.  
 FT SIGNAL 1 20 BY SIMILARITY.  
 FT CHAIN 21 114 BETA-MICROSEMINOPROTEIN.  
 FT DISULFID 22 38 BY SIMILARITY.  
 FT DISULFID 57 93 BY SIMILARITY.  
 FT DISULFID 60 69 OR 70 (BY SIMILARITY).  
 FT DISULFID 62 70 OR 69 (BY SIMILARITY).  
 FT DISULFID 84 107 BY SIMILARITY.  
 SQ SEQUENCE 114 AA; 13013 MW; A08C637ED81F9BED CRC64;

Query Match 46.7%; Score 7; DB 1; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 0.038;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WOTDNCE 8  
 |||||  
 52 WOTDNCE 58

Db 52 WOTDNCE 58

RESULT 3  
 CYC9 DESDE STANDARD; PRT; 326 AA.

ID CYC9 DESDE  
 AC Q9RNE6;

DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Nine-heme cytochrome c precursor (9Hcc).  
 OS Desulfovibrio desulfuricans.  
 CC Bacteria; Proteobacteria; Delta proteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio.  
 OX NCBI\_TaxID=876;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 27774;  
 RX MEDLINE=99400423; PubMed=10471375;  
 RA Saraiva L.M., da Costa P.N., Legall J.;  
 RT "Sequencing the gene encoding Desulfovibrio desulfuricans ATCC 27774 nine-heme cytochrome c."  
 RL Biochem. Biophys. Res. Commun. 262:629-634(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
 RC STRAIN=ATCC 27774;  
 RX MEDLINE=20022508; PubMed=10555582;  
 RA Matias P.M., Saraiva L.M., Soares C.M., Coelho A.V., Legall J., Carondo M.A.;  
 RT "Nine-heme cytochrome c from Desulfovibrio desulfuricans ATCC 27774: primary sequence determination, crystallographic refinement at 1.8 A and modelling studies of its interaction with the tetrahaem cytochrome c3."  
 RL J. Biol. Chem. 4:478-494(1999).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
 RC STRAIN=ATCC 27774;  
 RX MEDLINE=99448120; PubMed=10368280;  
 RA Matias P.M., Coelho R., Pereira I.A.C., Coelho A.V., Thompson A.W., Steker L., Legall J., Carondo M.A.;  
 RT "The primary and three-dimensional structures of a nine-haem cytochrome c from Desulfovibrio desulfuricans ATCC 27774 reveal a new member of the Hmc family."  
 RL Structure 7:119-130(1999).  
 CC -1- FUNCTION: MAY FORM PART OF A TRANSMEMBRANE REDOX COMPLEX THROUGH WHICH ELECTRONS ARE TRANSFERRED TO THE CYTOPLASM FOR REDUCTION OF SULFATE.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- SUBCELLULAR LOCATION: Periplasmic.  
 CC -1- PTM: BINDS 9 HEME GROUPS. ARRANGED INTO TWO TETRAHEME CLUSTERS AND THE EXTRA HEME 4 IS LOCATED ASYMMETRICALLY BETWEEN THE TWO REGIONS.  
 CC -1- SIMILARITY: Contains 9 cytochrome c domains.  
 CC -----  
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 CC -----  
 CC DR EMBL; AF186393; AAB56586.1; -  
 DR PIR; JC7094; JC7094.  
 DR PDB; 19HC; 01-DEC-99.  
 DR InterPro; IPR002322; Cyt CIII.  
 DR InterPro; IPR00345; CytC\_heme\_BS.  
 DR Pfam; PF02085; Cytochrome CIII; 1.  
 DR PRINTS; PR00609; CYTOCHROME C3.  
 DR PROSITE; PS00190; CYTOCHROME C; 9.  
 KW Electron transport; Heme; Periplasmic; Signal; Repeat; 3D-structure.  
 FT SIGNAL 1 30  
 FT CHAIN 31 326 NINE-HEME CYTOCHROME C.  
 FT METAL 67 70 IRON (HEME 1 AXIAL LIGAND).  
 FT METAL 70 70 IRON (HEME 3 AXIAL LIGAND).  
 FT BINDING 77 77 HEME 1 (COVALENT).  
 FT BINDING 80 80 HEME 1 (COVALENT).  
 FT METAL 81 81 IRON (HEME 1 AXIAL LIGAND).  
 FT METAL 82 82 IRON (HEME 2 AXIAL LIGAND).  
 FT BINDING 89 89 HEME 2 (COVALENT).

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FT BINDING 92 92 HEME 2 (COVALENT).
FT METAL 93 93 IRON (HEME 2 AXIAL LIGAND).
FT BINDING 111 111 IRON (HEME 5 AXIAL LIGAND).
FT BINDING 127 127 HEME 3 (COVALENT).
FT METAL 130 130 HEME 3 (COVALENT).
FT BINDING 131 131 IRON (HEME 3 AXIAL LIGAND).
FT BINDING 141 141 HEME 4 (COVALENT).
FT BINDING 144 144 HEME 4 (COVALENT).
FT METAL 145 145 IRON (HEME 4 AXIAL LIGAND).
FT BINDING 157 157 HEME 5 (COVALENT).
FT BINDING 160 160 HEME 5 (COVALENT).
FT METAL 161 161 IRON (HEME 5 AXIAL LIGAND).
FT METAL 227 227 IRON (HEME 6 AXIAL LIGAND).
FT METAL 230 230 IRON (HEME 8 AXIAL LIGAND).
FT METAL 248 248 IRON (HEME 4 AXIAL LIGAND).
FT BINDING 255 255 HEME 6 (COVALENT).
FT BINDING 258 258 HEME 6 (COVALENT).
FT METAL 259 259 IRON (HEME 6 AXIAL LIGAND).
FT METAL 260 260 IRON (HEME 7 AXIAL LIGAND).
FT BINDING 271 271 HEME 7 (COVALENT).
FT BINDING 274 274 HEME 7 (COVALENT).
FT METAL 275 275 IRON (HEME 7 AXIAL LIGAND).
FT METAL 294 294 IRON (HEME 9 AXIAL LIGAND).
FT BINDING 297 297 HEME 8 (COVALENT).
FT BINDING 300 300 HEME 8 (COVALENT).
FT METAL 301 301 IRON (HEME 8 AXIAL LIGAND).
FT BINDING 314 314 HEME 9 (COVALENT).
FT BINDING 317 317 HEME 9 (COVALENT).
FT METAL 318 318 IRON (HEME 9 AXIAL LIGAND).
SQ SEQUENCE 326 AA; 35025 MW; 2ED7025ADDF250E3 CRC64;

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Query Match 40.0%; Score 6; DB 1; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cy 5 DNCERT 10
    |||||
Db 75 DNCERT 80

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RESULT 4
ID MURD_LACPL STANDARD; PRT; 459 AA.
AC 088V80;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE UDP-N-acetylmuramoylalanine-D-glutamate ligase (EC 6.3.2.9) (UDP-N-
  acetylmuramoyl-L-alanyl-D-glutamate synthetase) (D-glutamic acid
  adding enzyme).
DE MURD OR LP 2197.
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
  Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCMB 8826 / WC831;
RA Kleebeezem W., Boekhorst J., van Kranenburg R., Molenaar D.,
  Kulpers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
  Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
  Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
  De Vos W.M., Sizer R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WC831.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
CC -1- FUNCTION: Cell wall formation. Catalyzes the addition of glutamate
  to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (UMA)
  (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanine +
  glutamate = ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-
  glutamate.
CC -1- PATHWAY: Peptidoglycan biosynthesis.

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CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the murCDEF family.
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  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AL935258; CAD64544.1; -
DR HAMAP: MF_00639; -; 1.
DR InterPro: IPR000713; Mur_ligase.
DR InterPro: IPR004101; Mur_ligase_C.
DR Pfam: PF01225; Mur_ligase; 1.
DR Pfam: PF02875; Mur_ligase_C; 1.
KW Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
  ATP-binding; Complete proteome.
FT NP BIND 119 125 ATP (POTENTIAL).
SQ SEQUENCE 459 AA; 50137 MW; 083AB3BE45C59DC9 CRC64;

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Query Match 40.0%; Score 6; DB 1; Length 459;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cy 4 TDNCERT 9
    |||||
Db 403 TDNCERT 408

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RESULT 5
ID LMA2_HUMAN STANDARD; PRT; 3110 AA.
AC F24043; Q14736; Q93022;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy
  chain).
DE LAMA2 OR LAM.
GN LAMA2 (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94124633; PubMed=8294519;
RA Vuolteenaho R., Nissinen M., Sainio K., Byers M., Eddy R.,
  Hirvonen H., Shows T.B., Sariola H., Engvall E., Trygvaason K.;
  "Human laminin M chain (merosin): complete primary structure,
  RT chromosomal assignment, and expression of the M and A chain in human
  fetal tissues.";
RL J. Cell Biol. 124:381-394(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97066955; PubMed=8910357;
RA Zhang X., Vuolteenaho R., Trygvaason K.;
  "Structure of the human laminin alpha2-chain gene (LAMA2), which is
  RT affected in congenital muscular dystrophy.";
RL J. Biol. Chem. 271:27664-27691(1996).
RN [3]
RP SEQUENCE OF 1981-3110 FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=90238994; PubMed=2185464;
RA Eris K., Ieiv I., Argraves W.S., Ruoslahti E., Engvall E.;
  "Merosin, a tissue-specific basement membrane protein, is a
  RT laminin-like protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3264-3268(1990).
RN [4]
RP VARIANTS GLN-545; HIS-619; LEU-919; HIS-2586 AND IYS-2614.
RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,

```

RA Marzluft G.A., Amato A.A., Mendell J.R.;  
RT "Novel single base polymorphisms and rare sequence variants in  
RT the laminin 2-chain coding region detected by RML/SSCP analysis.",  
RL Hum. Mutat. 13:174-174(1999).  
RN [5].  
RP ERATUM.  
RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,  
RA Marzluft G.A., Amato A.A., Mendell J.R.;  
RL Hum. Mutat. 13:340-340(1999).  
RN [6].  
RP VARIANT MDCA PRO-2564.  
RX MEDLINE=2147601; PubMed=1591858;  
RA He Y., Jones K.O., Vignier N., Morgan G., Chevallay M., Barois A.,  
RA Estournet-Mathaud B., Horii H., Mizuta T., Tome F.M.S., North K.N.,  
RA Guicheney P.;  
RT "Congenital muscular dystrophy with primary partial laminin alpha-2  
RT chain deficiency: molecular study.",  
RL Neurology 57:1339-1322(2001).  
RN [7].  
RP VARIANTS MDCA TYR-527 AND ARG-862.  
RX MEDLINE=2439669; PubMed=1255256;  
RA Tezak Z., Prandini P., Boscaro M., Marin A., Devaney J., Marino M.,  
RA Parin M., Trevisan C.P., Park J., Tyson W., Finkel R., Garcia C.,  
RA Angelini C., Hoffman E.P., Pegoraro E.;  
RT "Clinical and molecular study in congenital muscular dystrophy with  
RT partial laminin alpha-2 (LAMA2) deficiency.",  
RL Hum. Mutat. 21:103-111(2003).  
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin  
CC is thought to mediate the attachment, migration and organization  
CC of cells into tissues during embryonic development by interacting  
CC with other extracellular matrix components.  
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
CC different polypeptide chains (alpha, beta, gamma), which are bound  
CC to each other by disulfide bonds into a cross-shaped molecule  
CC comprising one long and three short arms with globules at each  
CC end. The alpha-2 chain is a subunit of laminin-2 (merosin) and  
CC laminin-4 (S-merosin).  
CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement  
CC membrane (major component).  
CC -1- TISSUE SPECIFICITY: Placenta, striated muscle, peripheral nerve,  
CC cardiac muscle, pancreas, lung, spleen, kidney, adrenal gland,  
CC skin, testis, meninges, choroid plexus, and some other regions of  
CC the brain; not in liver, thymus and bone.  
CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact  
CC with other laminin chains to form a coiled coil structure.  
CC -1- DOMAIN: Domains VI, IV and G are globular.  
CC -1- DISEASE: Defects in LAMA2 are the cause of merosin-deficient  
CC congenital muscular dystrophy type 1A (MDCA1A) [MIM:607855]. MDCA1A  
CC is characterized by difficulty walking, hypotonia, proximal  
CC weakness, hyporeflexia, and white matter hypodensity on MRI.  
CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.  
CC -1- SIMILARITY: Contains 2 laminin IV domains.  
CC -1- SIMILARITY: Contains 5 laminin G-like domains.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
DR EMBL; Z26653; CAAB1394.1; -;  
DR EMBL; U66736; AAB18388.1; -;  
DR EMBL; U66733; AAB18388.1; JOINED.  
DR EMBL; U66734; AAB18388.1; JOINED.  
DR EMBL; U66735; AAB18388.1; JOINED.  
DR EMBL; U66736; AAB18388.1; JOINED.  
DR EMBL; U66737; AAB18388.1; JOINED.  
DR EMBL; U66738; AAB18388.1; JOINED.  
DR EMBL; U66739; AAB18388.1; JOINED.  
DR EMBL; U66740; AAB18388.1; JOINED.

DR EMBL; U66741; AAB18388.1; JOINED.  
DR EMBL; U66742; AAB18388.1; JOINED.  
DR EMBL; U66743; AAB18388.1; JOINED.  
DR EMBL; U66744; AAB18388.1; JOINED.  
DR EMBL; U66745; AAB18388.1; JOINED.  
DR EMBL; U66746; AAB18388.1; JOINED.  
DR EMBL; U66747; AAB18388.1; JOINED.  
DR EMBL; U66748; AAB18388.1; JOINED.  
DR EMBL; U66749; AAB18388.1; JOINED.  
DR EMBL; U66750; AAB18388.1; JOINED.  
DR EMBL; U66751; AAB18388.1; JOINED.  
DR EMBL; U66752; AAB18388.1; JOINED.  
DR EMBL; U66753; AAB18388.1; JOINED.  
DR EMBL; U66754; AAB18388.1; JOINED.  
DR EMBL; U66755; AAB18388.1; JOINED.  
DR EMBL; U66756; AAB18388.1; JOINED.  
DR EMBL; U66757; AAB18388.1; JOINED.  
DR EMBL; U66758; AAB18388.1; JOINED.  
DR EMBL; U66759; AAB18388.1; JOINED.  
DR EMBL; U66760; AAB18388.1; JOINED.  
DR EMBL; U66761; AAB18388.1; JOINED.  
DR EMBL; U66762; AAB18388.1; JOINED.  
DR EMBL; U66763; AAB18388.1; JOINED.  
DR EMBL; U66764; AAB18388.1; JOINED.  
DR EMBL; U66765; AAB18388.1; JOINED.  
DR EMBL; U66766; AAB18388.1; JOINED.  
DR EMBL; U66767; AAB18388.1; JOINED.  
DR EMBL; U66768; AAB18388.1; JOINED.  
DR EMBL; U66769; AAB18388.1; JOINED.  
DR EMBL; U66770; AAB18388.1; JOINED.  
DR EMBL; U66771; AAB18388.1; JOINED.  
DR EMBL; U66772; AAB18388.1; JOINED.  
DR EMBL; U66773; AAB18388.1; JOINED.  
DR EMBL; U66774; AAB18388.1; JOINED.  
DR EMBL; U66775; AAB18388.1; JOINED.  
DR EMBL; U66776; AAB18388.1; JOINED.  
DR EMBL; U66777; AAB18388.1; JOINED.  
DR EMBL; U66778; AAB18388.1; JOINED.  
DR EMBL; U66779; AAB18388.1; JOINED.  
DR EMBL; U66780; AAB18388.1; JOINED.  
DR EMBL; U66781; AAB18388.1; JOINED.  
DR EMBL; U66782; AAB18388.1; JOINED.  
DR EMBL; U66783; AAB18388.1; JOINED.  
DR EMBL; U66784; AAB18388.1; JOINED.  
DR EMBL; U66785; AAB18388.1; JOINED.  
DR EMBL; U66786; AAB18388.1; JOINED.  
DR EMBL; U66787; AAB18388.1; JOINED.  
DR EMBL; U66788; AAB18388.1; JOINED.  
DR EMBL; U66789; AAB18388.1; JOINED.  
DR EMBL; U66790; AAB18388.1; JOINED.  
DR EMBL; U66791; AAB18388.1; JOINED.  
DR EMBL; U66792; AAB18388.1; JOINED.  
DR EMBL; U66793; AAB18388.1; JOINED.  
DR EMBL; U66794; AAB18388.1; JOINED.  
DR EMBL; U66795; AAB18388.1; JOINED.  
DR EMBL; M59832; AAA63215.1; -;  
DR PIR; PX0082; MGHUOH.  
DR HSP; O60675; IOUO.  
DR Genew; HGNC:6482; LAMA2.  
DR MIM; 156225; -;  
DR MIM; 607855; -;  
DR GO; GO:0005604; C:basement membrane; TAS.  
DR GO; GO:0005198; F:structural molecule activity; TAS.  
DR GO; GO:0007517; P:muscle development; TAS.  
DR InterPro; IPR008985; ConA\_like\_dom\_g1.  
DR InterPro; IPR006209; EGF\_like\_dom.  
DR InterPro; IPR008579; Gal\_bind\_like.  
DR InterPro; IPR000034; Laminin\_B.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR001791; Laminin\_G.  
DR InterPro; IPR008211; LamNT.  
DR Pfam; PF00052; laminin\_B\_2.  
DR Pfam; PF00053; laminin\_EGF\_14.  
DR Pfam; PF00054; laminin\_G\_5.  
DR Pfam; PF00055; laminin\_Nterm; 1.

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DR PRINTS; PR00011; EGF/LAMININ.
DR Prodom; PD003031; Laminin B; 1.
DR SMART; SMO0180; EGF Lam; 15.
DR SMART; SMO0281; LamB; 2.
DR SMART; SMO0282; LamG; 5.
DR SMART; SMO0136; LamT; 1.
DR PROSITE; PS00022; EGF_1; 11.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01248; LAMININ TYPE EGF; 14.
DR PROSITE; PS00025; LAM G DOMAIN; 5.
DR Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism;
KM Disease mutation.
FT SIGNAL 1 22 POTENTIAL.

Query Match 40.0%; Score 6; DB 1; Length 3110;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NCERTCT 11
DB 389 NCERTCT 394

RESULT 6
DEF4_ANDAU STANDARD; PRT; 37 AA.
ID DEF4_ANDAU STANDARD; PRT; 37 AA.
AC P56686; P81618;
DC 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 4 kDa defensin.
OS Androctonus australis (Sahara scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butiidae; Butiidae; Androctonus.
OX NCBI_TaxID=6858;
RN [1]
RP SEQUENCE AND CHARACTERIZATION.
RC STRAIN=Hector; TISSUE=Hemolymph;
RX MEDLINE=97094646; PubMed=8939880;
RA Ehret-Sabatie A., Loew D., Geyffon M., Fehlbauer P., Hoffmann J.A.,
RT "Characterization of novel cysteine-rich antimicrobial peptides from
scorpion blood."
RL J. Biol. Chem. 271:29537-29544(1996).
CC -1- FUNCTION: Active against Gram-positive bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=4206.8; METHOD=Electrospray.
CC -1- SIMILARITY: Belongs to the arthropod defensin family. Subfamily 2.
DR HSSP; P10891; IICA.
DR InterPro; IPR001542; Defensin anpod.
DR Pfam; PF01097; Arthro defensin; 1.
DR PROSITE; PS00425; ARTHROPOD_DEFENSINS; 1.
KM Antibiotic.
FT DISULFID 4 25 BY SIMILARITY.
FT DISULFID 11 33 BY SIMILARITY.
FT DISULFID 15 35 BY SIMILARITY.
SQ SEQUENCE 37 AA; 4212 MW; AB1363ECE3FB84C1 CRC64;

Query Match 33.3%; Score 5; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TCTCY 13
DB 32 TCTCY 36

RESULT 7
DEF4_LEI0H STANDARD; PRT; 38 AA.
ID DEF4_LEI0H STANDARD; PRT; 38 AA.
AC P41965;
DC 01-NOV-1995 (Rel. 32, Created)

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DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 4 kDa defensin (Antibacterial 4 kDa peptide).
OS Leirurus quinquestriatus hebraeus (Yellow scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butiidae; Butiidae; Leirurus.
OX NCBI_TaxID=6884;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph; PubMed=833834;
RX MEDLINE=93326112;
RA Cocciach S., Geyffon M., Bontems F., Bulet P., Bouet F., Menez A.,
RA Hoffmann J.A.,
RT "Purification and characterization of a scorpion defensin, a 4kDa
antibacterial peptide presenting structural similarities with insect
defensins and scorpion toxins."
RL Biochem. Biophys. Res. Commun. 194:17-22(1993).
CC -1- FUNCTION: Antibacterial protein against Gram-positive bacteria;
may act via membrane-permeabilization of these cells.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the arthropod defensin family. Subfamily 2.
DR HSSP; P10891; IICA.
DR InterPro; IPR001542; Defensin anpod.
DR Pfam; PF01097; Arthro defensin; 1.
DR PROSITE; PS00425; ARTHROPOD_DEFENSINS; 1.
KM Antibiotic.
FT DISULFID 4 25 BY SIMILARITY.
FT DISULFID 11 33 BY SIMILARITY.
FT DISULFID 15 35 BY SIMILARITY.
SQ SEQUENCE 38 AA; 4326 MW; DF35FB21EC33FB84 CRC64;

Query Match 33.3%; Score 5; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TCTCY 13
DB 32 TCTCY 36

RESULT 8
DEF1_AESCY STANDARD; PRT; 38 AA.
ID DEF1_AESCY STANDARD; PRT; 38 AA.
AC P80154;
DC 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Defensin.
OS Aeschna cyanea (Dragonfly) (Blue darner).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaepodera; Odonata; Anisoptera; Aeschnidae; Aeschna.
OX NCBI_TaxID=12921;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph; PubMed=1425705;
RX MEDLINE=93049356;
RA Bulet P., Cocciach S., Reuland M., Sauder F., Bischoff R., Hegy G.,
RA van Dorsselaer A., Hetru C., Hoffmann J.A.,
RT "A novel insect defensin mediates the inducible antibacterial
RT activity in larvae of the dragonfly Aeschna cyanea (Palaoptera,
RT Odonata)."
RL Eur. J. Biochem. 209:977-984(1992).
CC -1- FUNCTION: Mediates the inducible antibacterial activity in larvae
of A. cyanea.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the arthropod defensin family. Subfamily 2.
DR PIR; S27242; S27242.
DR InterPro; IPR001542; Defensin anpod.
DR Pfam; PF01097; Arthro defensin; 1.
DR PROSITE; PS00425; ARTHROPOD_DEFENSINS; 1.
KW Insect immunity; Antibiotic.
FT DISULFID 4 26

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FT DISULFID 11 34 BY SIMILARITY.  
 FT DISULFID 15 36 BY SIMILARITY.  
 SQ SEQUENCE 38 AA; 4180 MW; 7C884A8FDF54A46A CRC64;  
 Query Match 33.3%; Score 5; DB 1; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 3.8;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCTCY 13  
 DB 33 TCTCY 37

RESULT 9  
 DEFL DERVA STANDARD; PRT; 74 AA.  
 AC 086Q15;  
 DT 15-MAR-2004 (Rel. 43, Created)  
 DT 15-MAR-2004 (Rel. 43, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Defensin precursor (Varisin A1).  
 GN VSNAL.  
 OS Dermacentor variabilis (American dog tick).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
 OC Parasitiformes; Ixodida; Ixodidae; Dermacentor.  
 CX NCBI\_TaxID=34621;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Hemolymph;  
 RA Ceraul S.M., Schenshine D.E., Hynes W.L.;  
 RT "CDNA sequence of the defensin (varisin A1) from the hemocytes of the  
 hard tick Dermacentor variabilis.";  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 37-66, FUNCTION, SUBCELLULAR LOCATION, AND MASS  
 RP SPECTROMETRY.  
 RC TISSUE=Hemolymph;  
 RX MEDLINE=21332638; PubMed=11439245;  
 RA Johns R., Schenshine D.E., Hynes W.L.;  
 RT "Identification of a defensin from the hemolymph of the American dog  
 tick, Dermacentor variabilis.";  
 RL Insect Biochem. Mol. Biol. 31:857-865(2001).  
 CC -1- FUNCTION: Antibacterial activity against Gram-positive and Gram-  
 CC negative bacteria.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Hemolymph.  
 CC -1- MASS SPECTROMETRY: MW=4228.66; METHOD=MALDI; RANGE=37-74.  
 CC -1- SIMILARITY: Belongs to the arthropod defensin family. Subfamily 2.  
 CC -----  
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 CC -----  
 DR EMBL; AY181027; AAO24323.1;  
 DR InterPro: IPR001542; Defensin anod.  
 DR Pfam: PF01097; Arthropod defensin, 1.  
 DR PROSITE; PS00425; ARTHROPOD\_DEFENSINS; 1.  
 KW Antibiotic; Defensin; Signal.  
 FT SIGNAL 1 22  
 FT PROPEP 23 36  
 FT CHAIN 37 74  
 FT DISULFID 40 61  
 FT DISULFID 47 69  
 FT DISULFID 51 71  
 FT CONFLICT 63 63  
 SQ SEQUENCE 74 AA; 8040 MW; A5A29AF4E70DD0DB CRC64;  
 Query Match 33.3%; Score 5; DB 1; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 7;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 TCTCY 13  
 DB 68 TCTCY 72

RESULT 10  
 MSMB MACMU STANDARD; PRT; 114 AA.  
 AC P25142;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma  
 DE protein) (Prostate secretory protein PSP94) (PSP-94).  
 GN MSMB.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 CX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=91274357; PubMed=2054385;  
 RA Nole S., Mlikay M., Chretien M.;  
 RT "Prostatic secretory protein PSP94: gene organization and promoter  
 RT sequence in rhesus monkey and human.";  
 RL Biochim. Biophys. Acta 1089:247-249(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91244325; PubMed=2037304;  
 RA Nole S., St Louis D., Mlikay M., Chretien M.;  
 RT "Rapid evolution of prostatic protein PSP94 suggested by sequence  
 RT divergence between rhesus monkey and human cDNAs.";  
 RL Genomics 9:775-777(1991).  
 CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).  
 CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.  
 CC -----  
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 CC -----  
 DR EMBL; X57932; CAA41003.1;  
 DR EMBL; X57933; CAA41003.1; JOINED.  
 DR EMBL; X57934; CAA41003.1; JOINED.  
 DR EMBL; X57935; CAA41003.1; JOINED.  
 DR EMBL; M92161; AAA36903.1;  
 DR PIR; S16237; A54663.  
 DR InterPro: IPR008735; PSP94.  
 DR Pfam; PF05825; PSP94; 1.  
 KW Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 114  
 FT DISULFID 22 38  
 FT DISULFID 57 93  
 FT DISULFID 60 69  
 FT DISULFID 62 70  
 FT DISULFID 84 107  
 SQ SEQUENCE 114 AA; 13079 MW; C07A4EB984B276C CRC64;  
 Query Match 33.3%; Score 5; DB 1; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 TDNCE 8

Db 54 TDNCE 58

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RESULT 11
ACPS_MYCPN STANDARD; PRT; 119 AA.
ID ACPS_MYCPN
AC P75480;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Holo-(acyl-carrier protein) synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
DE ACPS OR MPN298 OR MP538.
OS Mycoplasma pneumoniae.
OC Bacteria: Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
[1]
SEQUENCE FROM N.A. / M129;
STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelfreith R., Hilbert H., Plagens H., Plickl E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae."
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. AcpS
CC family.
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-----
DR EMBL; AE000052; AAB96186.1; -
DR PIR; S73864; S73864.1; -
DR HAMAP; MF_00101; -; 1.
DR InterPro; IPR008278; 4-PPT transf.
DR InterPro; IPR002582; ACPs.
DR InterPro; IPR004568; Pantethn_tm.
DR Pfam; PF01648; ACPs; 1.
DR ProDom; PD004282; ACPs; 1.
DR Trifam; TRF00556; pantethn_tm; 1.
DR Transferrase; Lipid synthesis; Fatty acid biosynthesis; Magnesium;
KM Complete proteome.
KW METAL
FT METAL 8 MAGNESIUM (BY SIMILARITY).
FT METAL 60 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 119 AA; 13774 MW; 9394A16B4FCB131 CRC64;
Query Match 33.3%; Score 5; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yfQ.
GN yfQ OR B2448.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
[1]
SEQUENCE FROM N.A.
RC STRAIN=KL12 / MG1655;
RX MEDLINE=97426517; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
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DR EMBL; AE000332; AAC75501.1; -
DR PIR; G65019; G65019.
DR Ecogene; BG1478; yfQ.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 130 AA; 14394 MW; B4FCA92101994514 CRC64;
Query Match 33.3%; Score 5; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
PUR7_CHUTE STANDARD; PRT; 235 AA.
ID PUR7_CHUTE
AC O8KDT4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phosphoribosylaminimidazole-succinocarboxamide synthase (EC 6.3.2.6)
DE (SALCAR synthetase).
GN PURC OR CTO960.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID=1097;
[1]
SEQUENCE FROM N.A.
RP STRAIN=FLS / ATCC 49652 / DSM 12025;
RX MEDLINE=22103605; PubMed=12093501;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayan L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Nieman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathavan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum FLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium."
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
CC -1- CATALYTIC ACTIVITY: ATP + 5-amino-1-(5-phospho-D-
CC ribosyl)imidazole-4-carboxylate + L-aspartate = ADP + phosphate +
CC (S)-2-[5-amino-1-(5-phospho-D-ribosyl)imidazole-4-
CC carboxamido]succinate.

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CC -1- PATHWAY: De novo purine biosynthesis; seventh step.  
 CC -1- SIMILARITY: Belongs to the SAICAR synthetase family.  
 CC -----  
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 CC -----  
 DR EMBL; AB012861; AAM72195.1; -.  
 DR TIGR; CT0960; -.  
 DR HAMAP; MF\_00137; -; 1.  
 DR InterPro; IPR001636; SAICAR\_synt.  
 DR Pfam; PF01259; SAICAR\_synt; 1.  
 DR ProDom; PD003043; SAICAR\_synt; 1.  
 DR TIGRFAMs; TIGR00081; purC; 1.  
 DR PROSITE; PS01057; SAICAR\_SYNTHETASE\_1; FALSE\_NEG.  
 DR PROSITE; PS01058; SAICAR\_SYNTHETASE\_2; 1.  
 DR Purine biosynthesis; Ligase; Complete proteome.  
 KW SEQUENCE 235 AA; 26540 MW; 807AD30CD10BF4F CRC64;  
 SQ  
 Query Match 33.3%; Score 5; DB 1; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 WORDN 6  
 DB 16 WORDN 20  
 RESULT 14  
 YF63\_SYNY3 STANDARD; PRT; 295 AA.  
 ID YF63\_SYNY3 STANDARD; PRT; 295 AA.  
 AC P74594;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein slr1563.  
 GN slr1563.  
 OS Synecocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.  
 NC NCBI\_TaxID=1148;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=97061201; PubMed=8905231;  
 RA Kanehisa T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 RA Miyajima N., Hikosawa M., Sugiyama M., Sasamoto S., Kimura T.,  
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Natsu K., Okumura S.,  
 RA Shimizu S., Takeuchi C., Wada T., Watanabe A., Yanada M., Yasuda M.,  
 RA Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synecocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions.";  
 RL DNA Res. 3:109-136(1996).  
 CC -1- SIMILARITY: Belongs to the fructosamine kinase family.  
 CC -----  
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 CC -----  
 DR EMBL; D90916; BAA18702.1; -.  
 DR PIR; S76790; S76790.  
 DR InterPro; IPR005581; Fructosamin\_kin.  
 DR Pfam; PF03861; Fructosamin\_kin; 1.  
 KW Hypothetical protein; Transferase; Kinase; Complete proteome.  
 KW SEQUENCE 295 AA; 32813 MW; 2BCFE12496A83657 CRC64;  
 SQ

Query Match 33.3%; Score 5; DB 1; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 WORDN 6  
 DB 132 WORDN 136  
 RESULT 15  
 ISL2\_CHICK STANDARD; PRT; 319 AA.  
 ID ISL2\_CHICK STANDARD; PRT; 319 AA.  
 AC P53470;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Insulin gene enhancer protein ISL-2 (Islet-2) (Fragment).  
 GN ISL2 OR ISL-2.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE-Spinal cord;  
 RX MEDLINE=95094281; PubMed=7528105;  
 RA Tsuchida T., Enslin M., Morton S.B., Baldassare M., Edlund T.,  
 RA Jessell T.M., Pfaff S.L.;  
 RT "Topographic organization of embryonic motor neurons defined by  
 RT expression of LIM homeobox genes.";  
 RL Cell 79:957-970(1994).  
 CC -1- FUNCTION: Transcriptional factor that defines subclasses of  
 CC motoneurons that segregate into columns in the spinal cord and  
 CC select distinct axon pathways. Acts in conjunction with LIM-1,  
 CC LIM-3 and ISL-1.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DEVELOPMENTAL STAGE: Expressed prior to the formation of distinct  
 CC motor axon pathways and before the segregation of motor neurons  
 CC into columns. Expressed throughout the median and lateral motor  
 CC column.  
 CC -1- SIMILARITY: Contains 1 homeobox domain.  
 CC -1- SIMILARITY: Contains 2 LIM zinc-binding domains.  
 CC -----  
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 CC -----  
 DR EMBL; U35568; AAA62172.1; -.  
 DR PIR; I50370; I50370.  
 DR HSP; P32965; ICTL.  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR001781; LIM.  
 DR InterPro; IPR007107; LIM\_homeo.  
 DR Pfam; PF00046; homeobox; 1.  
 DR Pfam; PF00412; LIM; 2.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR ProDom; PD000094; LIM; 2.  
 DR SMART; SM00389; HOX; 1.  
 DR SMART; SM00132; LIM; 2.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS00478; LIM\_DOMAIN\_1; 1.  
 DR PROSITE; PS00423; LIM\_DOMAIN\_2; 2.  
 DR PROSITE; PS00771; HOMEBOX\_2; 1.  
 DR PROSITE; PS00771; HOMEBOX\_2; 1.  
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 KW Repeat; LIM domain; Metal-binding; Zinc; Multigene family.  
 KW NON TER  
 FT DOMAIN 1  
 FT DOMAIN 2  
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FT DNA BIND 150 209 HOMEBOX.  
 FT DOMAIN 214 319 GLN-RICH  
 SQ SEQUENCE 319 AA; 35027 MM; 2C86C5738121BCDF CRC64;

Query Match 33.3%; Score 5; DB 1; Length 319;  
 Best local Similarity 100.0%; Pred. No. 27;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ETCRC 12  
 ||||  
 Db 27 ETCRC 31

Search completed: March 11, 2004, 18:11:09  
 Job time : 3.78226 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2004, 18:08:03 ; Search time 5.08065 Seconds  
(without alignments)  
152.420 Million cell updates/sec

Title: US-09-977-406a-5  
Perfect score: 15  
Sequence: 1 EWQTDNCETCTCYET 15

Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size: 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCOTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	94	1 US-07-899-535A-1	Sequence 1, Appl
2	6	40.0	241	2 US-08-460-309-17	Sequence 17, Appl
3	6	40.0	241	2 US-08-125-077-17	Sequence 17, Appl
4	6	40.0	3088	4 US-09-562-702A-8	Sequence 8, Appl
5	6	40.0	3089	4 US-09-562-702A-4	Sequence 4, Appl
6	6	40.0	3110	4 US-09-562-702A-2	Sequence 2, Appl
7	6	40.0	3110	4 US-09-562-702A-6	Sequence 6, Appl
8	6	40.0	3110	4 US-09-561-709B-7	Sequence 7, Appl
9	6	40.0	3111	2 US-08-460-309-4	Sequence 4, Appl
10	6	40.0	3111	2 US-08-125-077-4	Sequence 4, Appl
11	5	33.3	9	4 US-08-481-968A-24	Sequence 24, Appl
12	5	33.3	9	4 US-08-154-712B-24	Sequence 24, Appl
13	5	33.3	38	4 US-09-030-619-199	Sequence 199, Appl
14	5	33.3	38	4 US-09-030-619-200	Sequence 200, Appl
15	5	33.3	58	4 US-09-621-976-5440	Sequence 5440, Appl
16	5	33.3	104	4 US-09-621-976-6750	Sequence 6750, Appl
17	5	33.3	231	4 US-09-265-540B-4	Sequence 4, Appl
18	5	33.3	243	2 US-08-460-309-15	Sequence 15, Appl
19	5	33.3	243	2 US-08-460-309-16	Sequence 16, Appl
20	5	33.3	243	2 US-08-125-077-15	Sequence 15, Appl
21	5	33.3	243	2 US-08-125-077-16	Sequence 16, Appl
22	5	33.3	316	4 US-09-543-681A-5873	Sequence 5873, Appl
23	5	33.3	392	4 US-09-424-978B-39	Sequence 39, Appl
24	5	33.3	396	4 US-09-424-978B-36	Sequence 36, Appl
25	5	33.3	454	4 US-09-134-000C-5977	Sequence 5977, Appl
26	5	33.3	716	2 US-08-484-993B-14	Sequence 14, Appl
27	5	33.3	716	2 US-08-484-158B-14	Sequence 14, Appl

28	5	33.3	716	2 US-08-484-596A-14	Sequence 14, Appl
29	5	33.3	716	2 US-08-480-150A-14	Sequence 14, Appl
30	5	33.3	716	3 US-08-458-731-14	Sequence 14, Appl
31	5	33.3	716	3 US-08-149-223A-14	Sequence 14, Appl
32	5	33.3	1288	4 US-09-546-934-4	Sequence 4, Appl
33	5	33.3	1289	4 US-09-546-934-1	Sequence 1, Appl
34	5	33.3	1969	4 US-09-418-710-72	Sequence 72, Appl
35	5	33.3	1972	4 US-09-418-710-21	Sequence 21, Appl
36	5	33.3	3075	2 US-08-460-309-5	Sequence 5, Appl
37	5	33.3	3075	2 US-08-125-077-5	Sequence 5, Appl
38	5	33.3	3075	2 US-08-125-077-5	Sequence 5, Appl
39	5	33.3	3106	4 US-09-562-702A-12	Sequence 12, Appl
40	5	33.3	3106	4 US-09-562-702A-10	Sequence 10, Appl
41	4	26.7	8	2 US-08-922-267A-70	Sequence 70, Appl
42	4	26.7	9	1 US-08-179-481-100	Sequence 100, Appl
43	4	26.7	9	2 US-08-347-197-1	Sequence 1, Appl
44	4	26.7	9	3 US-08-931-085-24	Sequence 24, Appl
45	4	26.7	10	4 US-09-139-802-39	Sequence 39, Appl
				4 US-09-659-786-39	Sequence 39, Appl

#### ALIGNMENTS

RESULT 1  
US-07-899-535A-1  
Sequence 1, Application US/07899535A  
Patent No. 5428011  
GENERAL INFORMATION:  
APPLICANT: Snelth, Anil R.  
APPLICANT: Gardel, Seema  
TITLE OF INVENTION: Pharmaceutical Preparations For  
TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate  
TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Mr. Jefferson Davis Highway, Suite 306  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/899,535A  
FILING DATE: 16-JUN-1992  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Loud, George A.  
REGISTRATION NUMBER: 25,814  
REFERENCE/DOCKET NUMBER: SSB-A835  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-415-0960  
TELEFAX: 703-415-0962  
TELEX: 24 8614  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 94 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
US-07-899-535A-1  
Query Match 100.0%; Score 15; DB 1; Length 94;  
Best Local Similarity 100.0%; Pred. No. 1.4e-11;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMOJNCECTCYET 15  
 Db 31 EMOJNCECTCYET 45

## RESULT 2

US-08-460-309-17  
 ; Sequence 17, Application US/08460309  
 ; Patent No. 5837496

## GENERAL INFORMATION:

APPLICANT: Enqvall, Eva  
 APPLICANT: Leivo, Ilmo  
 TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin  
 ; Fragments and Uses Thereof  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Campbell and Flores  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92122

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/460,309  
 FILING DATE:

## CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/125,077  
 FILING DATE: 22-SEP-1993  
 APPLICATION NUMBER: US PCT/US 94/10730  
 FILING DATE: 21-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/472,319  
 FILING DATE: 30-JAN-1990  
 PRIOR APPLICATION DATA:

## APPLICATION NUMBER: US 07/919,951

FILING DATE: 27-JUL-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-LA 9721  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949

## INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 241 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

US-08-460-309-17

## Query Match

Best Local Similarity 40.0%; Score 6; DB 2; Length 241;  
 Pred. No. 3;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCETCT 11  
 Db 103 NCETCT 108

## RESULT 3

US-08-125-077-17

; Sequence 17, Application US/08125077  
 ; Patent No. 5872231  
 ; Patent No. 5872231 5840863

GENERAL INFORMATION:  
 APPLICANT: Enqvall, Eva  
 APPLICANT: Leivo, Ilmo

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin  
 ; Fragments and Uses Thereof  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Campbell and Flores  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92122

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/125,077  
 FILING DATE: 22-SEP-1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US PCT/US 94/10730  
 FILING DATE: 21-SEP-1994  
 PRIOR APPLICATION DATA:

## APPLICATION NUMBER: US 07/472,319

FILING DATE: 30-JAN-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/919,951  
 FILING DATE: 27-JUL-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-LA 9721  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949

## INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 241 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

US-08-125-077-17

## Query Match

Best Local Similarity 40.0%; Score 6; DB 2; Length 241;  
 Pred. No. 3;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCETCT 11  
 Db 103 NCETCT 108

## RESULT 4

US-09-562-702A-8

; Sequence 8, Application US/09562702A  
 ; Patent No. 6632790

## GENERAL INFORMATION:

APPLICANT: Vurchenco, Peter  
 TITLE OF INVENTION: Laminin 2 and Methods for Its Use  
 ; Fragments and Uses Thereof  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Campbell and Flores  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92122

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/562,702A  
 FILING DATE: 2000-04-28  
 PRIOR APPLICATION NUMBER: 60/155,945  
 PRIOR FILING DATE: 1999-09-24  
 PRIOR APPLICATION NUMBER: 60/143,269  
 PRIOR FILING DATE: 1999-07-12  
 PRIOR APPLICATION NUMBER: 60/139,198  
 PRIOR FILING DATE: 1999-06-15  
 PRIOR APPLICATION NUMBER: 60/131,720  
 PRIOR FILING DATE: 1999-04-30  
 NUMBER OF SEQ ID NOS: 32  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO 8  
 LENGTH: 3088

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-8
Query Match          40.0%; Score 6; DB 4; Length 3088;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCETCT 11
DB 367 NCETCT 372

RESULT 5
US-09-562-702A-4
; Sequence 4, Application US/09562702A
; Patent No. 6632790.
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 3089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-4
Query Match          40.0%; Score 6; DB 4; Length 3089;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCETCT 11
DB 367 NCETCT 372

RESULT 6
US-09-562-702A-2
; Sequence 2, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-2
Query Match          40.0%; Score 6; DB 4; Length 3110;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCETCT 11
DB 389 NCETCT 394

RESULT 7
US-09-562-702A-6
; Sequence 6, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-6
Query Match          40.0%; Score 6; DB 4; Length 3110;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCETCT 11
DB 389 NCETCT 394

RESULT 8
US-09-561-709B-7
; Sequence 7, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgess, Robert
; APPLICANT: Champiaud, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunk, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
; CURRENT APPLICATION NUMBER: US/09/561,709B
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-7
Query Match          40.0%; Score 6; DB 4; Length 3110;
Best Local Similarity 100.0%; Pred. No. 31;
```

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCETCT 11  
|||||  
Db 389 NCETCT 394

## RESULT 9

US-08-460-309-4  
; Sequence 4, Application US/08460309  
; Patent No. 5837496  
; GENERAL INFORMATION:  
; APPLICANT: Engvall, Eva  
; APPLICANT: Leivo, Ilmo  
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin  
; NUMBER OF INVENTION: Fragments and Uses Thereof  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,309  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/125,077  
; FILING DATE: 22-SEP-1993  
; APPLICATION NUMBER: US PCT/US 94/10730  
; FILING DATE: 21-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/472,319  
; FILING DATE: 30-JAN-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/919,951  
; FILING DATE: 27-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LA 9721  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3111 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-460-309-4

Query Match 40.0%; Score 6; DB 2; Length 3111;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCETCT 11  
|||||  
Db 389 NCETCT 394

## RESULT 10

US-08-125-077-4  
; Sequence 4, Application US/08125077  
; Patent No. 5872231  
; Patent No. 5872231 5840863  
; GENERAL INFORMATION:

APPLICANT: Engvall, Eva  
APPLICANT: Leivo, Ilmo  
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin  
NUMBER OF INVENTION: Fragments and Uses Thereof  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/125,077  
FILING DATE: 22-SEP-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/US 94/10730  
FILING DATE: 21-SEP-1994  
APPLICATION NUMBER: US 07/472,319  
FILING DATE: 30-JAN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/919,951  
FILING DATE: 27-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LA 9721  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3111 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-125-077-4

Query Match 40.0%; Score 6; DB 2; Length 3111;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCETCT 11  
|||||  
Db 389 NCETCT 394

RESULT 11  
US-08-481-968A-24  
; Sequence 24, Application US/08481968A  
; Patent No. 6300490  
; GENERAL INFORMATION:  
; APPLICANT: Huber, Brian  
; APPLICANT: Richards, Cynthia  
; TITLE OF INVENTION: Molecular Constructs Comprising a Carcinoembryonic Antigen (CEA)  
; FILE REFERENCE: PB1087054  
; CURRENT APPLICATION NUMBER: US/08/481,968A  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 24  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Consensus sequence  
; FEATURE:  
; NAME/KEY: misc\_feature



OTHER INFORMATION: Consensus sequence B18 from transcriptional dictionary of Locker  
OTHER INFORMATION: and Buzard (1990).  
US-08-481-968A-24

Query Match 33.3%; Score 5; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCTCY 13  
Db 5 TCTCY 9

RESULT 12  
US-08-154-712B-24  
Sequence 24, Application US/08154712B  
Patent No. 6337209  
GENERAL INFORMATION:  
APPLICANT: Huber, Brian  
TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic Antigen Regu  
TITLE OF INVENTION: Sequence  
FILE REFERENCE: PB1087US3  
CURRENT APPLICATION NUMBER: US/08/154,712B  
CURRENT FILING DATE: 1993-11-19  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: Patent version 3.0  
SEQ ID NO 24  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Consensus sequence  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Consensus sequence B18 from transcriptional dictionary of Locker  
OTHER INFORMATION: and Buzard (1990).  
US-08-154-712B-24

Query Match 33.3%; Score 5; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCTCY 13  
Db 5 TCTCY 9

RESULT 13  
US-09-030-619-199  
Sequence 199, Application US/09030619B  
Patent No. 6503881  
GENERAL INFORMATION:  
APPLICANT: Krieger, Timothy J.  
APPLICANT: Taylor, Robert  
APPLICANT: Ertle, Douglas  
APPLICANT: Fraser, Janet R.  
APPLICANT: West, Michael H.P.  
APPLICANT: McNicol, Patricia J.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION  
TITLE OF INVENTION: WITH ANTIBIOTICS  
FILE REFERENCE: 660081.406  
CURRENT APPLICATION NUMBER: US/09/030,619B  
CURRENT FILING DATE: 1998-02-25  
NUMBER OF SEQ ID NOS: 232  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 199  
LENGTH: 38  
TYPE: PRT  
ORGANISM: Aeschna cyanea  
US-09-030-619-199

Query Match 33.3%; Score 5; DB 4; Length 38;  
Best Local Similarity 100.0%; Pred. No. 9.2;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCTCY 13  
Db 33 TCTCY 37

RESULT 14  
US-09-030-619-200  
Sequence 200, Application US/09030619B  
Patent No. 6503881  
GENERAL INFORMATION:  
APPLICANT: Krieger, Timothy J.  
APPLICANT: Taylor, Robert  
APPLICANT: Ertle, Douglas  
APPLICANT: Fraser, Janet R.  
APPLICANT: West, Michael H.P.  
APPLICANT: McNicol, Patricia J.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION  
TITLE OF INVENTION: WITH ANTIBIOTICS  
FILE REFERENCE: 660081.406  
CURRENT APPLICATION NUMBER: US/09/030,619B  
CURRENT FILING DATE: 1998-02-25  
NUMBER OF SEQ ID NOS: 232  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 200  
LENGTH: 38  
TYPE: PRT  
ORGANISM: Leiurus quinquestriatus  
US-09-030-619-200

Query Match 33.3%; Score 5; DB 4; Length 38;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCTCY 13  
Db 32 TCTCY 36

RESULT 15  
US-09-621-976-5440  
Sequence 5440, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Damas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 5440  
LENGTH: 58  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: -23...-1  
US-09-621-976-5440

Query Match 33.3%; Score 5; DB 4; Length 58;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WOTDN 6  
Db 47 WOTDN 51

Fri Mar 12 09:42:15 2004

us-09-977-406a-5.Orig.rai

Search completed: March 11, 2004, 18:14:42  
Job time : 6.08065 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2004, 17:45:41 ; Search time 2.78226 Seconds

(without alignments)  
280.726 Million cell updates/sec

Title: US-09-977-406a-5

Perfect score: 97

Sequence: 1 EWGTDNCECTCYET 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

141681

Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0

Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	114	1	MSMB_HUMAN
2	88	90.7	114	1	MSMB_PAPAN
3	79	81.4	114	1	MSMB_MACMU
4	68	70.1	114	1	MSPJ_SAGOE
5	56	57.7	112	1	MSPJ_SAGOE
6	53	54.6	111	1	MSMB_PIG
7	52	53.6	1172	1	TSF2_HUMAN
8	52	53.6	1172	1	TSF2_MOUSE
9	52	53.6	1173	1	TSPI_XENIA
10	51	52.6	114	1	MSPE_SAGOE
11	47	48.5	330	1	UL16_HSVJ
12	47	48.5	347	1	ASRA_SALTY
13	47	48.5	1178	1	TSF2_CHICK
14	46	47.4	1170	1	TSPI_BOVIN
15	46	47.4	1170	1	TSF2_BOVIN
16	45.5	46.9	398	1	MUBI_XENIA
17	45	46.4	772	1	2469_HUMAN
18	45	46.4	1170	1	TSPI_HUMAN
19	45	46.4	1170	1	TSPI_MOUSE
20	44.5	45.9	816	1	NEL2_MOUSE
21	44.5	45.9	816	1	NEL2_RAT
22	44.5	45.9	816	1	NEL2_CHICK
23	44.5	45.9	1572	1	BA12_HUMAN
24	44	45.4	387	1	BODG_MOUSE
25	44	45.4	387	1	BODG_RAT
26	43.5	44.8	1150	1	APMU_PIG
27	43	44.3	66	1	TRR2_ASCST
28	43	44.3	67	1	THBI_THERS
29	43	44.3	326	1	CYC9_DESDE
30	43	44.3	405	1	TMH_RAT
31	43	44.3	421	1	TMH_HUMAN
32	43	44.3	421	1	TMH_MOUSE
33	43	44.3	446	1	TBB2_DROBR

## ALIGNMENTS

34	43	44.3	446	1	TBB2_DROBE	P08840 drosophila
35	43	44.3	1173	1	NIFU_ENTNG	P19543 enterobacte
36	42.5	43.8	113	1	MSMB_RAT	P97580 rattus norv
37	42.5	43.8	1790	1	LMBI_DROME	P11046 drosophila
38	42.5	43.8	5376	1	ZAN_MOUSE	O08799 mus musculu
39	42	43.3	101	1	THST_THERS	Q9abw4 theromyzon
40	42	43.3	520	1	AMPA_MYCSA	P47707 mycoplasma
41	42	43.3	618	1	YMK3_CABEL	P14511 caenorhabdi
42	42	43.3	768	1	MEC4_CABEL	P24612 caenorhabdi
43	42	43.3	769	1	MEC4_CAEBL	Q17298 caenorhabdi
44	42	43.3	810	1	NEL1_RAT	Q62919 rattus norv
45	42	43.3	1233	1	MUSA_HUMAN	P98086 homo sapien

## RESULT 1

MSMB_HUMAN	STANDARD:	PRT:	114 AA.
ID	MSMB_HUMAN		
AC	P08118, P11993, Q13125, Q9UC59,		
DT	01-AUG-1988 (Rel. 08, Created)		
DT	01-AUG-1988 (Rel. 08, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94) (Seminal plasma beta-inhibin) (Immunoglobulin binding factor) (IGBF) (PN44).		
DE	Beta-inhibin (Immunoglobulin binding factor) (IGBF) (PN44).		
GN	MSMB OR PRSP.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=87161231; PubMed=3829888;		
RA	Whikay M., Nole S., Fournier S., Benjaminet S., Chapdelaine P.,		
RA	Paradis G., Dube J.Y., Tremblay R., Lazue C., Seidah N.G.,		
RA	Chretien M.;		
RT	"Molecular cloning and sequence of the cDNA for a 94-amino-acid		
RT	seminal plasma protein secreted by the human prostate.";		
RL	DNA 6:23-29(1987).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=91274357; PubMed=2054385;		
RA	Nole S., Whikay M., Chretien M.;		
RT	"Prostatic secretory protein PSP94: gene organization and promoter		
RT	sequence in rhesus monkey and human.";		
RL	Biochim. Biophys. Res. Commun. 108:1247-249(1991).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=90211299; PubMed=2322265;		
RA	Green C.B., Liu W.Y., Kwok S.C.M.;		
RT	"Cloning and nucleotide sequence analysis of the human beta-		
RT	microseminoprotein gene.";		
RL	Biochem. Biophys. Res. Commun. 167:1184-1190(1990).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=90073664; PubMed=2590204;		
RA	Uvslaeck M., Lindstroem C., Weiber H., Abrahamson P.-A., Lilja H.,		
RT	"Molecular cloning of a small prostate protein, known as beta-		
RT	microseminoprotein, PSP94 or beta-inhibin, and demonstration of		
RT	transcripts in non-genital tissues.";		
RL	Biochem. Biophys. Res. Commun. 164:1310-1315(1989).		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=94115955; PubMed=7506990;		
RA	Liu A.Y., Bracher R.C., Vessella R.L.;		
RT	"Decreased expression of prostatic secretory protein PSP94 in		
RT	prostate cancer.";		
RL	Cancer Lett. 74:91-99(1993).		
RN	[6]		



Query Match 100.0%; Score 97; DB 1; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCCTCYET 15  
 |||||  
 DB 51 KMQDNCCTCYET 65

## RESULT 2

MSMB\_PAPAN STANDARD; PRT; 114 AA.  
 AC Q28767;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Beta-microseminoprotein precursor (prostate secreted seminal plasma protein) (PSP94)  
 DE MSMB OR PSP94.  
 GN Papio anubis (Olive baboon).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Papio.  
 OC Cercopithecoidea; Papio.  
 OX NCBI\_TaxID=9555;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RX MEDLINE=97316893; PubMed=9174167;  
 RA Xian U.W., Wu D., Guo Y., Garde S., Shum D.T., Mbikay M., Zhong R., Chin U.L.;  
 RT "Molecular cloning and gene expression analysis of PSP94 (prostate secretory protein of 94 amino acids) in primates."  
 RT DNA Cell Biol. 16:627-638(1997).  
 CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).  
 CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.  
 CC CC  
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 CC -----  
 CC EMBL: U49786; AAB62726.1; -;  
 DR InterPro: IPR008735; PSP94.  
 DR Pfam: PF05825; PSP94; 1.  
 KW Signal.  
 FT CHAIN 1 20 BY SIMILARITY.  
 FT SIGNAL 1 114 BETA-MICROSEMINOPROTEIN.  
 FT DISULFID 22 38 BY SIMILARITY.  
 FT DISULFID 57 93 BY SIMILARITY.  
 FT DISULFID 60 69 OR 70 (BY SIMILARITY).  
 FT DISULFID 62 70 OR 69 (BY SIMILARITY).  
 FT DISULFID 84 107 BY SIMILARITY.  
 SQ SEQUENCE 114 AA; 13013 MW; A08C837ED81F98ED CRC64;  
 Query Match 90.7%; Score 88; DB 1; Length 114;  
 Best Local Similarity 86.7%; Pred. No. 2.1e-06;  
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Beta-microseminoprotein precursor (prostate secreted seminal plasma protein) (PSP94)  
 DE MSMB.  
 GN Papio anubis (Olive baboon).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Papio.  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=91274357; PubMed=2054385;  
 RA Nole S., Mbikay M., Chretien M.;  
 RT "Prostatic secretory protein PSP94: gene organization and promoter sequence in rhesus monkey and human."  
 RT Biochim. Biophys. Acta 1089:247-249(1991).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91244325; PubMed=2037304;  
 RA Nole S., St Louis D., Mbikay M., Chretien M.;  
 RT "Rapid evolution of prostatic protein PSP94 suggested by sequence divergence between rhesus monkey and human cDNAs."  
 RT Genomics 9:775-777(1991).  
 CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).  
 CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.  
 CC CC  
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 CC -----  
 CC EMBL: X57932; CAA41003.1; JOINED.  
 DR EMBL: X57933; CAA41003.1; JOINED.  
 DR EMBL: X57934; CAA41003.1; JOINED.  
 DR EMBL: X57935; CAA41003.1; JOINED.  
 DR EMBL: M92161; AAB36903.1; -;  
 DR PIR: S16237; A54663.  
 DR InterPro: IPR008735; PSP94.  
 DR Pfam: PF05825; PSP94; 1.  
 KW Signal.  
 FT CHAIN 1 20 BY SIMILARITY.  
 FT SIGNAL 1 114 BETA-MICROSEMINOPROTEIN.  
 FT DISULFID 22 38 BY SIMILARITY.  
 FT DISULFID 57 93 BY SIMILARITY.  
 FT DISULFID 60 69 OR 70 (BY SIMILARITY).  
 FT DISULFID 62 70 OR 69 (BY SIMILARITY).  
 FT DISULFID 84 107 BY SIMILARITY.  
 SQ SEQUENCE 114 AA; 13079 MW; C07A4EB9948B276C CRC64;

Query Match 81.4%; Score 79; DB 1; Length 114;  
 Best Local Similarity 73.3%; Pred. No. 4.3e-05;  
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EMQDNCCTCYET 15  
 |||||  
 DB 51 KMQDNCCTCYET 65

## RESULT 4

MSMB\_SAGOE STANDARD; PRT; 114 AA.  
 AC Q97949;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

```

DE Beta-microseminoprotein J1 precursor (msp-j1).
GN MSpJ.
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99421644; PubMed=10491085;
RA Maekinen M., Valtonen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
RT beta-microseminoprotein."
RL Eur. J. Biochem. 264:407-414(1999).
CC -!- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -!- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AJ010155; CAB38123.1; -.
DR EMBL: AJ010156; CAB38123.1; JOINED.
DR GO: GO:0005576; CAB38123.1; JOINED.
DR InterPro: IPR008735; PSp94.
DR Pfam: PF05825; PSp94; 1.
DR Signal.
KM SIGNAL.
FT CHAIN 1 20 POTENTIAL.
FT DISULFID 22 114 BETA-MICROSEMINOPROTEIN J1.
FT DISULFID 57 93 BY SIMILARITY.
FT DISULFID 60 69 BY SIMILARITY.
FT DISULFID 62 70 OR 70 (BY SIMILARITY).
FT DISULFID 84 107 OR 69 (BY SIMILARITY).
FT DISULFID 84 107 BY SIMILARITY.
SQ SEQUENCE 114 AA; 12746 MW; P3F05E013445BAP4 CRC64;

Query Match 70.1%; Score 68; DB 1; Length 114;
Best Local Similarity 64.3%; Pred. No. 0.0017;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 EMOTDNCECTCYE 14
DB 51 KWRIDNCDCTCRE 64

RESULT 5
MSPA_SAGOE STANDARD; PRT; 112 AA.
ID MSPA_SAGOE STANDARD; PRT; 112 AA.
AC O97936;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-microseminoprotein A1 precursor (msp-A1) (Fragment).
GN MSpA.
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99421644; PubMed=10491085;
RA Maekinen M., Valtonen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
RT beta-microseminoprotein."
RL Eur. J. Biochem. 264:407-414(1999).
CC -!- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
CC similarity).

```

```

CC -!- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -!- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AJ010158; CAB38124.1; -.
DR EMBL: AJ010159; CAB38124.1; JOINED.
DR GO: GO:0005576; C:extracellular; TAS.
DR InterPro: IPR002400; GP_cysknoc.
DR InterPro: IPR008735; PSp94.
DR Pfam: PF05825; PSp94; 1.
DR PRINTS: PR00438; GFCYSKNOT.
KM SIGNAL.
FT CHAIN 1 19 BY SIMILARITY.
FT DISULFID 20 112 BETA-MICROSEMINOPROTEIN A1.
FT DISULFID 21 37 BY SIMILARITY.
FT DISULFID 56 92 BY SIMILARITY.
FT DISULFID 59 68 OR 69 (BY SIMILARITY).
FT DISULFID 61 69 OR 68 (BY SIMILARITY).
FT DISULFID 83 106 BY SIMILARITY.
SQ SEQUENCE 112 AA; 12631 MW; D0A06BFC15C078B CRC64;

Query Match 57.7%; Score 56; DB 1; Length 112;
Best Local Similarity 53.8%; Pred. No. 0.094;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 MOTDNCECTCYE 14
DB 51 KWRIDNCECDCE 63

RESULT 6
MSMB_PIG STANDARD; PRT; 111 AA.
ID MSMB_PIG STANDARD; PRT; 111 AA.
AC C02836;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma
DE protein) (Prostate secretory protein PSp94) (PSP-94) (TSS07).
GN MSMB OR PSp94.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96117078; PubMed=8562060;
RA Tanaka T., Itahana K., Andoh N., Takeya T., Sato E.;
RT "Expression of prostatic secretory protein (PSP)-like protein in
RT porcine corpus luteum: Isolation and characterization of a new gene
RT encoding PSp94-like protein."
RL Mol. Reprod. Dev. 42:149-156(1995).
RN [2]
RP SEQUENCE OF 21-111.
RC TISSUE=seminal plasma;
RX MEDLINE=94161559; PubMed=8117114;
RA Fernlund P., Granberg L.B., Roepstorff P.;
RT "Amino acid sequence of beta-microseminoprotein from porcine seminal
RT plasma."
RL Arch. Biochem. Biophys. 309:70-76(1994).
CC -!- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -!- TISSUE SPECIFICITY: CORPORA LUTEA, MOSTLY IN THE LUTEAL CELLS
CC SURROUNDING BLOOD VESSELS.

```



FT	DISULFID	397	430	BY SIMILARITY.
FT	DISULFID	408	445	BY SIMILARITY.
FT	DISULFID	448	486	BY SIMILARITY.
FT	DISULFID	453	481	BY SIMILARITY.
FT	DISULFID	464	476	BY SIMILARITY.
FT	DISULFID	506	543	BY SIMILARITY.
FT	DISULFID	510	548	BY SIMILARITY.
FT	DISULFID	521	533	BY SIMILARITY.
FT	DISULFID	553	564	BY SIMILARITY.
FT	DISULFID	558	574	BY SIMILARITY.
FT	DISULFID	577	588	BY SIMILARITY.
FT	DISULFID	594	610	BY SIMILARITY.
FT	DISULFID	601	619	BY SIMILARITY.
FT	DISULFID	622	646	BY SIMILARITY.
FT	DISULFID	652	665	BY SIMILARITY.
FT	DISULFID	659	678	BY SIMILARITY.
FT	DISULFID	680	691	BY SIMILARITY.



[illegible]

FT DISULFID 595 611 BY SIMILARITY.  
 FT DISULFID 602 620 BY SIMILARITY.  
 FT DISULFID 623 647 BY SIMILARITY.  
 FT DISULFID 653 666 BY SIMILARITY.  
 FT DISULFID 660 679 BY SIMILARITY.  
 FT DISULFID 681 692 BY SIMILARITY.  
 FT DISULFID 708 716 BY SIMILARITY.  
 FT DISULFID 721 741 BY SIMILARITY.  
 FT DISULFID 757 777 BY SIMILARITY.  
 FT DISULFID 780 800 BY SIMILARITY.  
 FT DISULFID 816 836 BY SIMILARITY.  
 FT DISULFID 839 859 BY SIMILARITY.  
 FT DISULFID 877 897 BY SIMILARITY.  
 FT DISULFID 913 933 BY SIMILARITY.  
 FT DISULFID 949 1170 BY SIMILARITY.  
 FT CARBOHYD 155 158 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 705 705 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 711 711 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1070 1070 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 1173 AA; 130019 MW; A9F036DE516C0F24 CRC64;

Query Match 53.6%; Score 52; DB 1; Length 1173;  
 Best Local Similarity 58.3%; Pred. No. 3.6;  
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EWQDNCETCTC 12  
 Db 333 EWTVDSCTECTC 344

RESULT 10  
 MSPS\_SAGE STANDARD; PRT; 114 AA.  
 ID MSPS\_SAGE 097935;  
 AC 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Beta-microseminoprotein E1 precursor (msp-E1).  
 GN MSP.  
 OS Saguinus oedipus (Colton-top tamari).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.  
 OC NCBI\_TaxID=9490;  
 RX MEDLINE=99421644; PubMed=10491085;  
 RP SEQUENCE FROM N.A.  
 RT beta-microseminoprotein.  
 RT "New world, but not old world, monkeys carry several genes encoding  
 beta-microseminoprotein."  
 RL Eur. J. Biochem. 264:407-414(1999).  
 CC -!- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By  
 similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted. Sperm surface. (By similarity).  
 CC -!- SIMILARITY: Belongs to the beta-microseminoprotein family.  
 CC -----  
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 CC -----  
 CC EMBL; AJ010154; CAB38105.1;  
 DR GO; GO:0005576; C:extracellular; TAS.  
 DR InterPro; IPR008735; PSP94.  
 DR Pfam; PF05825; PSP94; 1.  
 KW Signal.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 114 BETA-MICROSEMINOPROTEIN E1.

FT DISULFID 22 38 BY SIMILARITY.  
 FT DISULFID 57 93 BY SIMILARITY.  
 FT DISULFID 60 69 OR 70 (BY SIMILARITY).  
 FT DISULFID 62 70 OR 69 (BY SIMILARITY).  
 FT DISULFID 84 107 BY SIMILARITY.  
 SQ SEQUENCE 114 AA; 12738 MW; 05E7A410125C94B2 CRC64;

Query Match 52.6%; Score 51; DB 1; Length 114;  
 Best Local Similarity 54.5%; Pred. No. 5.5;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 WQDNCETCTC 12  
 Db 52 WRTDCELCAC 62

RESULT 11  
 UL16\_HSV7J STANDARD; PRT; 330 AA.  
 AC P52359;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Protein U65.  
 GN U65.  
 OS Human herpesvirus (type 7 / strain J1) (HRV7).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OC NCBI\_TaxID=57278;  
 RX SEQUENCE FROM N.A.  
 RA Nicholas J.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL16,  
 CC HSV-6 ORF11R, EBV-1 46, HCMV UL94, EBV BGLE2, HSV 33, AND VZV 44.  
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 CC -----  
 CC EMBL; U43400; AAC54727.1;  
 DR PIR; T41967;  
 DR InterPro; IPR004286; UL16\_UL94.  
 DR Pfam; PF03044; UL16\_UL94; 1.  
 SQ SEQUENCE 330 AA; 37497 MW; FF32C19CEBF05901 CRC64;

Query Match 48.5%; Score 47; DB 1; Length 330;  
 Best Local Similarity 80.0%; Pred. No. 5.5;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TDNCETCTC 13  
 Db 233 TDNCETCTC 242

RESULT 12  
 ASRA\_SALTY STANDARD; PRT; 347 AA.  
 AC P26474;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Anaerobic sulfite reductase subunit A (anaerobic sulfite reductase  
 DE iron-sulfur subunit).  
 GN ASRA OR STM2548.  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OC NCBI\_TaxID=602;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ES303;  
 RX MEDLINE=91139599; PubMed=1704886;  
 RA Huang C.J., Barrett E.L.;  
 RT "Sequence analysis and expression of the *Salmonella typhimurium* *asr*  
 RT operon encoding production of hydrogen sulfide from sulfite.";  
 RL J Bacteriol. 173:1544-1553(1991).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=L72 / SGSC1412 / ATCC 700720;  
 RX MEDLINE=21534948; PubMed=11677609;  
 RA McCelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dance M., Du P., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of *Salmonella enterica* serovar *Typhimurium*  
 RT L72.";  
 RL Nature 413:852-856(2001).  
 CC -1- FUNCTION: ELECTRON TRANSFER PROTEIN FOR ANAEROBIC SULFITE  
 CC REDUCTASE SUBUNIT A.  
 CC -1- COPACTOR: Binds 2 4Fe-4S clusters.  
 CC -1- PATHWAY: Sulfite reduction.  
 CC -1- SUBUNIT: The anaerobic sulfite reductase seems to consist of three  
 CC subunits.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- INDUCTION: By sulfite. Repressed by oxygen.  
 CC -1- SIMILARITY: The iron-sulfur centers are similar to those of  
 CC bacterial-type 4Fe-4S ferredoxins.  
 CC -----  
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 CC -----  
 DR EMBL; M57706; AAA9275.1; -  
 DR EMBL; AE008816; AAL21442.1; -  
 DR PIR; A38453; A38453.  
 DR StyGene; SG10021; asrA.  
 DR InterPro; IPR001450; 4Fe4S\_ferredoxin.  
 DR Pfam; PF00037; fer4; 1.  
 DR PROSITE; PS00198; 4FE4S\_FERREDOXIN; 2.  
 KW Electron transport; Iron-sulfur; 4Fe-4S; Complete proteome.  
 FT METAL 230  
 FT METAL 233  
 FT METAL 236  
 FT METAL 240  
 FT METAL 312  
 FT METAL 315  
 FT METAL 318  
 FT METAL 322  
 SO SEQUENCE 347 AA; 39679 MW; 45B2C5DABF14236 CRC64;  
 Query Match 48.5%; Score 47; DB 1; Length 347;  
 Best Local Similarity 70.0%; Pred. No. 5.8;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 TDNCCTCTCY 13  
 DB 237 TTGCTCTCY 246  
 RESULT 13  
 TSP2 CHICK STANDARD; PRT; 1178 AA.  
 AC P35440.  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Thrombospondin 2 precursor.  
 GN THB2 OR TSP2.  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 CC NCBI\_TaxID=9031;  
 RX MEDLINE=91217026; PubMed=2022611;  
 RA Lawler J., Duquette M., Ferro P.;  
 RT "Cloning and sequencing of chicken thrombospondin.";  
 RL J Biol. Chem. 266:8039-8043(1991).  
 CC -1- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and  
 CC cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,  
 CC laminin and type V collagen.  
 CC -1- SUBUNIT: Homotrimer; disulfide-linked.  
 CC -1- SIMILARITY: Belongs to the thrombospondin family.  
 CC -1- SIMILARITY: Contains 1 WFPC domain.  
 CC -1- SIMILARITY: Contains 3 EGF-like domains.  
 CC -1- SIMILARITY: Contains 3 TSP type-1 domains.  
 CC -1- SIMILARITY: Contains 7 TSP type-3 domains.  
 CC -1- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL; M60853; AAA51437.1; -  
 DR PIR; A39804; A39804.  
 DR HSSP; P00740; 1EDM.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_Like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR000884; TSP1.  
 DR InterPro; IPR000885; TSP1.  
 DR InterPro; IPR003367; TSP3.  
 DR InterPro; IPR008859; TSPC.  
 DR InterPro; IPR003129; TSPN.  
 DR InterPro; IPR001007; WFC\_C.  
 DR Pfam; PF00008; EGF; 1.  
 DR Pfam; PF00090; TSP\_1; 3.  
 DR Pfam; PF02412; TSP\_3; 13.  
 DR Pfam; PF02412; TSP\_3; 13.  
 DR Pfam; PF02210; TSPN; 1.  
 DR Pfam; PF00093; WFC; 1.  
 DR PRINTS; PR01705; TSP1REPEAT.  
 DR SMART; SM00181; EGF; 2.  
 DR SMART; SM00209; TSP1; 3.  
 DR SMART; SM00210; TSPN; 1.  
 DR SMART; SM00214; WFC; 1.  
 DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS00026; EGF\_3; 2.  
 DR PROSITE; PS00092; TSP1; 3.  
 DR PROSITE; PS01208; WFC\_1; 1.  
 DR PROSITE; PS0184; WFC\_2; 1.  
 KW Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;  
 KW EGF-like domain; Signal.  
 FT SIGNAL 1  
 FT CHAIN 23  
 FT CHAIN 23  
 FT CHAIN 25  
 FT CHAIN 25  
 FT CHAIN 324  
 FT CHAIN 381  
 FT CHAIN 387  
 FT CHAIN 443  
 FT CHAIN 443  
 FT CHAIN 500  
 FT CHAIN 555  
 FT CHAIN 555  
 FT CHAIN 596  
 FT CHAIN 653  
 POTENTIAL.  
 THROMBOSPONDIN 2.  
 TSP N-TERMINAL.  
 HEPARIN-BINDING (POTENTIAL).  
 WFC.  
 TSP TYPE-1 1.  
 TSP TYPE-1 2.  
 TSP TYPE-1 3.  
 EGF-LIKE 1.  
 EGF-LIKE 2.  
 CALCIUM-BINDING (POTENTIAL).

```

FT DOMAIN 554 698 EGF-LIKE 3
FT DOMAIN 731 766 TSP TYPE-3 1.
FT DOMAIN 767 789 TSP TYPE-3 2.
FT DOMAIN 790 825 TSP TYPE-3 3.
FT DOMAIN 826 848 TSP TYPE-3 4.
FT DOMAIN 849 886 TSP TYPE-3 5.
FT DOMAIN 887 922 TSP TYPE-3 6.
FT DOMAIN 923 958 TSP TYPE-3 7.
FT DOMAIN 959 1178 C-TERMINAL.
FT SITE 934 935 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 399 431 BY SIMILARITY.
FT DISULFID 403 436 BY SIMILARITY.
FT DISULFID 414 421 BY SIMILARITY.
FT DISULFID 455 492 BY SIMILARITY.
FT DISULFID 459 497 BY SIMILARITY.
FT DISULFID 470 482 BY SIMILARITY.
FT DISULFID 512 549 BY SIMILARITY.
FT DISULFID 516 554 BY SIMILARITY.
FT DISULFID 527 539 BY SIMILARITY.
FT DISULFID 559 570 BY SIMILARITY.
FT DISULFID 564 580 BY SIMILARITY.
FT DISULFID 583 594 BY SIMILARITY.
FT DISULFID 600 616 BY SIMILARITY.
FT DISULFID 607 625 BY SIMILARITY.
FT DISULFID 628 652 BY SIMILARITY.
FT DISULFID 658 671 BY SIMILARITY.
FT DISULFID 665 684 BY SIMILARITY.
FT DISULFID 686 697 BY SIMILARITY.
FT DISULFID 713 721 BY SIMILARITY.
FT DISULFID 726 746 BY SIMILARITY.
FT DISULFID 762 782 BY SIMILARITY.
FT DISULFID 785 805 BY SIMILARITY.
FT DISULFID 821 841 BY SIMILARITY.
FT DISULFID 844 864 BY SIMILARITY.
FT DISULFID 882 902 BY SIMILARITY.
FT DISULFID 918 938 BY SIMILARITY.
FT DISULFID 954 1175 BY SIMILARITY.
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 590 590 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 716 716 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1075 1075 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1178 AA; 131816 MW; F37E02F42C8717A2 CRC64;

Query Match 48.5%; Score 47; DB 1; Length 1178;
Best Local Similarity 42.9%; Pred. No. 20;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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EX MEDLINE=98173773; PubMed=9507054;
RA Ueno A., Yamashita K., Nagata T., Tsurumi C., Miwa Y., Kitamura S.,
RA Inoue H.,
RT "cDNA cloning of bovine thrombospondin 1 and its expression in
RT odontoblasts and predermal cells."
RL Biochim. Biophys. Acta 1382:17-22(1998).
RN [2]
RP SEQUENCE OF 1-18 AND 710-1170 FROM N.A.
RC TISSUE=Arctic endothelium;
RA Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.;
RL Submitted (JUN-1995) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
CC cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
CC laminin, type V collagen and integrins alpha-Vbeta-1, alpha-
CC Vbeta-3 and alpha-5beta-1. May play a role in dentinogenesis
CC and/or maintenance of dentin and dental pulp.
CC -1- SUBUNIT: Homotrimer; disulfide-linked.
CC -1- TISSUE SPECIFICITY: Odontoblasts.
CC -1- SIMILARITY: Belongs to the thrombospondin family.
CC -1- SIMILARITY: Contains 1 WFC domain.
CC -1- SIMILARITY: Contains 3 EGF-like domains.
CC -1- SIMILARITY: Contains 3 TSP type-1 domains.
CC -1- SIMILARITY: Contains 7 TSP type-3 domains.
CC -1- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
CC -----
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DR EMBL; AB005287; BAA21115.1; -
DR EMBL; X87618; CAA60950.1; -
DR EMBL; X87619; CAA60951.1; -
DR PIR; S55501; S55501.
DR GlycosultDB; Q28178; -
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP1.
DR InterPro; IPR003367; TSP3.
DR InterPro; IPR008859; TSPC.
DR InterPro; IPR003129; TSPN.
DR InterPro; IPR001007; WFC_C.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00090; TSP1_3.
DR Pfam; PF02412; TSP3_13.
DR Pfam; PF05735; TSPC_1.
DR Pfam; PF02210; TSPN_1.
DR Pfam; PF00093; WFC_1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00181; EGF_3.
DR SMART; SM00209; TSP1_3.
DR SMART; SM00210; TSPN_1.
DR SMART; SM00214; WFC_1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS00092; TSP1_3.
DR PROSITE; PS01208; WFC_1; 1.
DR PROSITE; PS00184; WFC_2; 1.
KW Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;
KW EGF-like domain; Signal.
FT SIGNAL 1 18 BY SIMILARITY.
FT CHAIN 19 1170 THROMBOSPONDIN 1.
FT DOMAIN 19 232 HEPARIN-BINDING (POTENTIAL).
FT DOMAIN 24 221 TSP N-TERMINAL.
FT DOMAIN 316 373 WFC.
FT DOMAIN 379 429 TSP TYPE-1 1.
FT DOMAIN 435 490 TSP TYPE-1 2.

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FT DOMAIN 492 547 TSP TYPE-1 3.
FT DOMAIN 549 587 EGF-LIKE 1.
FT DOMAIN 588 645 EGF-LIKE 2. CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 646 690 EGF-LIKE 3.
FT DOMAIN 723 758 TSP TYPE-3 1.
FT DOMAIN 759 781 TSP TYPE-3 2.
FT DOMAIN 782 817 TSP TYPE-3 3.
FT DOMAIN 818 840 TSP TYPE-3 4.
FT DOMAIN 841 878 TSP TYPE-3 5.
FT DOMAIN 879 914 TSP TYPE-3 6.
FT DOMAIN 915 950 TSP TYPE-3 7.
FT DOMAIN 951 1170 C-TERMINAL.
FT SITE 926 928 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 270 270 INTERCHAIN (PROBABLE).
FT DISULFID 274 274 INTERCHAIN (PROBABLE).
FT DISULFID 391 423 BY SIMILARITY.
FT DISULFID 395 428 BY SIMILARITY.
FT DISULFID 406 413 BY SIMILARITY.
FT DISULFID 447 484 BY SIMILARITY.
FT DISULFID 451 489 BY SIMILARITY.
FT DISULFID 462 474 BY SIMILARITY.
FT DISULFID 504 541 BY SIMILARITY.
FT DISULFID 508 546 BY SIMILARITY.
FT DISULFID 519 531 BY SIMILARITY.
FT DISULFID 551 562 BY SIMILARITY.
FT DISULFID 556 572 BY SIMILARITY.
FT DISULFID 575 586 BY SIMILARITY.
FT DISULFID 592 608 BY SIMILARITY.
FT DISULFID 599 617 BY SIMILARITY.
FT DISULFID 620 644 BY SIMILARITY.
FT DISULFID 650 663 BY SIMILARITY.
FT DISULFID 657 676 BY SIMILARITY.
FT DISULFID 678 689 BY SIMILARITY.
FT DISULFID 705 713 BY SIMILARITY.
FT DISULFID 718 738 BY SIMILARITY.
FT DISULFID 754 774 BY SIMILARITY.
FT DISULFID 777 797 BY SIMILARITY.
FT DISULFID 813 833 BY SIMILARITY.
FT DISULFID 836 856 BY SIMILARITY.
FT DISULFID 894 930 BY SIMILARITY.
FT DISULFID 910 930 BY SIMILARITY.
FT DISULFID 946 1167 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 708 708 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1067 1067 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1085 1085 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 805 805 S -> G (IN REF. 2).
SQ SEQUENCE 1170 AA; 129533 MW; 0DD6ADF355FA031A CRC64;

Query Match 47.4%; Score 46; DB 1; Length 1170;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Db 1 330 EMTVDSCTECRC 341

RESULT 15
TSP2_BOVIN STANDARD; PRT; 1170 AA.
AC C95116; Q28180;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 26-FEB-2003 (Rel. 41, Last annotation update)
DE Thrombospondin 2 precursor (Corticotropic-induced secreted protein)
GN (CISF).
DE THBS2 OR TSP2 OR TSP-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.

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OX NCBI_TaxId=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Danik M., Chinn A., Lafeuillade M., Keramidas M., Agnesse-Germon S.,
RA Penhoat A., Chen H., Mosher D., Chambaz E.M., Feige J.J.,
RA Submitted (Mar-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RX SEQUENCE OF 1-522 FROM N.A.
RX MEDLINE=96331130; PubMed=8698834;
RA Lafeuillade B., Fellerin S., Keramidas M., Danik M., Chambaz E.M.,
RA Feige J.J.,
RT "Opposite regulation of thrombospondin-1 and corticotropin-induced
RT secreted protein/thrombospondin-2 expression by adrenocorticotrophic
RT hormone in adrenocortical cells."
RT J. Cell. Physiol. 167:164-172(1996).
RN [3]
RP SEQUENCE OF 318-831 FROM N.A.
RC TISSUE=ortic endothelium;
RA Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.;
RT "Cloning and sequencing of bovine thrombospondin stimulatory effect of
RT TGF-beta."
RT Submitted (May-1995) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
CC cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
CC laminin and type V collagen.
CC -! SUBUNIT: Homotrimer; disulfide-linked.
CC -! SIMILARITY: Belongs to the thrombospondin family.
CC -! SIMILARITY: Contains 1 VWFC domain.
CC -! SIMILARITY: Contains 3 EGF-like domains.
CC -! SIMILARITY: Contains 3 TSP type-1 domains.
CC -! SIMILARITY: Contains 7 TSP type-3 domains.
CC -! SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
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CC -----
DR EMBL; X69640; CAA65385.1; -
DR HSSP; P00740; IEDM.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR003867; TSP_3.
DR InterPro; IPR008859; TSPC.
DR InterPro; IPR003129; TSPN.
DR InterPro; IPR001007; VWFC_C.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF00090; TSP_1; 3.
DR Pfam; PF02412; TSP_3; 13.
DR Pfam; PF05735; TSPC; 1.
DR Pfam; PF02210; TSPN; 1.
DR Pfam; PF00093; VWC; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SMO0181; EGF_3.
DR SMART; SMO0209; TSP1_3.
DR SMART; SMO0210; TSPN; 1.
DR SMART; SMO0214; VWC; 1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 2.
DR PROSITE; PS50092; TSP1_3.
DR PROSITE; PS01208; VWFC_1; 1.
DR PROSITE; PS50184; VWFC_2; 1.
DR GlycoProtex; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;
KW EGF-like domain; Signal.
FT SIGNAL 1 18 POTENTIAL.

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FT CHAIN 19 1170 THROMBOSPONDIN 2.
FT DOMAIN 19 215 TSP N-TERMINAL.
FT DOMAIN 19 232 HEPARIN-BINDING (POTENTIAL).
FT DOMAIN 318 375 VWF.
FT DOMAIN 379 429 TSP TYPE-1 1.
FT DOMAIN 435 490 TSP TYPE-1 2.
FT DOMAIN 492 547 TSP TYPE-1 3.
FT DOMAIN 547 587 EGF-LIKE 1.
FT DOMAIN 588 645 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 646 690 EGF-LIKE 3.
FT DOMAIN 723 758 TSP TYPE-3 1.
FT DOMAIN 759 781 TSP TYPE-3 2.
FT DOMAIN 782 817 TSP TYPE-3 3.
FT DOMAIN 818 840 TSP TYPE-3 4.
FT DOMAIN 841 878 TSP TYPE-3 5.
FT DOMAIN 879 914 TSP TYPE-3 6.
FT DOMAIN 915 950 TSP TYPE-3 7.
FT DOMAIN 951 1170 C-TERMINAL.
FT SITE 926 928 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 266 266 INTERCHAIN (PROBABLE).
FT DISULFID 270 270 INTERCHAIN (PROBABLE).
FT DISULFID 391 423 BY SIMILARITY.
FT DISULFID 395 428 BY SIMILARITY.
FT DISULFID 406 413 BY SIMILARITY.
FT DISULFID 447 484 BY SIMILARITY.
FT DISULFID 451 489 BY SIMILARITY.
FT DISULFID 462 474 BY SIMILARITY.
FT DISULFID 504 541 BY SIMILARITY.
FT DISULFID 508 546 BY SIMILARITY.
FT DISULFID 519 531 BY SIMILARITY.
FT DISULFID 551 572 BY SIMILARITY.
FT DISULFID 556 572 BY SIMILARITY.
FT DISULFID 575 586 BY SIMILARITY.
FT DISULFID 592 608 BY SIMILARITY.
FT DISULFID 599 617 BY SIMILARITY.
FT DISULFID 617 644 BY SIMILARITY.
FT DISULFID 620 644 BY SIMILARITY.
FT DISULFID 650 663 BY SIMILARITY.
FT DISULFID 657 676 BY SIMILARITY.
FT DISULFID 678 689 BY SIMILARITY.
FT DISULFID 705 713 BY SIMILARITY.
FT DISULFID 718 738 BY SIMILARITY.
FT DISULFID 754 774 BY SIMILARITY.
FT DISULFID 777 797 BY SIMILARITY.
FT DISULFID 813 833 BY SIMILARITY.
FT DISULFID 836 856 BY SIMILARITY.
FT DISULFID 874 894 BY SIMILARITY.
FT DISULFID 910 930 BY SIMILARITY.
FT DISULFID 946 1167 BY SIMILARITY.
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 582 582 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 708 708 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 936 936 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1067 1067 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 535 535 A -> V (IN REF. 3).
FT CONFLICT 748 748 S -> T (IN REF. 3).
SQ SEQUENCE 1170 AA; 129862 MW; 9CF1FBF58B89A051 CRC64;

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Query Match 47.4%; Score 46; DB 1; Length 1170;
Best Local Similarity 54.5%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 2 WQDNCERTCTC 12
Db 333 WYVDSTKCTC 343

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Search completed: March 11, 2004, 17:53:18  
Job time : 4.78226 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2004, 17:45:41 ; Search time 11.871 Seconds  
(without alignments)  
280.726 Million cell updates/sec

Title: US-09-977-406A-58

Perfect score: 368  
Sequence: 1 EMQDNCETCTCYETETISCC.....YIVVEKKDPKCTSVSEWII 64

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 111681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	368	100.0	114 1 MSMB_HUMAN	P08118 homo sapien
2	314	85.3	114 1 MSMB_PAPAN	Q28767 papio anubi
3	307	83.4	114 1 MSMB_MACMU	P25142 macaca mula
4	283	76.9	112 1 MSPA_SAGO	O97936 saguinus oe
5	268	72.8	114 1 MSPJ_SAGO	O97949 saguinus oe
6	239	64.9	114 1 MSPJ_SAGO	O97935 saguinus oe
7	213	57.9	111 1 MSMB_PIG	O02826 sus scrofa
8	187.5	51.0	113 1 MSMB_RAT	P97580 rattus norv
9	179.5	48.8	113 1 MSMB_MOUSE	O08540 mus muscul
10	178	48.4	90 1 MSMB_STRCA	P83242 struthio ca
11	79	21.5	940 1 CHRDR_BRARE	O57472 brachydanio
12	73	19.8	1064 1 FEPL_STRPU	P10079 strongyloce
13	70	19.0	816 1 NEPL_MOUSE	Q61220 mus muscul
14	70	19.0	816 1 NEPL_MOUSE	Q62918 rattus norv
15	69	18.8	8545 1 ANCI_CAEEL	Q9444 caenorhabdi
16	68	18.5	1173 1 TSP1_XENLA	P35448 xenopus lae
17	66.5	18.1	1178 1 TSP2_CHICK	P35440 gallus gall
18	66	17.9	1429 1 LI12_CAEEL	P45585 caenorhabdi
19	65.5	17.8	348 1 IDD_MOUSE	P81543 mus muscul
20	65.5	17.8	350 1 IDD_MOUSE	P81543 mus muscul
21	65.5	17.8	689 1 SP11_HUMAN	Q8158 homo sapien
22	65.5	17.8	810 1 NEPL_RAT	Q62919 rattus norv
23	65	17.7	816 1 NEPL_CHICK	O90827 gallus gall
24	64.5	17.5	563 1 MUC5B_BOVIN	P88091 bos taurus
25	64.5	17.5	941 1 CHRDR_XENLA	Q91713 xenopus lae
26	64	17.4	66 1 TTR2_ASCSU	P01049 ascaris suu
27	63.5	17.3	1170 1 TSP1_BOVIN	Q8178 bos taurus
28	63.5	17.3	4349 1 FAT2_HUMAN	Q9458 homo sapien
29	63	17.1	539 1 WNT4_DROME	P08598 drosophila
30	62.5	17.0	96 1 FEPL_AQUAE	O67065 aquifex aeo
31	62.5	17.0	113 1 RBX2_HUMAN	Q9466 homo sapien
32	62.5	17.0	113 1 RBX2_MOUSE	Q94661 mus muscul
33	62.5	17.0	162 1 MTCD_TERTH	Q95W33 tetrahyena

## ALIGNMENTS

RESULT 1	ID	MSMB_HUMAN	STANDARD	PRT	114 AA.
AC	P08118	P11999, Q13125, Q9UC59,			
DT	01-AUG-1988	(Rel. 08, Created)			
DT	01-AUG-1988	(Rel. 08, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94) (Seminal plasma beta-inhibin) (Immunoglobulin binding factor) (IGBF) (PN44).				
DE	MSMB OR PRSP.				
GN	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NOBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=87161231; PubMed=3829888;				
RA	Mikay M., Nolat S., Fournier S., Benjannet S., Chappellaine P.,				
RA	Paradis G., Dube J.Y., Tremblay R., Lazare C., Seidah N.G.,				
RA	Chretien M.,				
RT	"Molecular cloning and sequence of the cDNA for a 94-amino-acid				
RT	seminal plasma protein secreted by the human prostate.";				
RL	DNA 6:23-29(1987).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91274357; PubMed=2054385;				
RA	Nolat S., Mikay M., Chretien M.,				
RT	"Prostatic secretory protein PSP94: gene organization and promoter				
RT	sequence in rhesus monkey and human.";				
RL	Biochim. Biophys. Acta 1089:247-249(1991).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90211299; PubMed=2322265;				
RA	Green C.B., Liu W.Y., Kwok S.C.M.,				
RT	"Cloning and nucleotide sequence analysis of the human beta-				
RT	microseminoprotein gene.";				
RL	Biochem. Biophys. Res. Commun. 167:1184-1190(1990).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90073664; PubMed=2550204;				
RA	Olivaack M., Lindstrom C., Weidner H., Abrahamsson P.-A., Lilja H.,				
RA	Lundwall A.,				
RT	"Molecular cloning of a small prostate protein, known as beta-				
RT	microseminoprotein, PSP94 or beta-inhibin, and demonstration of				
RT	transcripts in non-genital tissues.";				
RL	Biochem. Biophys. Res. Commun. 164:1310-1315(1989).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Prostate;				
RA	MEDLINE=94115955; PubMed=7506990;				
RA	Liu A.Y., Bradner R.C., Vessella R.L.,				
RT	"Decreased expression of prostatic secretory protein PSP94 in				
RT	prostate cancer.";				
RL	Cancer Lett. 74:91-99(1993).				
RN	[6]				

34	62.5	17.0	1170 1 TSP1_HUMAN	P07996 homo sapien
35	62.5	17.0	1170 1 TSP1_MOUSE	P35441 mus musculu
36	62.5	17.0	5376 1 ZAN_MOUSE	O88799 mus musculu
37	62	16.8	119 1 ANTA_HAEGH	P16242 haemerteria
38	62	16.8	552 1 DNLI_VACCV	P16272 vaccinia vi
39	62	16.8	552 1 DNLI_VARV	P33798 variola vir
40	62	16.8	1019 1 ENTR_HUMAN	P98073 homo sapien
41	62	16.8	1038 1 SOG_DROME	Q24025 drosophila
42	61	16.6	136 1 ANTA_HAEOF	P15358 haemerteria
43	61	16.6	552 1 DNLI_VACCC	P20492 vaccinia vi
44	61	16.6	863 1 LDVR_CHICK	P98165 gallus gall
45	61	16.6	1121 1 WDR6_HUMAN	Q9nmw5 homo sapien

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RN      Int. J. Biochem. Cell Biol. 27:603-611(1995).
[14]
RP      SEQUENCE OF 21-32.
RX      MERLINNE-21648993; PubMed=11788998;
RA      Ghafoori B., Stahlbon B., Tagesson C., Lindahl M.;
RT      "Newly identified proteins in human nasal lavage fluid from
RT      non-smokers and smokers using two-dimensional gel electrophoresis and
RT      peptide mass fingerprinting.";
RL      Proteomics 2:112-120(2002).
CC      -1- FUNCTION: Inhibits the secretion of PSH by pituitary cells.
CC      -1- SUBCELLULAR LOCATION: Secreted. Sperm surface.
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=PSP94;
CC      IsoId=P08118-1; Sequence=Displayed;
CC      Name=PSP57;
CC      IsoId=P08118-2; Sequence=VSP_003375, VSP_003276;
CC      -1- TISSUE SPECIFICITY: Strongly expressed in prostate, liver, kidney,
CC      breast and penis. Also expressed in pancreas, esophagus, stomach,
CC      duodenum, colon, trachea, lung, salivary glands and fallopian
CC      tube. PSP94 is expressed in lung and breast, whereas PSP57 is
CC      found in kidney and bladder.
CC      -1- MISCELLANEOUS: SPECIFIC RECEPTORS FOR THIS PROTEIN ARE FOUND ON
CC      SPERMATOZOA AND IN THE PROSTATE.
CC      -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sb-sib.ch).
CC      -----
DR      EMBL; M34376; AAAS9871.1; -.
DR      EMBL; M34373; AAAS9871.1; JOINED.
DR      EMBL; M34374; AAAS9871.1; JOINED.
DR      EMBL; M34375; AAAS9871.1; JOINED.
DR      EMBL; M15885; AAA36635.1; -.
DR      EMBL; X57928; CAA41002.1; -.
DR      EMBL; X57929; CAA41002.1; JOINED.
DR      EMBL; X57930; CAA41002.1; JOINED.
DR      EMBL; X57931; CAA41002.1; JOINED.
DR      EMBL; S67815; AAB29732.1; -.
DR      EMBL; U22178; AAA83556.1; -.
DR      EMBL; U78976; AAB37355.1; -.
DR      EMBL; BC005257; AAH05257.1; -.
DR      EMBL; AJ133356; CAB39325.1; -.
DR      PIR; A34567; A34567.
DR      PIR; G01730; G01730.
DR      Genew; HGNC:7372; MSMB.
DR      MIT; 157145; -.
DR      GO; GO:0005615; C:extracellular space; TAS.
DR      GO; GO:0005634; C:nucleus; TAS.
DR      InterPro; IPR008735; PSP94, 1.
RV      Signal; Polymorphism; Alternative splicing.
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FT      DISULFID       84            107
FT      VARSPIC        37             77
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FT      DISULFID       57             93
FT      DISULFID       60             79
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FT      VARSPIC        37             77
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FT      -----
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FT      DISULFID       57             93
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FT      -----
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FT      DISULFID       60             79
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FT      DISULFID       60             79
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Query Match 100.0%; Score 368; DB 1; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 2,2e-33;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60  
 DB 51 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 110  
 QY 61 EMI 64  
 DB 111 EMI 114

## RESULT 2

MSMB\_PAPAN STANDARD; PRT; 114 AA.  
 AC Q28767;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (PSP94) (PSP-94).  
 GN MSMB OR PSP94.  
 OS Papio anubis (Olive baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Papio.  
 OC Cercopithecoidea; Papio.  
 OX NCBI\_TaxID=9555;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RX MEDLINE=97316893; PubMed=9174167;  
 RA Xuan U.L.; Wu D.; Guo Y.; Garde S.; Shum D.T.; Molkay M.; Zhong R.; Chai U.L.;  
 RT "Molecular cloning and gene expression analysis of PSP94 (prostate secretory protein of 94 amino acids) in primates.";  
 RL DNA Cell Biol. 16:627-638(1997).  
 CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).  
 CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.  
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 CC OR send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
 DR EMBL: U49786; AAB62726.1; -  
 DR InterPro: IPR008735; PSP94.  
 DR Pfam: PF05825; PSP94; 1.  
 DR Signal.  
 KW Signal.  
 FT CHAIN 1 20 BY SIMILARITY.  
 FT CHAIN 21 114 BETA-MICROSEMINOPROTEIN.  
 FT DISULFID 22 38 BY SIMILARITY.  
 FT DISULFID 57 93 BY SIMILARITY.  
 FT DISULFID 60 69 OR 70 (BY SIMILARITY).  
 FT DISULFID 62 70 OR 69 (BY SIMILARITY).  
 FT DISULFID 84 107 BY SIMILARITY.  
 FT DISULFID 84 107 BY SIMILARITY.  
 SQ SEQUENCE 114 AA; 13013 MW; A08C837ED81F98BD CRC64;

Query Match 85.3%; Score 314; DB 1; Length 114;  
 Best Local Similarity 78.1%; Pred. No. 1,6e-27;  
 Matches 50; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60  
 DB 51 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 110  
 QY 61 EMI 64

DB 111 QMI 114

## RESULT 3

MSMB\_MACMU STANDARD; PRT; 114 AA.  
 AC P25142;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (PSP94) (PSP-94).  
 GN MSMB.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=91274357; PubMed=2054385;  
 RA Nole S.; Molkay M.; Chretien M.;  
 RT "Prostatic secretory protein PSP94: gene organization and promoter sequence in rhesus monkey and human.";  
 RL Biochim. Biophys. Acta 1089:247-249(1991).  
 CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).  
 CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.  
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 CC OR send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
 DR EMBL: X57932; CAA41003.1; JOINED.  
 DR EMBL: X57933; CAA41003.1; JOINED.  
 DR EMBL: X57934; CAA41003.1; JOINED.  
 DR EMBL: X57935; CAA41003.1; JOINED.  
 DR EMBL: M92161; AAA63903.1; -  
 DR PIR: S16237; A54663  
 DR InterPro: IPR008735; PSP94.  
 DR Pfam: PF05825; PSP94; 1.  
 DR Signal.  
 KW Signal.  
 FT CHAIN 1 20 BY SIMILARITY.  
 FT CHAIN 21 114 BETA-MICROSEMINOPROTEIN.  
 FT DISULFID 22 38 BY SIMILARITY.  
 FT DISULFID 57 93 BY SIMILARITY.  
 FT DISULFID 60 69 OR 70 (BY SIMILARITY).  
 FT DISULFID 62 70 OR 69 (BY SIMILARITY).  
 FT DISULFID 84 107 BY SIMILARITY.  
 FT DISULFID 84 107 BY SIMILARITY.  
 SQ SEQUENCE 114 AA; 13079 MW; C07A4B9984B276C CRC64;

Query Match 83.4%; Score 307; DB 1; Length 114;  
 Best Local Similarity 76.6%; Pred. No. 9,2e-27;  
 Matches 49; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60  
 DB 51 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 110

OY 61 EMTI 64  
DB 111 QMIL 114

## RESULT 4

MSPA\_SAGOE

ID MSPA\_SAGOE STANDARD; PRT; 112 AA.

AC 097936;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE 28-FEB-2003 (Rel. 41, Last annotation update)

DE Beta-microseminoprotein A1 precursor (msp-A1) (Fragment).

GN MSPA.

OS Saginus oedipus (Cotton-top tamarin).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.

OX NCBI\_TaxID=9490;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9421644; PubMed=10491085;

RA Maekinen M., Valtanen-Andre C., Lundwall A.;

RT "New world, but not old world, monkeys carry several genes encoding

beta-microseminoprotein."

RL Eur. J. Biochem. 264:407-414(1999).

CC -!- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By

similarity).

CC -!- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).

CC -!- SIMILARITY: Belongs to the beta-microseminoprotein family.

CC -----

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CC -----

CC EMBL; AJ010158; CAB38124.1; JOINED.

DR EMBL; AJ010159; CAB38124.1; JOINED.

DR GO; GO:0005576; C:extracellular; TAS.

DR InterPro; IPR002400; GP\_cys\_knot.

DR Pfam; PF05825; PSp94; 1.

DR PRINTS; PRO0438; GFCYSKNOT.

KM Signal.

FT SIGNAL

FT CHAIN

FT DISULFID

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DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Beta-microseminoprotein U1 precursor (msp-U1).

GN MSPA.

OS Saginus oedipus (Cotton-top tamarin).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.

OX NCBI\_TaxID=9490;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9421644; PubMed=10491085;

RA Maekinen M., Valtanen-Andre C., Lundwall A.;

RT "New world, but not old world, monkeys carry several genes encoding

beta-microseminoprotein."

RL Eur. J. Biochem. 264:407-414(1999).

CC -!- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By

similarity).

CC -!- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).

CC -!- SIMILARITY: Belongs to the beta-microseminoprotein family.

CC -----

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CC -----

CC EMBL; AJ010155; CAB38123.1; JOINED.

DR EMBL; AJ010156; CAB38123.1; JOINED.

DR GO; GO:0005576; C:extracellular; NAS.

DR InterPro; IPR008735; PSp94; 1.

DR Pfam; PF05825; PSp94; 1.

DR Signal.

FT SIGNAL

FT CHAIN

FT DISULFID

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Query Match

Best Local Similarity 72.8%; Score 268; DB 1; Length 114;

Matches 44; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

OY 1 EMTI 64

DB 111 QMIL 114

RESULT 6

MSPA\_SAGOE

ID MSPA\_SAGOE STANDARD; PRT; 114 AA.

AC 097935;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE 28-FEB-2003 (Rel. 41, Last annotation update)

DE Beta-microseminoprotein E1 precursor (msp-E1).

GN MSPA.

OS Saginus oedipus (Cotton-top tamarin).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.

OX NCBI\_TaxID=9490;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9421644; PubMed=10491085;

RA Maekinen M., Valtanen-Andre C., Lundwall A.;

RT "New world, but not old world, monkeys carry several genes encoding

beta-microseminoprotein."

RL Eur. J. Biochem. 264:407-414(1999).

CC -!- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By

similarity).

CC -!- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).

CC -!- SIMILARITY: Belongs to the beta-microseminoprotein family.

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CC -----

CC EMBL; AJ010155; CAB38123.1; JOINED.

DR EMBL; AJ010156; CAB38123.1; JOINED.

DR GO; GO:0005576; C:extracellular; NAS.

DR InterPro; IPR008735; PSp94; 1.

DR Pfam; PF05825; PSp94; 1.

DR Signal.

FT SIGNAL

FT CHAIN

FT DISULFID

FT DISULFID

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FT DISULFID

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RX MEDLINE=99421644; PubMed=10491085;
RA Meekinen M., Valtonen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
beta-microseminoprotein."
RL Eur. J. Biochem 264:407-414(1999).
CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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CC -----
DR EMBL, AJ010154; CAB8105.1;
DR GO, GO:000576; C:extracellular; TAS.
DR InterPro, IPR008735; PSP94.
DR Pfam, PF05825; PSP94; 1.
KW Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 114 BETA-MICROSEMINOPROTEIN EI.
FT DISULFID 22 38 BY SIMILARITY.
FT DISULFID 57 93 BY SIMILARITY.
FT DISULFID 60 69 OR 70 (BY SIMILARITY).
FT DISULFID 62 70 OR 69 (BY SIMILARITY).
FT DISULFID 84 107 BY SIMILARITY.
SQ SEQUENCE 114 AA; 12738 MW; 05E7A410125694B2 CRC64;

Query Match
Best Local Similarity 64.9%; Score 239; DB 1; Length 114;
Matches 39; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 2 MOTDNCETCTCYETISCTLTSTPVGYDKDNCQRIFFKEDKYIVVEKKDPKKTCSYSE 61
DB 52 WRTDCELCACRDIIEICCSLVSTPVGYDKNCKRIKFKETCKISVVEKIDPFRGCVSG 111
QY 62 WI 63
DB 112 WI 113

RESULT 7
MSMB_PIG STANDARD; PRT; 111 AA.
ID MSMB_PIG
AC 002826;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma
protein) (PSP94) (PSP-94) (15507).
GN MSMB OR PSP94.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96117078; PubMed=8562060;
RA Tanaka T., Itahana K., Andoh N., Takeya T., Sato E.;
RT "Expression of prostatic secretory protein (PSP)-like protein in
rat porcine corpus luteum: isolation and characterization of a new gene
encoding PSP94-like protein."
RL Mol. Reprod. Dev. 42:149-156(1995).
RN [2]
RP SEQUENCE OF 21-111.
RC TISSUE=Seminal Plasma;
RX MEDLINE=94161559; PubMed=8117114;
RA Fernlund P., Granberg L.B., Roepstorff P.;
RT "Amino acid sequence of beta-microseminoprotein from porcine seminal

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RT plasma."
RL Arch. Biochem. Biophys. 309:70-76(1994).
CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- TISSUE SPECIFICITY: CORPORA LUTEA, MOSTLY IN THE LUTEAL CELLS
SURROUNDING BLOOD VESSELS.
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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CC -----
DR EMBL, S80724; AAB5071.1;
DR InterPro, IPR008735; PSP94.
DR Pfam, PF05825; PSP94; 1.
KW Signal; Pyroliidone carboxylic acid.
FT SIGNAL 1 20
FT CHAIN 21 111 BETA-MICROSEMINOPROTEIN.
FT DISULFID 22 35 BY SIMILARITY.
FT DISULFID 54 90 BY SIMILARITY.
FT DISULFID 57 66 OR 67 (BY SIMILARITY).
FT DISULFID 59 67 OR 66 (BY SIMILARITY).
FT DISULFID 81 104 BY SIMILARITY.
FT MOD RES 21 21 PYROLIIDONE CARBOXYLIC ACID.
SQ SEQUENCE 111 AA; 12246 MW; ABR3A067A23765E CRC64;

Query Match
Best Local Similarity 57.9%; Score 213; DB 1; Length 111;
Matches 33; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 2 MOTDNCETCTCYETISCTLTSTPVGYDKDNCQRIFFKEDKYIVVEKKDPKKTCSYSE 61
DB 49 WTKDCEBETCGQNMISCNLTALPTGYDYNCKQILNKKTCTIVVEKKDCKTCDVYG 108
QY 62 WI 64
DB 109 WVL 111

RESULT 8
MSMB_RAT STANDARD; PRT; 113 AA.
ID MSMB_RAT
AC P97580;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma
protein) (PSP94) (PSP-94).
GN MSMB OR PSP94.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=96434855; PubMed=8837741;
RA Fernlund P., Granberg L.B., Larsson I.;
RT "Cloning of beta-microseminoprotein of the rat: a rapidly evolving
mucosal surface protein."
RL Arch. Biochem. Biophys. 334:73-82(1996).
CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface. PRESENT IN THE
SECRETIONS OF THE AIRWAYS, THE GASTROINTESTINAL AND THE UROGENITAL
TRACTS.
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.

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CC  
 CC EMBL/ U65486; AB19102.1; -  
 CC InterPro: IPR009041; PMP inhibitor.  
 CC InterPro: IPR008735; PSP94.  
 CC Pfam: PF05825; PSP94; 1.

CC  
 CC SIGNAL  
 CC FT CHAIN 1 20 POTENTIAL.  
 CC FT DISULFID 21 113 BETA-MICROSEMINOPROTEIN.  
 CC FT DISULFID 22 38 BY SIMILARITY.  
 CC FT DISULFID 56 92 BY SIMILARITY.  
 CC FT DISULFID 59 68 OR 69 (BY SIMILARITY).  
 CC FT DISULFID 61 69 OR 68 (BY SIMILARITY).  
 CC FT DISULFID 83 106 BY SIMILARITY.  
 CC SEQUENCE 113 AA; 12750 MW; 060246793AF24B31 CRC64;

Query Match 51.0%; Score 187.5; DB 1; Length 113;  
 Best Local Similarity 54.0%; Pred. No. 8.8e-14;  
 Matches 34; Conservative 6; Mismatches 22; Indels 1; Gaps 1;

OY 2 MOTDNCETCTCYETISCTIVSTPVGYDKNCORIFKEDCKYIVVEKDPKTCVSE 61  
 DB 52 WK-KNCEWCFCEKTAITCTKTLTPSYDKKRCQGFHSENYTVERTNPKGTCPVG 110  
 OY 62 WI 64  
 DB 111 WTI 113

RESULT 9  
 MSMB\_MOUSE STANDARD; PRT; 113 AA.  
 ID MSMB\_MOUSE  
 AC O08540;  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma  
 DE protein) (Prostate secretory protein PSP94) (PSP-94).  
 GN MSMB OR PSP94.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 CC NCBI\_TaxID=10090;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN=CD-1;  
 CC Xuan J.W., Mokay M., Wu D., Guo Y., Chin J.L.;  
 CC "Rapid evolution of PSP94 cDNA sequence in rodents";  
 CC Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).  
 CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.

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CC  
 CC EMBL/ U69840; AB49683.1; -  
 CC MGD; MGI:97166; MsmD.  
 CC InterPro: IPR008735; PSP94.  
 CC Pfam: PF05825; PSP94; 1.  
 CC Signal.

FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 113 BETA-MICROSEMINOPROTEIN.  
 FT DISULFID 22 38 BY SIMILARITY.  
 FT DISULFID 56 92 BY SIMILARITY.  
 FT DISULFID 59 68 OR 69 (BY SIMILARITY).  
 FT DISULFID 61 69 OR 68 (BY SIMILARITY).  
 FT DISULFID 83 106 BY SIMILARITY.  
 FT SEQUENCE 113 AA; 12844 MW; 892DAD4BEF49379 CRC64;

Query Match 48.4%; Score 179.5; DB 1; Length 113;  
 Best Local Similarity 49.2%; Pred. No. 6.5e-13;  
 Matches 30; Conservative 10; Mismatches 20; Indels 1; Gaps 1;

OY 2 MOTDNCETCTCYETISCTIVSTPVGYDKNCORIFKEDCKYIVVEKDPKTCVSE 61  
 DB 52 WK-KNCTWCSCKITICTTATPLSYDKNDVQFHPENCTISVDRKPKGTCAVDS 110  
 OY 62 W 62  
 DB 111 W 111

RESULT 10  
 MSMB\_STRCA STANDARD; PRT; 90 AA.  
 ID MSMB\_STRCA  
 AC P83242;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Beta-microseminoprotein.  
 GN MSMB.  
 OS Struthio camelus (Ostrich).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;  
 CC Struthio.  
 CC NCBI\_TaxID=8901;  
 CC [1]  
 CC SEQUENCE, AND DISULFIDE BONDS.  
 CC TISSUE=Plutitary;  
 CC MEDLINE=21490993; PubMed=11604528;  
 CC Lazure C., Villeneuve M., Gauthier D., Naude R.J., Mbikay M.;  
 CC "Characterization of ostrich (Struthio camelus) beta-  
 CC microseminoprotein (MSB): identification of homologous sequence in  
 CC EST databases and analysis of their evolution during speciation";  
 CC Protein Sci. 10:2207-2218(2001).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.  
 CC PIR: A59385; A59385  
 CC GO: 0005576; Cytocellular; TAS.  
 CC InterPro: IPR008735; PSP94.  
 CC Pfam: PF05825; PSP94; 1.  
 CC Amidation.  
 CC FT DISULFID 2 16  
 CC FT DISULFID 34 70  
 CC FT DISULFID 37 46  
 CC FT DISULFID 39 47 OR 47.  
 CC FT DISULFID 61 84 OR 46.  
 CC FT DISULFID 83 90  
 CC MOD RES 90 90  
 CC SEQUENCE 90 AA; 10447 MW; B4AC6FBE7148652 CRC64;

Query Match 48.4%; Score 178; DB 1; Length 90;  
 Best Local Similarity 50.9%; Pred. No. 7.6e-13;  
 Matches 29; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

OY 3 QTDNCECTCYETISCTIVSTPVGYDKNCORIFKEDCKYIVVEKDPKTCVSE 59  
 DB 30 RENCRCGCSRDARCTLTFTPVGNKCKKVFENKSNYDVQKDPDSKECFV 86

RESULT 11  
 CHRD\_BRARE STANDARD; PRT; 940 AA.  
 ID CHRD\_BRARE  
 AC 057472; Q9DEB8;

DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Chordin precursor (Chordin protein).  
 GN CHD.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NC NCBI\_Taxid=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL  
 RP STAGE.  
 RC TISSUE=Gastrula;  
 RX MEDLINE=98104254; PubMed=9441687;  
 RA Miller-Bertoglio V.E., Fisher S., Sanchez A., Mullins M.C.,  
 RA Halpern M.E.;  
 RT "Differential regulation of chordin expression domains in mutant  
 RT zebrafish";  
 RL Dev. Biol. 192:537-550(1997).  
 RN [2]  
 RP SEQUENCE OF 1-42 FROM N.A.  
 RA Fujii R., Hibi M., Hirano T., Shimizu T.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Dorsalizing factor. Key developmental protein that  
 CC dorsalizes early vertebrate embryonic tissues by binding to  
 CC ventralizing TGF-beta family bone morphogenetic proteins (BMPs)  
 CC and sequestering them in latent complexes (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1- TISSUE SPECIFICITY: During gastrulation, levels are highest in  
 CC the organizer region. Also present in the developing brain and in  
 CC paraxial mesoderm and ectoderm.  
 CC -1- DEVELOPMENTAL STAGE: First detected shortly after the midblastula  
 CC transition. Levels increase during gastrulation, persist through  
 CC early somitogenesis, but then decrease and are gone by 24  
 CC hours.  
 CC -1- SIMILARITY: Belongs to the chordin family.  
 CC -1- SIMILARITY: Contains 4 CHRD domains.  
 CC -1- SIMILARITY: Contains 4 WMFC domains.  
 CC -----  
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 CC -----  
 DR EMBL: AF034606; AB93485.1; -  
 DR EMBL: AB043968; BAB18642.1; -  
 DR ZFIN: ZDB-GENE-990415-33; chd.  
 DR InterPro: IPR006559; SOG.  
 DR InterPro: IPR001007; WMF\_C.  
 DR Pfam: PF00093; WFC; 4.  
 DR SMART: SM00566; SOG; 3.  
 DR SMART: SM00214; WMC; 4.  
 DR PROSITE: PSS0933; CHRD; 4.  
 DR PROSITE: PSS01206; WMFC\_1; 3.  
 DR PROSITE: PSS0184; WMFC\_2; 4.  
 KM Developmental protein; Repeat; Glycoprotein; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 940 CHORDIN.  
 FT DOMAIN 42 118 WMFC 1.  
 FT DOMAIN 162 277 CHRD 1.  
 FT DOMAIN 279 398 CHRD 2.  
 FT DOMAIN 404 519 CHRD 3.  
 FT DOMAIN 525 652 CHRD 4.  
 FT DOMAIN 689 748 WMFC 2.  
 FT DOMAIN 767 836 WMFC 3.  
 FT DOMAIN 855 919 WMFC 4.  
 FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 430 430 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 940 AA; 104999 MW; B855CAF84FA623AC CRC64;

Query Match 21.5%; Score 79; DB 1; Length 940;  
 Best Local Similarity 32.8%; Pred. No. 0.4;  
 Matches 21; Conservative 10; Mismatches 25; Indels 8; Gaps 3;  
 QY 1 EW--CTDNCCTCTCYETETISCTLTSPVGYDKNCQRIPKED-CXKIYVERKDPKTKC 57  
 DB 703 CMTPTGYNCTCTCKKTVIC-----DVMCTLTSCHTVGPEDQCCPICEKSKETA 757  
 QY 58 SYSE 61  
 DB 758 AVER 761  
 RESULT 12  
 FBP1\_STRPU STANDARD; PRT; 1064 AA.  
 ID FBP1\_STRPU  
 AC P10079;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Fibropellin I precursor (Epidermal growth factor-related protein 1)  
 DE (UEGF-1).  
 GN EGF1.  
 OS Strongylocentrotus purpuratus (Purple sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Echinoidea; Echinodermata; Echinodermata; Strongylocentrotidae;  
 OC Strongylocentrotus.  
 NC NCBI\_Taxid=7668;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90112459; PubMed=2514273;  
 RA Delgadillo-Reynoso M.G., Rollo D.R., Hursh D.A., Raff R.A.;  
 RT "Structural analysis of the uegf gene in the sea urchin  
 RT strongylocentrotus purpuratus reveals more similarity to vertebrate  
 RT than to invertebrate genes with EGF-like repeats.";  
 RL J. Mol. Evol. 29:314-327(1989).  
 RN [2]  
 RP SEQUENCE OF 279-476 AND 781-1064 FROM N.A.  
 RX MEDLINE=87319677; PubMed=3498216;  
 RA Hursh D.A., Andrews M.E., Raff R.A.;  
 RT "A sea urchin gene encodes a polypeptide homologous to epidermal  
 RT growth factor.";  
 RL Science 237:1487-1490(1987).  
 RN [3]  
 RP AVIDIN-LIKE DOMAIN.  
 RX MEDLINE=89196806; PubMed=2784773;  
 RA Hunt L.T., Barker W.C.;  
 RT "Avidin-like domain in an epidermal growth factor homolog from a sea  
 RT urchin.";  
 RL PNASB 76:311760-1764(1989).  
 RN [4]  
 RP CHARACTERIZATION.  
 RX MEDLINE=91285254; PubMed=2060714;  
 RA Bisgrove B.W., Andrews M.E., Raff R.A.;  
 RT "Fibropellins, products of an EGF repeat-containing gene, form a  
 RT unique extracellular matrix structure that surrounds the sea urchin  
 RT embryo.";  
 RL Dev. Biol. 146:89-99(1991).  
 CC -1- FUNCTION: Form the apical lamina, a component of the extracellular  
 CC matrix.  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR. IN VESICLES IN THE CYTOPLASM  
 CC OF UNFERTILIZED EGGS. THEN TO THE BASE OF THE HYALIN LAYER  
 CC THROUGHOUT DEVELOPMENT AND FINALLY IN THE APICAL LAMINA IN LATE  
 CC EMBRYOS AND EARLY LARVAE.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Name=IA;  
 CC Name=IA;  
 CC IsoId=PI0079-1; Sequence=Displayed;  
 CC Name=IB;  
 CC IsoId=PI0079-2; Sequence=VSP 000451;  
 CC -1- DEVELOPMENTAL STAGE: Moderate levels in unfertilized eggs and  
 CC during early cleavage, then rapidly increases in abundance between

late morula and mesenchyme blastula stages to maximal levels maintained through subsequent stages. Expressed both maternally and zygotically.

-1- SIMILARITY: Contains 21 EGF-like domains.

-1- SIMILARITY: Contains 1 CUB domain.

-1- SIMILARITY: THE C-TERMINAL DOMAIN OF THIS PROTEIN IS SIMILAR TO AVIDIN/STREPTAVIDIN.

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EMBL; L08692; AAA62164.1; -

EMBL; L08692; AAA62163.1; -

EMBL; X17530; CAA35571.1; -

EMBL; M17421; AAA30050.1; -

EMBL; X17533; CAA35573.1; -

PIR; A40136; A40136.

HSSP; P01132; IEGF.

InterPro; IPR000152; Asx\_hydroxyl\_S.

InterPro; IPR005469; Avidin.

InterPro; IPR005468; Avidin/str.

InterPro; IPR000859; CUB.

InterPro; IPR000742; EGF\_2.

InterPro; IPR001881; EGF\_Ca.

InterPro; IPR001438; EGF\_11.

InterPro; IPR006209; EGF\_like.

Pfam; PF04382; Avidin; 1.

Pfam; PF00431; CUB; 1.

Pfam; PF00008; EGF; 21.

PRINTS; PR00709; AVIDIN.

PRINTS; PR00010; EGBLOOD.

SMART; SM00042; CUB; 1.

SMART; SM00179; EGF\_Ca; 20.

PROSITE; PS00010; ASX\_HYDROXYL; 19.

PROSITE; PS00577; AVIDIN; 1.

PROSITE; PS00022; EGF\_1; 19.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01186; EGF\_2; 19.

PROSITE; PS50026; EGF\_3; 21.

PROSITE; PS01187; EGF\_Ca; 18.

Biochem; Alternative splicing; EGF-like domain; Repeat; Signal;

KW Glycoprotein; Calcium-binding.

FT SIGNAL 1 19

FT CHAIN 1 1064

FT DOMAIN 20 55

FT DOMAIN 62 175

FT DOMAIN 176 212

FT DOMAIN 214 250

FT DOMAIN 252 288

FT DOMAIN 290 326

FT DOMAIN 328 364

FT DOMAIN 366 402

FT DOMAIN 404 440

FT DOMAIN 442 478

FT DOMAIN 480 516

FT DOMAIN 518 554

FT DOMAIN 556 592

FT DOMAIN 594 630

FT DOMAIN 632 668

FT DOMAIN 670 706

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QY 1 EMOQNCERT-CTCYETETISCTTVSPGVYDKNCORIFKEDCKYIVE 49  
 DB 22 ECSDPFCENGSTGCEGEGS--YICQCPMGYDGCNCOR-FGSGNGVYVFD 68

RESULT 13  
 NEIL2\_MOUSE STANDARD; PRT; 816 AA.

AC 061220;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Protein kinase C-binding protein NEIL2 precursor (NEIL-like protein 2)  
 DE (NEIL2 OR NEIL1).  
 GN NEIL2 OR NEIL1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NEIL2\_TaxID=10090;  
 RN [1]  
 RA SEQUENCE FROM N.A.  
 RA Elkins D.A., Rossi J.  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP TSP N-TERMINAL DOMAIN.  
 RX MEDLINE=98153258; PubMed=9480764;  
 RA Beckmann G., Hanke J., Bork P., Reich J.;  
 RT "Merging extracellular domains: fold prediction for laminin G-like  
 RT and amino-terminal thrombospondin-like modules based on homology to  
 RT pentaxins".  
 RL J. Mol. Biol. 275:725-730(1998).  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.  
 CC -1- SIMILARITY: Contains 5 WFPC domains.  
 CC -1- SIMILARITY: Contains 6 EGF-like domains.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: U59230; AAB02924.1; ALT\_INIT.  
 DR HSSP: P00740; ISDM.  
 DR MGD: MGI:1858510; Neil2.  
 DR InterPro: IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro: IPR008985; Cona\_like\_1ec\_g1.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR006209; EGF\_Like.  
 DR InterPro: IPR001791; Laminin\_G.  
 DR InterPro: IPR003129; TSPN.  
 DR InterPro: IPR001007; VWF\_C.  
 DR Pfam: PF00008; EGF\_4.  
 DR Pfam: PF02210; TSPN\_1.  
 DR Pfam: PF00093; WFC\_2.  
 DR SMART: SM00179; EGF\_Ca\_3.  
 DR SMART: SM00282; LamiG\_1.  
 DR SMART: SM00210; TSPN\_1.  
 DR SMART: SM00214; VWC\_2.  
 DR PROSITE: PS00010; ASX\_HYDROXYL\_3.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01166; EGF\_2; 3.  
 DR PROSITE: PS00026; EGF\_3; 6.  
 DR PROSITE: PS01167; EGF\_CA\_3.  
 DR PROSITE: PS01208; VWF\_C\_1; 2.  
 DR PROSITE: PS50184; VWF\_C\_2; 2.  
 KM Glycoprotein; EGF-like domain; Repeat; Signal.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 816 PROTEIN KINASE C-BINDING PROTEIN NEIL2.  
 FT DOMAIN 30 258 TSP N-TERMINAL.

FT DOMAIN 272 331 WFC 1.  
 FT DOMAIN 332 396 WFC 2.  
 FT DOMAIN 397 439 EGF-LIKE 1.  
 FT DOMAIN 440 481 EGF-LIKE 2.  
 FT DOMAIN 482 522 EGF-LIKE 3.  
 FT DOMAIN 521 553 EGF-LIKE 4.  
 FT DOMAIN 555 601 EGF-LIKE 5.  
 FT DOMAIN 602 637 EGF-LIKE 6.  
 FT DOMAIN 638 693 CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 698 756 CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 758 813 WFC 4.  
 FT DISULFID 401 413 WFC 5.  
 FT DISULFID 407 422 BY SIMILARITY.  
 FT DISULFID 424 438 BY SIMILARITY.  
 FT DISULFID 444 457 BY SIMILARITY.  
 FT DISULFID 451 466 BY SIMILARITY.  
 FT DISULFID 468 480 BY SIMILARITY.  
 FT DISULFID 486 499 BY SIMILARITY.  
 FT DISULFID 493 508 BY SIMILARITY.  
 FT DISULFID 510 521 BY SIMILARITY.  
 FT DISULFID 525 535 BY SIMILARITY.  
 FT DISULFID 529 541 BY SIMILARITY.  
 FT DISULFID 543 552 BY SIMILARITY.  
 FT DISULFID 559 572 BY SIMILARITY.  
 FT DISULFID 566 581 BY SIMILARITY.  
 FT DISULFID 583 600 BY SIMILARITY.  
 FT DISULFID 606 619 BY SIMILARITY.  
 FT DISULFID 613 628 BY SIMILARITY.  
 FT CARBOHYD 225 53 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT CARBOHYD 225 53 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT CARBOHYD 225 225 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT CARBOHYD 228 298 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT CARBOHYD 517 517 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT CARBOHYD 615 615 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT CARBOHYD 635 635 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 SQ SEQUENCE 816 AA; 91163 MW; 5BDD0A946F87E74D CRC64;

Query Match 19.0%; Score 70; DB 1; Length 816;  
 Best Local Similarity 34.0%; Pred. No. 3.3;  
 Matches 18; Conservative 4; Mismatches 19; Indels 12; Gaps 3;

QY 2 MOTDNCERTCTCYETETISCTTV-----STPGVYDKNCORIFKEDCKY 45  
 DB 287 W-TDCKKCTCLNGTICETILVCPADPCPSAPAYVYDKCKEC--KSTQCF 336

RESULT 14  
 NEIL2\_RAT STANDARD; PRT; 816 AA.

AC 062818;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Protein kinase C-binding protein NEIL2 precursor (NEIL-like protein 2).  
 DE NEIL2 OR NEIL1.  
 GN Rattus norvegicus (Rat).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RA SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
 RX MEDLINE=20017976; PubMed=10548494;  
 RA Kuroda S., Oyasu M., Kawakami M., Kanayama N., Tanizawa K., Saito N.,  
 RA Abe T., Matsunashi S., Ting K.;  
 RT "Biochemical characterization and expression analysis of neural  
 RT thrombospondin-1-like proteins NEIL1 and NEIL2.";  
 RL Biochem. Biophys. Res. Commun. 265:79-86(1999).  
 RN [2]  
 RP TSP N-TERMINAL DOMAIN.  
 RX MEDLINE=98153258; PubMed=9480764;  
 RA Beckmann G., Hanke J., Bork P., Reich J.;

FT	DISULFID	630	636		BY SIMILARITY.	
FT	CARBONYD	53		N-LINKED (GLCNAC. .)	(POTENTIAL).	.
FT	CARBONYD	225	225	N-LINKED (GLCNAC. .)	(POTENTIAL).	.
FT	CARBONYD	293	293	N-LINKED (GLCNAC. .)	(POTENTIAL).	.
FT	CARBONYD	298	298	N-LINKED (GLCNAC. .)	(POTENTIAL).	.
FT	CARBONYD	517	517	N-LINKED (GLCNAC. .)	(POTENTIAL).	.
FT	CARBONYD	615	615	N-LINKED (GLCNAC. .)	(POTENTIAL).	.
FT	CARBONYD	635	635	N-LINKED (GLCNAC. .)	(POTENTIAL).	.
SQ	SEQUENCE	816 AA;	90952 MM;	A999E76078060D6B	CRCE64;	
Query Match		19.0%	Score 70;	DB 1;	Length 816;	
Best Local Similarity		34.0%;	Pred. No. 3.3;			
Matches	18;	Conservative	4;	Mismatches	19;	Indels 12; Gaps 3
QY	2	WOTDNCECTCYETEISCTIV-----STPVGYDKDNCGRIKKEEDCKY	45			
Dc	287	W-TDGCKNCTCLNGTIOCEIIVCPAPDCPKASAPAYVDGCKCEC--KSTQCF	336			

```

RESULT 15
ANCL CAEEL STANDARD; PRT: 8545 AA.
ID ANCL CAEEL
AC Q9N4M4; 061841; 061842;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NCCL anchorage protein 1 (Anchorage 1 protein) (Nesprin homolog) .
CN ANCL 1 OR ZK973.6 OR T03A1.3/T03A1.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
CX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE OF 1-1751 FROM N.A., FUNCTION, CHARACTERIZATION, AND
RP INTERACTION WITH F-ACTIN AND UNC-84.
RC STRAIN=Bristol N2;
RX MEDLINE=22264052; PubMed=12169658;
RA Starr D.A., Har M.;
RT "Role of ANCL-1 in tethering nuclei to the actin cytoskeleton.";
RL Science 298:406-409(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Gattung S., Goela D., Brody M.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISIONS.
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 688-1243 FROM N.A.
RX MEDLINE=22269693; PubMed=12408664;
RA Zhang Q., Ragnauth C., Greener M.J., Shanahan C.M., Roberts R.G.;
RT "The nesprins are giant actin-binding proteins, orthologous to
Drosophila melanogaster muscle protein MSP-300.";
RL Genomics 80:447-481(2002).
RN
RL
CC -1: FUNCTION: Plays a central role in nuclear and mitochondrial
anchoring. Probably connects nuclei to the cytoskeleton by
interacting with unc-84 at the nuclear envelope and with F-actin
in the cytoplasm, creating a bridge across the nuclear envelope
between the cytoskeleton and the nucleus.
CC -1: SUBUNIT: Interacts with F-actin via its N-terminal domain.
CC -1: Interacts indirectly with unc-84.
CC -1: SUBCELLULAR LOCATION: Type IV membrane protein (Potential). The
largest part of the protein is cytoplasmic, while its C-terminal
part is associated either with the nuclear envelope, most probably
the outer nuclear membrane, or with mitochondrial membrane.
CC -1: TISSUE SPECIFICITY: Ubiquitously expressed in all postembryonic
cells.
CC -1: DEVELOPMENTAL STAGE: First expressed in L1 larvae, and thereafter.
CC -1: DOMAIN: The large coiled coil domains are composed of 6 nearly
exact repeats of 903 residues. The last repeat is partial. These
repeats are conserved in Hawai (CB4056), Australia (AB4) and

```



CC Germany (RC301) strains. The length of the repeat may be  
 CC maintained because of a selective advantage to keep the protein  
 CC large and allow a single molecule to extent more than 0,5  
 CC micrometers.  
 CC -1- DOMAIN: The Klarsicht domain, which contains a potential  
 CC transmembrane domain, is essential for the nuclear envelope  
 CC targeting.  
 CC -1- SIMILARITY: Belongs to the nesprin family.  
 CC -1- SIMILARITY: Contains 1 actin-binding domain.  
 CC -1- SIMILARITY: Contains 2 calponin-homology (CH) domains.  
 CC -1- SIMILARITY: Contains 1 Klarsicht domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 CC DR EMBL; AY157938; AAN35200.1; -;  
 CC DR EMBL; AC006834; AAF40010.3; -;  
 CC DR EMBL; AY126454; AAM95163.1; -;  
 CC DR HSSP; P46939; 10NG  
 CC WormPep; ZK873.6; CE33588.  
 CC DR InterPro; IPR001589; Actbind\_actnin.  
 CC DR InterPro; IPR003103; BAG.  
 CC DR InterPro; IPR001715; Calponin-like.  
 CC DR InterPro; IPR002017; Spectrin.  
 CC DR SMART; SM000264; Bag; 6.  
 CC DR SMART; SM00033; CH; 2.  
 CC DR PROSITE; PS00018; ACTININ\_1; 1.  
 CC DR PROSITE; PS00020; ACTININ\_2; FALSE\_NEG.  
 CC DR K2 Structural protein; Cytoskeleton; Actin-binding; Transmembrane;  
 CC KW Coiled coil; Repeat.  
 CC FT DOMAIN 1 8494  
 CC FT TRANSLEM 8495 8513  
 CC FT  
 CC FT DOMAIN 8514 8545  
 CC FT DOMAIN 1 325  
 CC FT DOMAIN 23 130  
 CC FT DOMAIN 222 325  
 CC FT DOMAIN 3241 8199  
 CC FT REPEAT 3241 4143  
 CC FT REPEAT 4144 5097  
 CC FT REPEAT 5098 6000  
 CC FT REPEAT 6001 6903  
 CC FT REPEAT 6904 7806  
 CC FT REPEAT 7807 8199  
 CC FT REPEAT 754 774  
 CC FT DOMAIN 1072 1101  
 CC FT DOMAIN 1215 1236  
 CC FT DOMAIN 1324 1384  
 CC FT DOMAIN 1574 1629  
 CC FT DOMAIN 1725 1754  
 CC FT DOMAIN 1950 1981  
 CC FT DOMAIN 2103 2580  
 CC FT DOMAIN 2682 2712  
 CC FT DOMAIN 2852 2949  
 CC FT DOMAIN 3002 3119  
 CC FT DOMAIN 3178 3295  
 CC FT DOMAIN 3346 3417  
 CC FT DOMAIN 3482 3552  
 CC FT DOMAIN 3587 3703  
 CC FT DOMAIN 3781 3839  
 CC FT DOMAIN 3902 4022  
 CC FT DOMAIN 4114 4198  
 CC FT DOMAIN 4249 4320  
 CC FT DOMAIN 4436 4506  
 CC FT DOMAIN 4541 4657  
 CC FT DOMAIN 4735 4793  
 CC FT DOMAIN 4856 4976

FT DOMAIN 5035 5152  
 FT DOMAIN 5203 5274  
 FT DOMAIN 5339 5409  
 FT DOMAIN 5444 5560  
 FT DOMAIN 5638 5696  
 FT DOMAIN 5759 5879  
 FT DOMAIN 5938 6055  
 FT DOMAIN 6106 6177  
 FT DOMAIN 6242 6312  
 FT DOMAIN 6347 6463  
 FT DOMAIN 6541 6599  
 FT DOMAIN 6662 6782  
 FT DOMAIN 6841 6958  
 FT DOMAIN 7009 7080  
 FT DOMAIN 7145 7215  
 FT DOMAIN 7250 7366  
 FT DOMAIN 7444 7502  
 FT DOMAIN 7565 7685  
 FT DOMAIN 7744 7861  
 FT DOMAIN 7912 7983  
 FT DOMAIN 8048 8118  
 FT DOMAIN 8153 8204  
 FT DOMAIN 8273 8329  
 FT DOMAIN 8370 8390  
 FT DOMAIN 8486 8545  
 FT DOMAIN 1455 1458  
 FT DOMAIN 3021 3029  
 FT DOMAIN 3924 3932  
 FT DOMAIN 4878 4886  
 FT DOMAIN 5781 5789  
 FT DOMAIN 6684 6692  
 FT DOMAIN 7587 7595  
 SQ SEQUENCE 8545 AA; 956470 MW; 02A94D94BBE19E3 CRC64;  
 Query Match 18.8%; Score 69; DB 1; Length 8545;  
 Best Local Similarity 27.6%; Pred. No. 40;  
 Matches 21; Conservative 9; Mismatches 24; Indels 22; Gaps 3;  
 QY 10 CTCVETELISCC-----TLVSPVGYDKNCORIFPKEDC-----KYIV 48  
 DB 353 CTRHLSNGECGRIRREFIRHPLPLIIVKAVDVELVIEKMDICIRELTKARR 412  
 QY 49 EKXD-PKTCGVSEMI 63  
 DB 413 SERDLPEPPASIAWTI 428

Search completed: March 11, 2004, 17:53:19  
 Job time : 12.871 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2004, 17:49:21 ; Search time 18.0645 Seconds

(without alignments)  
340.793 Million cell updates/sec

Title: US-09-977-406a-58

Perfect score: 368

Sequence: 1 FMQTDNCFCTCTCTETETSCC.....YIVVEKKDKPKTCSVSEWII 64

Scoring table: BIOSUM62

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: PIR\_78:\*\*  
2: PIR1:\*\*  
3: PIR2:\*\*  
4: PIR3:\*\*  
5: PIR4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	368	100.0	114	2 A34567	beta-microseminopr
2	307	83.4	114	2 A54663	seminal plasma pro
3	212	57.6	91	2 S41663	Beta-microseminopr
4	178	48.4	90	2 A59385	Beta-microseminopr
5	85.5	23.2	884	2 T18649	hypothetical prote
6	76	20.7	219	2 D88990	protein C36C5.12
7	73	19.8	154	2 A96544	hypothetical prote
8	73	19.8	1064	2 A40136	fibropellin Ia - s
9	71.5	19.4	198	2 T28990	hypothetical prote
10	69.5	18.9	429	2 T21113	hypothetical prote
11	69	18.8	814	2 T33140	hypothetical prote
12	69	18.6	1535	2 S46224	peroxidasin - fru
13	68.5	18.6	1376	2 S63966	collagen alpha 5 c
14	66.5	18.1	355	2 T29944	hypothetical prote
15	66.5	18.1	1178	2 A39804	thrombospondin pre
16	66	17.9	1360	2 T33922	hypothetical prote
17	66	17.9	1429	2 S06434	homocit protein
18	65.5	17.8	200	2 E88986	protein C17B7.9 [1
19	65.5	17.8	227	2 E88987	protein C17B7.3 [1
20	65.5	17.8	371	2 A49515	phosphoprotein 75
21	65.5	17.8	546	2 UC4798	seizure-related me
22	65.5	17.8	550	2 T37579	DiGeorge syndrome
23	65.5	17.8	810	2 T10756	Nel-homolog protei
24	65	17.7	835	2 JP0076	Nel protein - chic
25	64.5	17.5	204	2 T28985	hypothetical prote
26	64.5	17.5	320	2 T28985	hypothetical prote
27	64.5	17.5	320	2 A36054	mucin homololog - bo
28	64.5	17.5	941	1 A55195	choirin precursor
29	64	17.4	66	1 T1AC	typsin inhibitor

30	64	17.4	347	2 T15149	hypothetical prote
31	64	17.4	392	2 T32311	hypothetical prote
32	63.5	17.3	335	2 D88997	protein C17B7.2 [1
33	62.5	17.0	96	2 F70379	ferredoxin 12Fe-2S
34	62.5	17.0	203	2 H88990	protein C36C5.15
35	62.5	17.0	1170	2 TSHUP1	thrombospondin 1 p
36	62.5	17.0	1170	2 A40558	thrombospondin 1 p
37	62.5	17.0	5376	2 T42215	zonadhesin - mouse
38	62	16.8	119	2 A34816	anticoagulant prot
39	62	16.8	552	1 JQ1788	DNA ligase (ATP) (
40	62	16.8	552	1 JQ1857	DNA ligase (ATP) (
41	62	16.8	552	2 A72171	DNA ligase (ATP) (
42	62	16.8	552	2 T28595	DNA ligase (ATP) (
43	62	16.8	869	1 J54858	VLDL receptor prec
44	62	16.8	1019	1 A56318	enteropeptidase 1E
45	62	16.8	1038	2 T13177	sog protein - Fru

## ALIGNMENTS

RESULT 1  
A34567  
beta-microseminoprotein precursor - human  
N/Alternate names: beta-inhibin; prostatic secretory protein; PSP-94; seminal plasma pr  
C/Species: Homo sapiens (man)  
C/Date: 13-Jul-1990 #sequence revision 13-Jul-1990 #text change 20-Aug-1999  
C/Accession: A34567; A26451; A29777; A30984; A60673; S16238; I52682  
R/Green, C.B.; Liu, W.Y.; Kwok, S.C.M.  
Biochem. Biophys. Res. Commun. 167, 1184-1190, 1990  
A/Title: Cloning and nucleotide sequence analysis of the human beta-microseminoprotein  
A/Reference number: A34567; MUID:90211299; PMID:2322265  
A/Accession: A34567  
A/Status: not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-114 <GRE>  
A/Cross-references: GB:M34376; NID:9514370; PID:AAA59871.1; PID:9514372  
R/Akiyama, K.; Yoshioke, Y.; Schmid, K.; Offner, G.D.; Troxler, R.F.; Teuda, R.; Hara,  
Biochim. Biophys. Acta 829, 288-294, 1985  
A/Title: The amino acid sequence of human beta-microseminoprotein.  
A/Reference number: A29777; MUID:8519974; PMID:2995056  
A/Accession: A29777  
A/Molecule type: protein  
A/Residues: 21-58, 'PT', 61-113 <AKI>  
R/Seidat, N.G.; Arabat, N.J.; Rochemont, J.; Sheth, A.R.; Chretien, M.  
FEBS Lett. 175, 349-355, 1984  
A/Title: Complete amino acid sequence of human seminal plasma beta-inhibin. Prediction  
A/Reference number: A30984; MUID:85004133; PMID:6434350  
A/Accession: A30984  
A/Molecule type: protein  
A/Residues: 21-112, 'G', 114 <SEI>  
R/Reiber, H.; Andersson, C.; Murre, A.; Rannevik, G.; Lindstrom, C.; Lillja, H.; Fernlu  
Am. J. Pathol. 137, 593-604, 1990  
A/Title: Beta microseminoprotein is not a prostate-specific protein.  
A/Reference number: A60673; MUID:90379237; PMID:2205099  
A/Accession: A60673  
A/Molecule type: protein  
A/Residues: 21, 'X', 23-34 <MEI>  
R/Experimental source: gastric juice  
R/Moiet, S.; Moikay, M.; Chretien, M.  
Biochim. Biophys. Acta 1089, 247-249, 1991  
A/Title: Prostatic secretory protein (PSP-94): gene organization and promoter sequence i  
A/Reference number: S16237; MUID:91274357; PMID:2054385  
A/Accession: S16238  
A/Molecule type: DNA

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A:Residues: 1-114 <NOL>
A:Cross-references: EMBL:X57928; NID:G35760; PIDD:CAA1002.1; PID:G825707
A>Note: the authors translated the codon ACT for residue 54 as Trp
R:Lin, A.Y.; Bracher, R.C.; Vessella, R.L.
Cancer Lett. 74, 91-99, 1993
A>Title: Decreased expression of prostatic secretory protein PSP94 in prostate cancer.
A:Reference number: 152682; MUID:94115955; PMID:7506990
A:Accession: 152682
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-114 <RES>
A:Cross-references: GB:S67815; NID:G460566; PIDD:AA829732.1; PID:G460569
C:Comment: This protein is a component of seminal plasma as well as secretory fluids from
C:Genetics:
A:Gene: GDB:MSMB
A:Cross-references: GDB:128042; OMIM:157145
A:Map position: 10q11.2-10q11.2
A:Introns: 1/3; 37/1; 72/2
C:Superfamily: seminal plasma protein
C:Keywords: semen
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-114/Product: seminal plasma protein #status experimental <MAT>

Query Match          100.0%; Score 368; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.8e-31;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60
DB 51 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 110

QY 61 EWII 64
DB 111 EWII 114

RESULT 2
A54663
Seminal plasma protein PSP-94 precursor - rhesus macaque
N:Alternate names: prostatic secretory protein PSP94
C:Species: Macaca mulatta (rhesus macaque)
C>Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 20-Aug-1999
A:Accession: S16237; A54663
R:Nolet, S.; Mdkay, M.; Chretien, M.
Biochim. Biophys. Acta 1089, 247-249, 1991
A>Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in
A:Reference number: S16237; MUID:91274357; PMID:2054385
A:Accession: S16237
A:Molecule type: DNA
A:Residues: 1-114 <NO2>
A:Cross-references: EMBL:X57932; NID:G38094; PIDD:CAA1003.1; PID:G829152
A>Note: the authors translated the codon ACT for residue 54 as Trp
R:Nolet, S.; St-Louis, D.; Mdkay, M.; Chretien, M.
Genomics 9, 775-777, 1991
A>Title: Rapid evolution of prostatic protein PSP-94 suggested by sequence divergence be
A:Reference number: A54663; MUID:91244325; PMID:2037304
A:Accession: A54663
A:Molecule type: mRNA
A:Residues: 1-114 <NO1>
A:Cross-references: GB:M92161; NID:G342280; PIDD:AAA36903.1; PID:G342281
C:Genetics:
A:Introns: 1/3; 37/1; 72/2
C:Superfamily: seminal plasma protein
F:1-20/Domain: signal sequence #status predicted <SIG>

Query Match          83.4%; Score 307; DB 2; Length 114;
Best Local Similarity 76.6%; Pred. No. 4e-25;
Matches 49; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 61 EWII 64
DB 111 EWII 114

RESULT 3
S41663
beta-microseminoprotein - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
A:Accession: S41663
R:Fernlund, P.; Granberg, L.B.; Roepstorff, P.
Arch. Biochem. Biophys. 309, 70-76, 1994
A>Title: Amino acid sequence of beta-microseminoprotein from porcine seminal plasma.
A:Reference number: S41663; MUID:94161559; PMID:8117114
A:Accession: S41663
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-91 <PR>
C:Superfamily: seminal plasma protein

Query Match          57.6%; Score 212; DB 2; Length 91;
Best Local Similarity 52.4%; Pred. No. 2.6e-15;
Matches 33; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 2 MQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 61
DB 29 MKTKCEBCTCGQDAISCCNTAIPGYPDNCKQILNKTKCTYIVVEKKDPKKTCDVTG 88

QY 62 WII 64
DB 89 WII 91

RESULT 4
A59385
Beta-microseminoprotein - Ostrich (Struthio camelus)
C:Species: Ostrich (Struthio camelus)
C>Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 11-Jan-2002
A:Accession: A59385
R:Lazare, C.
submitted to the Protein Sequence Database, March 2001
A:Description: Characterization of ostrich (Struthio camelus).
A:Reference number: A59385
A:Accession: A59385
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-90 <LA2>
A:Experimental source: Pituitary extracts
A:Note: Structurally related to mammalian Prostate Secretory Protein
C:Keywords: amidated carboxyl end
F:2-16/34-70/37-46/39-47/61-84/Disulfide bonds: #status predicted
F:90/Modified site: amidated carboxyl end (Val) #status experimental

Query Match          48.4%; Score 178; DB 2; Length 90;
Best Local Similarity 50.9%; Pred. No. 9e-12;
Matches 29; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 3 QTDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 59
DB 30 RTENCRCGSRDANRCCTLVHTPVGINKKCKVFNKSCNYDVQKDSKECFV 86

RESULT 5
T18649
hypothetical protein B0024.14 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
R:McMurray, A.
submitted to the EMBL Data Library, April 1996
A:Reference number: Z19001
A:Accession: T18649
```

A:Status: Preliminary; translated from GB/EMBL/DDBC  
A:Molecule type: DNA  
A:Residues: 1-884 <Full>  
A:Cross-references: EMBL/Z71178, PIDN:CAA94886.1, GSPDB:GNO0023, CESP:B0024.14  
A:Experimental source: clone B0024  
C:Genetics:  
A:Gene: CESP:B0024.14  
A:Map position: 5  
A:Introns: 46/3; 84/1; 212/1; 307/2; 345/2; 394/1; 424/2; 481/1; 596/1; 702/1; 765/3; 85

Query Match 23.2%; Score 85.5; DB 2; Length 884;  
Best Local Similarity 32.3%; Pred. No. 0.25;  
Matches 20; Conservative 12; Mismatches 27; Indels 3; Gaps 2;

OY 1 EMQTDNCCTCTCYEHEISCTIVSPVGYDNDNCORIFKED--CKYIVVEKKDPKTKS 58  
Db 441 EWMSGCCHCTC-ENKQFCSLICTPTPSCALBKNVQNEDECCPCITQKKPKHSNS 459  
OY 59 VS 60  
Db 500 LA 501

RESULT 6  
D88990  
Protein C36C5.12 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001  
C:Accession: D88990  
R:Anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog  
A:Reference number: A75000; MUID:99069613; PMID:19851916  
A>Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C\_ele  
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: D88990  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-219 <STO>  
A:Cross-references: GB:chr\_V, PIDN:AAB65934.1; PID:G2315401; GSPDB:GNO0023; CESP:C36C5.1  
C:Genetics:  
A:Gene: C36C5.12  
A:Map position: 5  
C:Superfamily: Caenorhabditis elegans hypothetical protein COI.B7.7

Query Match 20.7%; Score 76; DB 2; Length 219;  
Best Local Similarity 25.6%; Pred. No. 0.84;  
Matches 21; Conservative 8; Mismatches 23; Indels 30; Gaps 3;

OY 6 NCETCTCYETSISCT---LVSTPVGYD-----KDNCGRIFFK 40  
Db 119 NCEAVVIHEDPDCSDKLTKAKSVCFDNNDDPIPDGIHLSEDKKVKRKKTCKRYFGK 178  
OY 41 EDCKYIVVEKKDPKTKSVSEM 62  
Db 179 DDCM----KKEIVETCSQKEM 195

RESULT 7  
A86544  
hypothetical protein FAM5.5 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: A86544  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federici, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Knaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

```

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A|Reference number: A86141; MUID:21016719; PMID:11130712
A|Accession: A86544
A>Status: preliminary
A|Molecule type: DNA
A|Residues: 1-154 <STO>
A|Cross-references: GB:A8005173; NID:g11072061; PIDN:AA828918.1; GSPDB:GN00141
C|Genetics:
A|Gene: FAM5.5
A|Map position: 1

Query Match      19.8%; Score 73; DB 2; Length 154;
Best Local Similarity 21.4%; Pred.No. 1.3;
Matches 15; Conservative 17; Mismatches 26; Indels 12; Gaps 2;

QY      7  CECTCYETTESCCCTVSTPYGVKDN-----QRIFKKDDCKIVVEK---DPK 54
Db       78 CKSQGMNTVAACSNKCVDIAYDNNCGACKNOCKFTOTCRGECVYLAYDKRHGBCN 137
          ||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      55 KTCGVSEWII 64
          :||::||::||::||::||::||::||::||::||::||::||::||::||
Db      138 HSCLVGEFCV 147

RESULT 8
A0136
fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)
M|Alternate names: epidermal growth factor homolog precursor
N|Contains: alternatively spliced fibropellin Ib (EGFI)
C|Species: Strongylocentrotus purpuratus (purple urchin)
C|Date: 13-May-1992 #sequence_revision 17-Sep-1997 #text_change 21-Jul-2000
C|Accession: A40136; B40136; C40136; A29316; A43131
R|Delgado-Rio-Reynoso, M.G.; Rollo, D.R.; Hursh, D.A.; Raff, R.A.
J|Mol. Evol. 29, 314-327, 1989
A>Title: Structural analysis of the uGF gene in the sea urchin Strongylocentrotus purp
A|Reference number: A40136; MUID:90112459; PMID:2514273
A|Accession: A40136
A>Status: preliminary
A|Molecule type: mRNA
A|Residues: 1-114 <DEP>
A|Cross-references: GB:X17530; NID:g10225; PID:667061
A|Accession: B40136
A>Status: preliminary; not compared with conceptual translation
A|Molecule type: DNA
A|Residues: 181-251,329-370,'R','372-408','RA',411-441 <DE2>
A|Accession: C40136
A>Status: preliminary; not compared with conceptual translation
A|Molecule type: DNA
A|Residues: 'K',747-821,898-978 <DE3>
R|Hursh, D.A.; Andrews, M.E.; Raff, R.A.
Science 237, 1487-1490, 1987
A>Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.
A|Reference number: A29316; MUID:87319677; PMID:3498216
A|Accession: A29316
A>Status: preliminary
A|Molecule type: mRNA
A|Residues: 'S',280-481,786-1064 <HUR>
A|Cross-references: GB:M17421; NID:g161474; PIDN:AAA30050.1; PID:g552260
R|Hunt, L.T.; Barker, W.C.
FASEB J. 3, 1760-1764, 1989
A>Title: Avdlin-like domain in an epidermal growth factor homolog from a sea urchin.
A|Reference number: A43131; MUID:89196806; PMID:2784773
A|Contents: annotation
C|Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib
C|Superfamily: Clr/Cis repeat homology; EGF homology
F|1-19/Domain: signal sequence #status predicted <SIG>
F|20-1064/Product: fibropellin I #status predicted <FLB>
F|23-54/Domain: EGF homology <EG01>
F|57-175/Domain: Clr/Cis repeat homology <CLR>
F|180-211/Domain: EGF homology <EG02>
F|218-249/Domain: EGF homology <EG03>
F|256-287/Domain: EGF homology <EG04>
F|294-325/Domain: EGF homology <EG05>

```



	Matches	12;	Conservative	4;	Mismatches	13;	Indels	4;	Gaps	1;
Qy	2	WQDNCEFTCTCYETETISC----	CTIVSTPVGVD	30						
		: : :								
Db	1481	WSPDVCETKCNCFHGQVNCIRRCGEVSPGVD	1513							

## RESULT 13

```

collagen alpha 5 chain - sea urchin (Strongylocentrotus purpuratus) (fragment)
[C]Species: Strongylocentrotus purpuratus (purple urchin)
C|Date: 20-Jul-1996 #sequence_rev108-Nov-1996 #text_change 25-Apr-1997
R|Accession: S63986; S64638
R|Exposito, J.Y.; Boute, N.; Deleage, G.; Garrone, R.
R|Eur. J. Biochem. 234, 59-65, 1995
A|Title: Characterization of two genes coding for a similar four-cysteine motif of the a
A|Reference number: S63985; MUID:96096722; PMID:852969
A|Accession: S63986
A|Status: nucleic acid sequence not shown
A|Molecule type: DNA
A|Residues: 1-1376 <EXP>
A|Cross-references: EMBL:X89804
R|Exposito, J.Y.
submitted to the EMBL Data Library, July 1995
A|Reference number: S64637
A|Accession: S64638
A|Molecule type: DNA
A|Residues: 1-658, 'G', 660-870, 'G', 872-901, 'H', 903-1185, 'T', 1187-1214, 'Y', 1216-1376 <EX>
A|Cross-references: EMBL:X89804
C|Genetics:
A|Gene: COLP5alpha
A|Intons: 73/1; 136/2; 221/1; 369/1; 517/1; 659/1; 799/1; 948/1; 1093/1; 1236/1
C|Superfamily: von Willebrand factor type C repeat homology
C|Keywords: extracellular matrix
F,15-73/Domain: von Willebrand factor type C repeat homology <VMC>

Query Match      18.6%; Score 68.5; DB 2; Length 1376;
Best Local Similarity 27.5%; Pred. No. 26;
Matches 19; Conservative 6; Mismatches 23; Indels 21; Gaps 3;

Oy      1 EMQIDNCEPCCYEPEISCCCTLVSPGVGDNDNCORFKKED-----CKYIV-YE 49
       |||||
Db      28 EWKDEECTTCADNVATTTCV-----ESCQPAFCAPIPPESECCCLCPYNVRV 77

Oy      50 KKDPKRTCS 58
       :|::|
Db      78 RVTPETITS 86

```

## RESULT 14

hypothetical protein T20D4.10 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_rev:10110 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T29944  
R:Minx, P.; Graves, T.  
submitted to the EMBL Data Library, November 1996  
A:Description: The sequence of C. elegans cosmid T20D4.  
A:Reference number: Z20712  
A:Accession: T29944  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-355 <MIN>  
A:Cross-references: EMBL:U00029; PIDW:AA037587.1; GSPDB:GN00023; CESP:T20D4.10  
A:Experimental source: strain Bristol N2; clone T20D4  
C:Genetics:  
A:Gene: CESP:T20D4.10  
A:Map position: 5  
A:Introns: 44/3, 161/3, 195/1, 343/3

```
QY      32 DNGQRIKKEDCKYIVKEKDPKKTCSVSEW 62
      : : | | : | | : | | | |
Db      151 ETCKRYFGKDDCM-----MKVEKETGGQGEW 176
```

RESULT 15

thrombospondin precursor - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A39804  
 R:Rawler, J.; Duquette, M.; Ferro, P.  
 J. Biol. Chem. 265, 8039-8043, 1991  
 A:Title: Cloning and sequencing of chicken thrombospondin.  
 A:Reference number: A39804; MUID:91217026; PMID:2022631  
 A:Accession: A39804  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1178 <LAW>  
 A:Cross-references: GB:W60853; NID:G212763; PIDN:AAA5137.1; PID:G212764  
 C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von Willebrand factor type C repeat homology <VWC>  
 F:325-333/Domain: von Willebrand factor type C repeat homology <THR1>  
 F:386-437/Domain: thrombospondin type 1 repeat homology <THR1>  
 F:447-498/Domain: thrombospondin type 1 repeat homology <THR2>  
 F:499-555/Domain: thrombospondin type 1 repeat homology <THR3>  
 F:658-697/Domain: EGF homology <EGF>

Search completed: March 11, 2004, 17:56:00  
Job time : 19.0645 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2004, 17:49:21 ; Search time 12.7016 Seconds

(without alignments)  
340.793 Million cell updates/sec

Title: US-09-977-406A-88

Perfect score: 268  
Sequence: 1 SCYFIPNKGVGSDTRKCMD.....HPINSEWQTNCECTCYET 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR\_78.\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	268	100.0	114	2	A34567
2	218	81.3	114	2	A54563
3	135.5	50.6	91	2	S41663
4	93	34.7	77	2	G01730
5	67	25.0	1292	2	T09229
6	67	25.0	2476	2	T34022
7	66	24.6	1280	2	A39117
8	66	24.6	2813	2	A59385
9	64.5	24.1	90	2	B59431
10	64.5	24.1	1499	2	T42724
11	63.5	23.7	1501	2	T21305
12	62.5	23.3	2214	2	T12225
13	61.5	22.9	5376	2	T12225
14	61	22.8	1535	2	S46224
15	60.5	22.6	884	2	T18649
16	60	22.4	1465	2	T23056
17	59.5	22.2	628	2	T02602
18	58.5	21.8	275	2	A36415
19	58.5	21.8	377	2	T28558
20	58.5	21.8	377	2	H36849
21	58.5	21.8	377	2	T37403
22	58.5	21.8	377	2	T2165
23	58.5	21.8	377	2	T42518
24	58	21.6	437	2	S05478
25	58	21.6	1700	2	S08167
26	57.5	21.5	398	2	A35281
27	57	21.3	230	2	C30286
28	57	21.3	1172	1	TSH022
29	57	21.3	1172	2	A42587

30	57	21.3	2481	2	A43908	fibronectin - Afri
31	56.5	21.1	961	2	H86181	hypothetical prote
32	56.5	21.1	2477	2	S14428	fibronectin precu
33	56	20.9	186	2	E86320	beta-galactosidase
34	56	20.9	649	2	H72283	DPP receptor TKV,
35	55.5	20.7	509	2	I45713	hypothetical prote
36	55.5	20.7	629	2	T25571	collagen alpha 5 c
37	55.5	20.7	1376	2	S63986	hypothetical prote
38	55.5	20.7	2229	2	T16199	hypothetical prote
39	55.5	20.7	3084	1	MMMSA	laminin alpha-1 ch
40	55.5	20.7	3133	2	S52093	hemocytin - silkw
41	55	20.5	810	2	T10756	Nel-homolog protei
42	55	20.5	915	2	T21773	hypothetical prote
43	55	20.5	927	2	T21772	hypothetical prote
44	54.5	20.3	159	2	T33696	hypothetical prote
45	54.5	20.3	229	2	A69762	hypothetical prote

## ALIGNMENTS

RESULT 1  
A34567  
beta-microseminoprotein precursor - human  
N/Alternate names: beta-inhibin; prostatic secretory protein; PSP-94; seminal plasma pr  
C/Species: Homo sapiens (man)  
C/Date: 13-Jul-1990 #sequence revision 13-Jul-1990 #ext change 20-Aug-1999  
C/Accession: A34567; A26451; A29777; A30984; A60673; S16238; I2662  
R/Green, C.B.; Liu, W.Y.; Kwok, S.C.M.  
Biochem. Biophys. Res. Commun. 167, 1184-1190, 1990  
A/Title: Cloning and nucleotide sequence analysis of the human beta-microseminoprotein  
A/Reference number: A34567; PMID:90211299; PMID:2322265  
A/Status: not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-114 <GRE>  
A/Cross-references: GB:M34376; NID:G514370; PIDN:AAA59871.1; PID:G514372  
R/Mikay, M.; Nolte, S.; Fournier, S.; Benjannet, S.; Chapelaine, P.; Paradis, G.; Dub  
DNA 6, 23-29, 1987  
A/Title: Molecular cloning and sequence of the cDNA for a 94-amino-acid seminal plasma  
A/Reference number: A26451; PMID:87161231; PMID:3829888  
A/Accession: A26451  
A/Molecule type: mRNA  
A/Residues: 1-114 <MB1>  
A/Cross-references: GB:M15885; NID:G338414; PIDN:AAA3635.1; PID:G338415  
R/Akiyama, K.; Yoshioke, Y.; Schmidt, K.; Offner, G.D.; Troxler, R.F.; Tsuda, R.; Hara,  
Biochim. Biophys. Acta 829, 288-294, 1985  
A/Title: The amino acid sequence of human beta-microseminoprotein.  
A/Reference number: A29777; PMID:85199974; PMID:3995056  
A/Accession: A29777  
A/Molecule type: protein  
A/Residues: 21-58, 'PT', 61-113 <AKI>  
R/Seidman, N.G.; Arbatli, N.J.; Rochemont, J.; Sheeh, A.R.; Chretien, M.  
FEBS Lett. 175, 349-355, 1984  
A/Title: Complete amino acid sequence of human seminal plasma beta-inhibin. Prediction  
A/Reference number: A30984; PMID:85004133; PMID:5434350  
A/Accession: A30984  
A/Molecule type: protein  
A/Residues: 21, 'X', 23-34 <SEI>  
R/Weiber, H.; Anderson, C.; Murrie, A.; Rannevik, G.; Lindstroem, C.; Lilja, H.; Fernlu  
Am. J. Pathol. 137, 593-604, 1990  
A/Title: Beta microseminoprotein is not a prostate-specific protein.  
A/Reference number: A60673; PMID:90379237; PMID:2205099  
A/Accession: A60673  
A/Molecule type: protein  
A/Residues: 21, 'X', 23-34 <WEI>  
A/Experimental source: gastric juice  
R/Nolte, S.; Mikay, M.; Chretien, M.  
Biochim. Biophys. Acta 1089, 247-249, 1991  
A/Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence i  
A/Reference number: S16237; PMID:91274357; PMID:2054385  
A/Accession: S16238  
A/Molecule type: DNA

A:Residues: 1-114 <NO>  
 A:Cross-references: EMBL:X57928; NID:G35760; PIDN:CAA41002.1; PID:G825707  
 A>Note: The authors translated the codon ACT for residue 54 as Trp  
 R.Liu, A.Y.; Brader, R.C.; Vessella, R.L.  
 Cancer Lett. 74, 91-99, 1993  
 A>Title: Decreased expression of prostatic secretory protein PSP94 in prostate cancer.  
 A:Reference number: 152682; MUID:94115955; PMID:7506990  
 A:Accession: 152682  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-114 <RES>  
 A:Cross-references: GB:S67815; NID:G460569; PIDN:AA829732.1; PID:G460569  
 A:Comment: This protein is a component of seminal plasma as well as secretory fluids from  
 C:Genetics:  
 A:Gene: GDB:MSMB  
 A:Cross-references: GDB:128042; OMIM:157145  
 A:Map position: 10q11.2-10q11.2  
 A:Introns: 1/3; 37/1; 72/2  
 C:Superfamily: seminal plasma protein  
 C:Keywords: semen  
 F.1-10/Domain: signal sequence #status predicted <SIG>  
 F.1-114/Product: seminal plasma protein #status experimental <MAT>

Query Match 100.0%; Score 268; DB 2; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-25;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SCYFIPNEGVPDSTRKCMCLKGNKHPINSEWQNDNCCTCYET 45  
 DB 21 SCYFIPNEGVPDSTRKCMCLKGNKHPINSEWQNDNCCTCYET 65

## RESULT 2

AS4663  
 seminal plasma protein PSP-94 precursor - rhesus macaque  
 M:Alternate names: prostatic secretory protein PSP94  
 C:Species: Macaca mulatta (rhesus macaque)  
 C>Date: 02-Jun-1995 #sequence\_revision 02-Jun-1995 #text\_change 20-Aug-1999  
 C:Accession: S16237; AS4663  
 R:Nolet, S.; Moikay, M.; Chretien, M.  
 Biochim. Biophys. Acta 1089, 247-249, 1991  
 A>Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in  
 A:Reference number: S16237; MUID:91274557; PMID:2054385  
 A:Accession: S16237  
 A:Molecule type: DNA  
 A:Residues: 1-114 <NO2>  
 A:Cross-references: EMBL:X57932; NID:G38094; PIDN:CAA41003.1; PID:G829152  
 A>Note: the authors translated the codon ACT for residue 54 as Trp  
 R.Nolet, S.; St-Louis, D.; Moikay, M.; Chretien, M.  
 Genomics 9, 775-777, 1991  
 A>Title: Rapid evolution of prostatic protein PSP-94 suggested by sequence divergence be  
 A:Reference number: AS4663; MUID:91244525; PMID:2037304  
 A:Accession: AS4663  
 A:Molecule type: mRNA  
 A:Residues: 1-114 <NO>  
 A:Cross-references: GB:M92161; NID:G342280; PIDN:AA36903.1; PID:G342281  
 C:Genetics:  
 A:Introns: 1/3; 37/1; 72/2  
 C:Superfamily: seminal plasma protein  
 F.1-20/Domain: signal sequence #status predicted <SIG>

Query Match 81.3%; Score 218; DB 2; Length 114;  
 Best Local Similarity 80.0%; Pred. No. 5.8e-19;  
 Matches 36; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 SCYFIPNEGVPDSTRKCMCLKGNKHPINSEWQNDNCCTCYET 45  
 DB 21 SCYFIPNEGVPDSTRKCMCLKGNKHPINSEWQNDNCCTCYET 65

RESULT 3  
 S41663  
 beta-microseminoprotein - pig

C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
 C:Accession: S41663  
 R:Perlund, P.; Graberg, L.B.; Roepstorff, P.  
 Arch. Biochem. Biophys. 309, 70-76, 1994  
 A>Title: Amino acid sequence of beta-microseminoprotein from porcine seminal plasma.  
 A:Reference number: S41663; MUID:94161559; PMID:8117114  
 A:Accession: S41663  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-91 <PER>  
 C:Superfamily: seminal plasma protein

Query Match 50.6%; Score 135.5; DB 2; Length 91;  
 Best Local Similarity 53.7%; Pred. No. 3.3e-09;  
 Matches 22; Conservative 6; Mismatches 10; Indels 3; Gaps 1;

OY 2 CYFIPNEGVPDSTRKCMCLKGNKHPINSEWQNDNCCTCYET 42  
 DB 2 CYFIPNEGVPDSTRKCMCLKGNKHPINSEWQNDNCCTCYET 39

## RESULT 4

G01730  
 PSP97 - human  
 C:Species: Homo sapiens (man)  
 C>Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 20-Aug-1999  
 C:Accession: G01730  
 R:Xian, J.W.; Chin, J.L.; Guo, Y.; Chambers, A.F.; Finkelman, M.A.; Clarke, M.W.  
 submitted to the EMBL Data Library, March 1995  
 A:Reference number: G08240  
 A:Accession: G01730  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-77 <XUA>  
 A:Cross-references: EMBL:U22178; NID:G885984; PIDN:AA83556.1; PID:G885985  
 C:Superfamily: seminal plasma protein

Query Match 34.7%; Score 93; DB 2; Length 77;  
 Best Local Similarity 81.0%; Pred. No. 0.00034;  
 Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 SCYFIPNEGVPDSTRKCMCLKGNKHPINSEWQNDNCCTCYET 41  
 DB 21 SCYFIPNEGVPDSTRKCMCLKGNKHPINSEWQNDNCCTCYET 41

## RESULT 5

T09229  
 galactose binding adhesin heavy chain - Entamoeba histolytica  
 C:Species: Entamoeba histolytica  
 C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
 C:Accession: T09229  
 R:Purdy, J.E.; Mann, B.J.; Shugart, E.C.; Petri, W.A.  
 Mol. Biochem. Parasitol. 62, 53-59, 1993  
 A>Title: Analysis of the gene family encoding the Entamoeba histolytica galactose-speci  
 A:Reference number: Z16622; MUID:94158976; PMID:8114826  
 A:Accession: T09229  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1292 <PUR>  
 A:Cross-references: EMBL:L14815; NID:G290648; PID:G290649  
 C:Genetics:  
 A:Gene: hgl3  
 C:Keywords: lectin

Query Match 25.0%; Score 67; DB 2; Length 1292;  
 Best Local Similarity 31.7%; Pred. No. 6;  
 Matches 13; Conservative 6; Mismatches 10; Indels 12; Gaps 1;

OY 17 KCMCLKGNKHPINSEWQNDNCCTCYET 45  
 DB 1099 KCVESKSGDSOKITHKWEIDTFRSNNPKRNCERTATCQT 1139

## RESULT 6

T34022  
 zonadhesin - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 02-Sep-2000  
 C:Accession: T34022  
 R:Hardy, D.M.; Garbers, D.L.  
 J. Biol. Chem. 270, 26025-26028, 1995  
 A:Title: A sperm membrane protein that binds in a species-specific manner to the egg ext  
 A:Reference number: Z21464; MUID:96064658; PMID:7592795  
 A:Accession: T34022  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-2476 <HAR>  
 A:Cross-references: EMBL:U40024; NID:G1066465; PID:G1066466; PIDN:AA4486.1  
 A:Experimental source: strain Meishan; testis  
 C:Genetics:  
 A:Gene: Zan  
 C:Function:  
 A:Description: may be involved in sperm adhesion to the zona pellucida

Query Match 25.0%; Score 67; DB 2; Length 2476;  
 Best local Similarity 40.7%; Pred. No. 11;  
 Matches 11; Conservative 3; Mismatches 11; Indels 2; Gaps 1;  
 QY 18 CMDLKGKHPINSMQTDN--CETCTC 42  
 DB 1513 CTTQRGSYHPVGSWYTDNSCRCTC 1539

## RESULT 7

A39117  
 170K lectin precursor - Entamoeba histolytica (fragment)  
 C:Species: Entamoeba histolytica  
 C:Date: 30-Aug-1991 #sequence\_revision 17-Apr-1993 #text\_change 09-Sep-1997  
 C:Accession: A39117  
 R:Tannich, E.; Ebert, F.; Horstmann, R.D.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 1849-1853, 1991  
 A:Title: Primary structure of the 170-kDa surface lectin of pathogenic Entamoeba histolytica  
 A:Reference number: A39117; MUID:91156704; PMID:2000392  
 A:Accession: A39117  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1280 <TAN>  
 A:Cross-references: GB:M60498; NID:G158958; PID:G158959  
 C:Keywords: transmembrane protein

Query Match 24.6%; Score 66; DB 2; Length 1280;  
 Best local Similarity 31.7%; Pred. No. 7.8;  
 Matches 11; Conservative 6; Mismatches 10; Indels 12; Gaps 1;  
 QY 17 KCMDLKGKHPINSMQTDN--CETCTCYFT 45  
 DB 1087 KCVESKSGDKITHKWEIDTERSNIDKPPNPCEATACDQT 1127

## RESULT 8

VWHD  
 von Willebrand factor precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 04-Dec-1986 #sequence\_revision 30-Jun-1993 #text\_change 22-Jun-1999  
 C:Accession: A34480; S02377; A37139; S23676; A25298; A25469; A23366; S23645; A94  
 R:Mancuso, D.J.; Tukey, E.A.; Westfield, L.A.; Morrall, N.K.; Shelton-Inloes, B.B.; Sor  
 J. Biol. Chem. 264, 19514-19527, 1989  
 A:Title: Structure of the gene for human von Willebrand factor.  
 A:Reference number: A34480; MUID:90062044; PMID:2584182  
 A:Accession: A34480  
 A:Molecule type: DNA  
 A:Residues: 1-2813 <EMAN>  
 A:Cross-references: EMBL:M25864  
 R:Bonthron, D.; Orkin, S.H.

Eur. J. Biochem. 171, 51-57, 1988  
 A:Title: The human von Willebrand factor gene. Structure of the 5' region.  
 A:Reference number: S02377; MUID:88111704; PMID:2828057  
 A:Accession: S02377

A:Molecule type: DNA  
 A:Residues: 1-177 <BO2>  
 A:Cross-references: EMBL:X06828  
 R:Mancuso, D.J.; Tukey, E.A.; Westfield, L.A.; Lester-Mancuso, T.L.; Le Beau, M.M.; Sor  
 Biochemistry 30, 253-269, 1991  
 A:Title: Human von Willebrand factor gene and pseudogene: structural analysis and diffe  
 A:Reference number: A37139; MUID:91105089; PMID:1988024  
 A:Accession: A37139  
 A:Molecule type: DNA  
 A:Residues: 990-1947 <MAD>  
 A:Cross-references: GB:M60675; NID:G340357; PIDN:AAA61295.1; PID:G553810  
 A:Note: the authors translated the codon CGC for residue 156 as Gln  
 R:Collins, C.J.; Underahl, J.P.; Levene, R.B.; Ravera, C.P.; Morin, M.J.; Domagalian,  
 Proc. Natl. Acad. Sci. U.S.A. 84, 4393-4397, 1987  
 A:Title: Molecular cloning of the human gene for von Willebrand factor and identificati  
 A:Reference number: S23676; MUID:87260814; PMID:3496594  
 A:Accession: S23676  
 A:Molecule type: DNA  
 A:Residues: 2731-2813 <COL>  
 A:Cross-references: EMBL:M16945  
 R:Bonthron, D.; Orr, E.C.; Mitsuoka, L.M.; Ginsburg, D.; Hardin, R.I.; Orkin, S.H.  
 Nucleic Acids Res. 14, 7125-7127, 1986  
 A:Title: Nucleotide sequence of pre-pro-von Willebrand factor cDNA.  
 A:Reference number: A25298; MUID:87016349; PMID:485923  
 A:Accession: A25298  
 A:Molecule type: mRNA  
 A:Residues: 1-470, 'V', 472-2813 <BON>  
 A:Cross-references: EMBL:X04385  
 R:Verweij, C.L.; Diegarde, P.J.; Hart, M.; Pannekoek, H.  
 EMBO J. 5, 1839-1847, 1986  
 A:Title: Full-length von Willebrand factor (vWF) cDNA encodes a highly repetitive prote  
 A:Reference number: A91044; MUID:87004550; PMID:3019665  
 A:Accession: A25469  
 A:Molecule type: mRNA  
 A:Residues: 1-470, 'V', 472-493, 'R', 485-1022, 'K', 1024-1025, 'E', 1027-1400 <VER>  
 A:Cross-references: EMBL:X04146  
 R:Verweij, C.L.; Diegarde, P.J.; Hart, M.; Pannekoek, H.  
 EMBO J. 5, 3074, 1986  
 A:Reference number: A91056  
 A:Accession: A25366  
 A:Molecule type: mRNA  
 A:Residues: 1021-1030 <VER>  
 A:Note: this is a revision to the sequence from reference A91044  
 R:Shelton-Inloes, B.B.; Broze Jr., G.J.; Miletich, J.P.; Sadler, J.E.  
 Biochem. Biophys. Res. Commun. 144, 657-665, 1987  
 A:Title: Evolution of human von Willebrand factor: cDNA sequence polymorphisms, repeate  
 A:Reference number: S23618; MUID:87213253; PMID:3495266  
 A:Accession: S23618  
 A:Molecule type: mRNA  
 A:Residues: 1-120 <SH2>  
 A:Cross-references: EMBL:M17588; NID:G799330; PIDN:AAA65940.1; PID:G340316  
 A:Accession: S23645  
 A:Molecule type: protein  
 A:Residues: 23-56 <SH3>  
 R:Sadler, J.E.; Shelton-Inloes, B.B.; Sorace, J.M.; Harlan, J.M.; Tlanti, K.; Davie, E.I.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 6394-6398, 1985  
 A:Title: Cloning and characterization of two cDNAs coding for human von Willebrand fact  
 A:Reference number: A94060; MUID:86016708; PMID:2864688  
 A:Accession: A94060  
 A:Molecule type: mRNA  
 A:Residues: 'MA', 739, 'C', 744-769, 'H', 771-788, 'A', 790-803, 'S', 805-873, 1289-1471, 'D', 1473.  
 A:Note: the authors translated the codon TCG for residue 2168 as Cys  
 R:Shelton-Inloes, B.B.; Tlanti, K.; Sadler, J.E.  
 Biochemistry 25, 3164-3171, 1986  
 A:Title: cDNA sequences for human von Willebrand factor reveal five types of repeated dk  
 A:Reference number: A90504; MUID:86269894; PMID:3488076  
 A:Accession: A90504  
 A:Molecule type: mRNA

A:Residues: 781-788, 'A', 790-1424 <SHE>  
 A:Note: 852-Gln, 857-Asp, and 1381-Thr were also found  
 R:Ginsburg, D.; Handlin, R.I.; Bonthron, D.T.; Donlon, T.A.; Bruns, G.A.P.; Latt, S.A.; C  
 Science 228, 1401-1406, 1985  
 A:Title: Human von Willebrand factor (vWF): isolation of complementary DNA (cDNA) clones  
 A:Reference number: A44178; PMID:85244588; PMID:3874428  
 A:Accession: A44178  
 A:Molecule type: mRNA  
 A:Residues: 2621-2813 <GIN>  
 A:Cross-references: EMBL:X0208; NID:G340308; PIDN:AA61293.1; PID:G340309  
 R:Vervaeke, C.L.; de Vries, C.J.M.; Distel, B.; van Zonneveld, A.J.; van Kessel, A.G.; va  
 Nucleic Acids Res. 13, 4659-4717, 1985  
 A:Title: Construction of cDNA coding for human von Willebrand factor using antibody prod  
 A:Reference number: S07363; PMID:85269603; PMID:3875078  
 A:Accession: S07363  
 A:Molecule type: mRNA  
 A:Residues: 2731-2813 <VR3>  
 A:Cross-references: EMBL:X02672; NID:G37939; PIDN:CAA26503.1; PID:G37940  
 R:Lynch, D.C.; Zimmerman, T.S.; Collins, C.J.; Brown, M.; Morin, M.J.; Ling, E.H.; Livin  
 Cell 41, 49-56, 1985  
 A:Title: Molecular cloning of cDNA for human von Willebrand factor: authentication by a  
 A:Reference number: S23678; PMID:85201687; PMID:3873280  
 A:Accession: S23678  
 A:Molecule type: mRNA  
 A:Residues: 2731-2813 <LYN>  
 A:Cross-references: EMBL:X03028  
 R:Tiliani, K.; Kumer, S.; Takio, K.; Ericsson, L.H.; Wade, R.D.; Ashida, K.; Walsh, K.A.;  
 Biochemistry 25, 3171-3184, 1986  
 A:Title: Amino acid sequences of human von Willebrand factor.  
 A:Reference number: A90505; PMID:85269895; PMID:3524673  
 A:Accession: A90505  
 A:Molecule type: protein  
 A:Residues: 764-788, 'A', 790-1471, 'D', 1473-2813 <TIT>  
 A:Note: 789-Thr was also found  
 R:Chopek, M.W.; Girma, J.F.; Fujikawa, K.; Davie, E.W.; Tilani, K.  
 Biochemistry 25, 3146-3155, 1986  
 A:Title: Human von Willebrand factor: a multivalent protein composed of identical subunit  
 A:Reference number: A23464; PMID:85269892; PMID:3015159  
 A:Accession: A23464  
 A:Molecule type: protein  
 A:Residues: 764-773, 2803-2813 <CHO>  
 R:Dent, J.A.; Berkowitz, S.D.; Ware, J.; Kasper, C.K.; Ruggeri, Z.M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 6306-6310, 1990  
 A:Title: Identification of a cleavage site directing the immunohistochemical detection of mol  
 A:Reference number: A36013; PMID:90349604; PMID:2385594  
 A:Accession: A36013  
 A:Molecule type: protein  
 A:Residues: 1606-1617 <DEN>  
 R:Pay, P.J.; Kawai, Y.; Wagner, D.D.; Ginsburg, D.; Ohlsson-Wilhelm, B.M.;  
 Science 232, 995-998, 1986  
 A:Title: Protopolypeptide of von Willebrand factor circulates in blood and is identical to  
 A:Reference number: A60913; PMID:85208144; PMID:3486471  
 A:Accession: A60913  
 A:Molecule type: protein  
 A:Residues: 576-590 <PAY>  
 A:Gene: GDB: VWF  
 C:Genetics:  
 A:Cross-references: GDB:119125; OMIM:193400  
 A:Map position: 12p13.3-12p13.2  
 A:Intron: 19/1, 74/1, 108/2, 178/1, 219/3, 292/1, 333/1, 370/2, 386/1, 431/3, 478/1, 51  
 5/1, 1724/1, 1771/1, 1819/1, 1874/1, 1888/3, 1948/1, 2021/3, 2086/1, 2200/1, 2266/3, 230  
 C:Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von  
 C:Keywords: blood coagulation; cell binding; connective tissue; disulfide bond; duplicat  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-763/Product: von Willebrand antigen II #status predicted <MA1>  
 F:34-386/Domain: type D repeat 1 <DD1>  
 F:387-745/Domain: type D repeat 2 <DD2>  
 F:698-700/Region: cell attachment (R-G-D) motif  
 F:764-2813/Product: von Willebrand factor #status predicted <MA2>  
 F:784-865/Domain: D' <DDD>  
 F:788-833, 2216-2261/Region: duplication  
 F:826-853, 2400-2515, 2544-2662/Region: duplication  
 F:842-1130, 1934-2203/Region: duplication

F:866-1241/Domain: type D repeat 3 <DD3>  
 F:1275-1443/Domain: von Willebrand factor type A repeat homology <VWA1>  
 F:1496-1654/Domain: von Willebrand factor type A repeat homology <VWA2>  
 F:1689-1854/Domain: von Willebrand factor type A repeat homology <VWA3>  
 F:1947-2295/Domain: type D repeat 4 <DD4>  
 F:2296-2330/Domain: type B repeat 1 <VB1>  
 F:2340-2365/Domain: type B repeat 2 <VB2>  
 F:2375-2399/Domain: type B repeat 3 <VB3>  
 F:2430-2497/Domain: von Willebrand factor type C repeat homology <VWC1>  
 F:2507-2509/Region: cell attachment (R-G-D) motif  
 F:2581-2647/Domain: von Willebrand factor type C repeat homology <VWC2>  
 F:2587-1231, 1515, 1574, 2223, 2290, 2357, 2400, 2546, 2585, 2790/Binding site: carbohydrate (asn  
 F:1147/Binding site: carbohydrate (asn) (covalent) #status atypical  
 F:1248, 1255, 1256, 1468, 1477, 1487, 1679, 2298/Binding site: carbohydrate (Thr) (covalent) #  
 F:1253, 1486/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 24.6%; Score 66; DB 1; Length 2813;  
 Best Local Similarity 27.6%; Pred. No. 16;  
 Matches 16; Conservative 8; Mismatches 18; Indels 16; Gaps 2;

Query 1 SCYFFPNEG-----VPGDSTRKMDLGNKHPINSEWQTDN--CETCTC 42  
 DB 2226 SCGDHPSECFPCPPDKRMLESGVPEEACTOCIGEDVGHQFLKAWVDHQPCCCTC 2283

RESULT 9  
 A:53385  
 Beta-microseminoprotein - Ostrich (Struthio camelus)  
 C:Species: Ostrich (Struthio camelus)  
 C:Date: 31-Dec-2001 #sequence\_revision 31-Dec-2001 #text\_change 11-Jan-2002  
 C:Accession: A59385  
 R:Lazure, C.  
 Submitted to the Protein Sequence Database, March 2001  
 A:Description: Characterization of ostrich (struthio camelus).  
 A:Reference number: A59385  
 A:Accession: A59385  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-90 <LAZ>  
 A:Experimental source: Pituitary extracts  
 A:Note: Structurally related to mammalian Prostate Secretory Protein  
 C:Keywords: amidated carboxyl end  
 F:2-16, 34-70, 37-46, 39-47, 61-84/Disulfide bonds: #status predicted  
 F:30/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 24.1%; Score 64.5; DB 2; Length 90;  
 Best Local Similarity 37.5%; Pred. No. 0.99;  
 Matches 12; Conservative 6; Mismatches 13; Indels 1; Gaps 1;

Query 11 PGDSTRKMDLGNKHPINSEWQTDN-CETCTC 42  
 DB 9 PGSDSGCT-LDQKXYPGEISRTENYCRSC 39

RESULT 10  
 A:59431  
 Rho GTPase activating protein 5 (p190-B) [imported] - human  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Jun-2002 #sequence\_revision 03-Jun-2002 #text\_change 23-Sep-2002  
 C:Accession: B59431  
 R:Barbello, P.D.; Miyamoto, S.; Utani, A.; Brill, S.; Yamada, K.M.; Hall, A.; Yamada, Y.  
 J. Biol. Chem. 270, 30919-30926, 1995  
 A:Title: p190-B, a new member of the Rho GAP family, and Rho are induced to cluster aft  
 A:Reference number: B59431; PMID:96125066; PMID:8537347  
 A:Accession: B59431  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1499 <BUR>  
 A:Cross-references: GB:NP\_001164; PID:G4502221; PIDN:NP\_001164.1.

Query Match 24.1%; Score 64.5; DB 2; Length 1499;  
 Best Local Similarity 48.1%; Pred. No. 14;  
 Matches 13; Conservative 6; Mismatches 5; Indels 3; Gaps 1;

QY 11 PGDSTRKMDLKGKHPINSEWQDNC 37  
 Db 1004 PSDRSRYRLDLEGNEYPVHS--TPNC 1027

RESULT 11  
 T42724  
 p190-B protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000  
 C/Accession: T42724  
 R:Burtejo, P.D.; Finegold, A.A.; Kozak, C.A.; Yamada, Y.; Takami, H.  
 B:Jochim, Biophys. Acta 1443, 203-210, 1998  
 A>Title: Cloning, genomic organization and chromosomal assignment of the mouse p190-B gene  
 A:Reference number: Z22244; MUID:99051598; PMID:9838117  
 A:Accession: T42724  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1501 <BUR>  
 A:Cross-references: EMBL:U67160; NID:g1762974; PID:g1762975; PIDN:AAD2768.1  
 C:Genetics:  
 A:Map position: 12

Query Match 23.7%; Score 63.5; DB 2; Length 1501;  
 Best Local Similarity 44.4%; Pred. No. 18;  
 Matches 12; Conservative 7; Mismatches 5; Indels 3; Gaps 1;

QY 11 PGDSTRKMDLKGKHPINSEWQDNC 37  
 Db 1003 PSDRSRYRLDLEGNEYPVHS--TPNC 1026

RESULT 12  
 T16305  
 hypothetical protein F40F4.6 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C/Accession: T16305  
 R:Wilson, R.  
 A:Submitted to the EMBL Data Library, November 1995  
 A:Description: The sequence of C. elegans cosmid F40F4.  
 A:Reference number: Z16493  
 A:Accession: T16305  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-2214 <WIL>  
 A:Cross-references: EMBL:U40420; NID:g1065513; PID:g1065514; PIDN:AAA81430.1; CESP:F40F4  
 C:Genetics:  
 A:Gene: CESP:F40F4.6  
 A:Introns: 57/3; 95/1; 302/3; 323/1; 380/1; 404/1; 468/1; 507/2; 547/3; 595/3; 1532/1; 1

Query Match 23.3%; Score 62.5; DB 2; Length 2214;  
 Best Local Similarity 38.7%; Pred. No. 34;  
 Matches 12; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

QY 8 EGVPDGS-TRKMDLKGKHPINSEWQDNC 37  
 Db 1271 DGSPDPTPQCYFNGRSGDANKWTTDTTC 1301

RESULT 13  
 T42215  
 zonadhesin - mouse  
 N:Alternate names: sperm-specific membrane protein  
 C:Species: Mus musculus (house mouse)  
 C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
 C/Accession: T42215  
 R:Gao, Z.; Garbers, D.L.  
 J: Biol. Chem. 273, 3415-3421, 1998  
 A>Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane protein  
 A:Reference number: Z22080; MUID:98123114; PMID:9452463  
 A:Accession: T42215

A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-5376 <GAO>  
 A:Cross-references: EMBL:U97068; NID:g3327420; PID:g3327421; PIDN:AAC26680.1  
 C:Genetics:  
 A:Gene: Zan  
 A:Map position: 5  
 C:Function:  
 A:Description: functions in multiple cell adhesion processes  
 A>Note: found exclusively on the apical region of the sperm head  
 C:Keywords: cell adhesion

Query Match 22.9%; Score 61.5; DB 2; Length 5376;  
 Best Local Similarity 42.3%; Pred. No. 16+02;  
 Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 18 CMDLKGKHPINSEWQDNC-ETCTC 42  
 Db 4324 CDAQGDILIPANKTWLTRGCAQKTC 4349

RESULT 14  
 S46224  
 peroxidasein - fruit fly (Drosophila sp.)  
 C:Species: Drosophila sp.  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Oct-2000  
 C/Accession: S46224  
 R:Nelson, R.E.; Fessler, L.I.; Takagi, Y.; Blumberg, B.; Keene, D.R.; Olson, P.F.; Park, E.M.O. J. 13, 3438-3447, 1994  
 A>Title: Peroxidasein: a novel enzyme-matrix protein of Drosophila development.  
 A:Reference number: S46224; MUID:94341255; PMID:8062820  
 A:Accession: S46224  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1535 <NEL>  
 A:Cross-references: GB:U11052; NID:g531384; PIDN:AAA61568.1; PID:g531385  
 C:Superfamily: peroxidasein; myeloperoxidase homology; proteoglycan amino-terminal homol  
 F:19-44/domain: proteoglycan amino-terminal homology <PAH4>  
 F:661-1350/domain: myeloperoxidase homology <MPX>

Query Match 22.8%; Score 61; DB 2; Length 1535;  
 Best Local Similarity 38.5%; Pred. No. 37;  
 Matches 10; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

QY 18 CMDLKGKHPINSEWQDNCETCTCY 43  
 Db 1467 CVDDKGTTRLNNEVWSPVCTKNCIF 1492

RESULT 15  
 T18649  
 hypothetical protein B0024.14 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C/Accession: T18649  
 R:McMurry, A.  
 A:Submitted to the EMBL Data Library, April 1996  
 A:Reference number: Z19001  
 A:Accession: T18649  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-884 <WIL>  
 A:Cross-references: EMBL:Z71178; PIDN:CAA94886.1; GSPDB:GN00023; CESP:B0024.14  
 A:Experimental source: clone B0024  
 A:Gene: CESP:B0024.14  
 A:Map position: 5  
 A:Introns: 46/3; 84/1; 212/1; 307/2; 345/2; 394/1; 424/2; 481/1; 596/1; 702/1; 765/3; 85

Search completed: March 11, 2004, 17:56:02  
Job time : 14.7016 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2004, 17:45:41 ; Search time 8.34677 Seconds

(without alignments)  
280.726 Million cell updates/sec

Title: US-09-977-406a-88

Sequence: 1 SCVFINEGVGDSTRKCMD.....HPINSEWQDNCETCTCYET 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt 42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	268	100.0	114	1 MSMB_HUMAN	P08118 homo sapien
2	224	83.6	114	1 MSMB_PAPAN	Q28767 papio anubi
3	218	81.3	114	1 MSMB_VACCU	P25142 macaca mula
4	195	72.8	114	1 MSPJ_SAGOE	O97949 saguinus oe
5	190	70.9	112	1 MSPA_SAGOE	O97936 saguinus oe
6	154	57.5	114	1 MSPB_SAGOE	O97935 saguinus oe
7	135.5	50.6	111	1 MSMB_PIG	O02826 sus scrofa
8	90.5	33.8	113	1 MSMB_RAT	P97560 rattus norv
9	87.5	32.6	113	1 MSMB_MOUSE	O08540 mus musculu
10	73	27.2	2482	1 VWF_FIG	Q28833 sus scrofa
11	68	25.4	2812	1 ZAN_HUMAN	Q9Y433 homo sapien
12	67	25.0	1276	1 GILI_ENTHI	P32022 entamoeba h
13	67	24.6	2476	1 ZAN_PIG	Q28963 sus scrofa
14	66	24.6	1285	1 S117_ENTHI	P23502 entamoeba h
15	66	24.6	2813	1 VWF_HUMAN	P04275 homo sapien
16	65	24.3	2282	1 ZAN_MOUSE	P57999 cryotolagus
17	64.5	24.1	90	1 MSMB_STRCA	P83242 struthio ca
18	64.5	24.1	1499	1 RHGS_HUMAN	Q13017 homo sapien
19	63.5	23.7	1501	1 RHGS_MOUSE	P97333 mus musculu
20	63	23.5	1218	1 JAG1_HUMAN	P78504 homo sapien
21	62	23.1	2813	1 VWF_CANPA	Q28255 canis fami
22	61.5	22.9	5376	1 ZAN_MOUSE	O88799 mus musculu
23	59.5	22.2	940	1 CHR_BRARE	O57472 brachydanio
24	58.5	21.8	275	1 VAI6_VACCV	P16710 vaccinia vi
25	58.5	21.8	377	1 VAI6_VARY	P23841 vaccinia vi
26	58.5	21.8	378	1 VAI6_VACCC	P20093 vaccinia vi
27	58	21.6	437	1 PROF_MOUSE	P11680 mus musculu
28	58	21.6	1700	1 BAR3_CHITE	O03336 chironomus
29	58	21.6	3130	1 DPO2_HUMAN	O60673 homo sapien
30	57.5	21.5	398	1 MBI1_XENIA	P88555 xenopus lae
31	57	21.3	1172	1 TSP2_HUMAN	P25442 homo sapien
32	57	21.3	1172	1 TSP2_MOUSE	O03350 mus musculu
33	57	21.3	1173	1 TSP1_XENIA	P35448 xenopus lae

34	57	21.3	1210	1	AT19_MOUSE	P59509 mus musculu
35	57	21.3	2481	1	JAG2_MOUSE	O9495 mus musculu
36	57	21.3	2481	1	FINC_XENIA	O91740 xenopus lae
37	56.5	21.1	2477	1	FINC_MOUSE	P11276 mus musculu
38	56.5	21.1	2477	1	FINC_RAT	P04937 rattus norv
39	56	20.9	810	1	NEI1_HUMAN	Q92832 homo sapien
40	55.5	20.7	2386	1	FINC_MOUSE	P02751 homo sapien
41	55.5	20.7	3084	1	LMAL_MOUSE	P19137 mus musculu
42	55.5	20.7	3133	1	HMCT_BOMMO	P98092 bombyx mori
43	55	20.5	810	1	NEI1_RAT	O62919 rattus norv
44	55	20.5	816	1	NEI2_MOUSE	O61220 mus musculu
45	55	20.5	902	1	CLC2_CAVPO	O96045 cavia porce

## ALIGNMENTS

RESULT 1  
ID MSMB\_HUMAN STANDARD; PRT; 114 AA.  
AC P08118; P11999; Q13125; Q9UC59;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94) (Seminal plasma beta-inhibin) (Immunoglobulin binding factor) (IGBF) (PN44).  
GN MSMB OR PRSP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87161231; PubMed=3829868;  
RA Mikiy M., Nolet S., Fournier S., Benjannet S., Chappelaine P., Paradis G., Dube J.Y., Tremblay R., Lazure C., Seidah N.G., Chretien M.;  
RA "Molecular cloning and sequence of the cDNA for a 94-amino-acid RT seminal plasma protein secreted by the human prostate.";  
RL DNA 6:23-29 (1987).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91274357; PubMed=2054385;  
RA Noler S., Mikiy M., Chretien M.;  
RT "Prostatic secretory protein PSP94: gene organization and promoter sequence in rhesus monkey and human.";  
RL Biochim. Biophys. Acta 1089:247-249 (1991).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90211299; PubMed=2322265;  
RA Green C.B., Liu W.Y., Kwok S.C.M.;  
RT "Cloning and nucleotide sequence analysis of the human beta-microseminoprotein gene.";  
RL Biochem. Biophys. Res. Commun. 167:1184-1190 (1990).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90073664; PubMed=2590204;  
RA Uvshaeck M., Lindstrom C., Weidner H., Abrahamsson P.-A., Lilja H., Lundvall A.;  
RT "Molecular cloning of a small prostate protein, known as beta-microseminoprotein, PSP94 or beta-inhibin, and demonstration of transcripts in non-genital tissues.";  
RL Biochem. Biophys. Res. Commun. 164:1310-1315 (1989).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX TISLITE=Prostate;  
RC MEDLINE=94115955; PubMed=7506990;  
RA Liu A.Y., Brader R.C., Vessella R.L.;  
RT "Decreased expression of prostatic secretory protein PSP94 in prostate cancer.";  
RN Cancer Lett. 74:91-99 (1993).  
RN [6]

RP SEQUENC FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.  
RC TISSUE=Prostate; PubMed=7566962;  
RX MEDLINE=96032566; PubMed=7566962;  
RA Xuan J.W., Chin J.L., Guo Y., Chambers A.F., Finkelmann M.A.,  
RA Clarke M.W.;  
RT "Alternative splicing of PSP94 (prostatic secretory protein of 94  
RT amino acids) mRNA in prostate tissue.";  
RL Oncogene 11:1041-1047(1995).  
RN [17]  
RP SEQUENCE FROM N.A.  
RA Balfaj-Gupta M., Clarke M.W.;  
RT "Prostate specific protein (PSP94) expression in a human endometrial  
RT cell line (KLE).";  
RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.  
RN [8]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RX MEDLINE=42388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schler G.D.,  
RA Altschul S.F., Ziegler B., Buerow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farnet A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.U., Ushid T.B., Toshynski S., Carninci P., Pange C.,  
RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallahy S.J.,  
RA Bosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Mundy D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey U., Helton E., Kettelman M., Maan A.A., Rodrigues S., Sanchez A.,  
RA Whiting M., Maan A., Young A.C., Shevchenko T., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield J.V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [9]  
RP SEQUENCE OF 2-72 FROM N.A.  
RX MEDLINE=99421644; PubMed=10491085;  
RA Maekinen M., Valtonen-Andre C., Lundwall A.;  
RT "New world, but not old world, monkeys carry several genes encoding  
RT beta-microseminoprotein.";  
RL Eur. J. Biochem. 264:407-414(1999).  
RN [10]  
RP SEQUENCE OF 21-113.  
RX MEDLINE=85199974; PubMed=3595056;  
RA Akiyama K., Yoshida Y., Schmid K., Offner G.D., Troxler R.F.,  
RA Tenda R., Hara M.;  
RT "The amino acid sequence of human beta-microseminoprotein.";  
RL Biochim. Biophys. Acta 829:288-294(1985).  
RN [11]  
RP SEQUENCE OF 21-114.  
RX MEDLINE=85004133; PubMed=6434350;  
RA Seidah N.G., Abbatti N.J., Rochement J., Sheh A.R., Chretien M.;  
RT "Complete amino acid sequence of human seminal plasma beta-inhibin.  
RT Prediction of post-Gln-Arg cleavage as a maturation site.";  
RL FEBS Lett. 175:349-355(1984).  
RN [12]  
RP SEQUENCE OF 21-50 AND 113-114.  
RX MEDLINE=92028964; PubMed=1930232;  
RA Liang Z.G., Kamada M., Koide S.S.;  
RT "Structural identity of immunoglobulin binding factor and prostatic  
RT secretory protein of human seminal plasma.";  
RL Biochem. Biophys. Res. Commun. 180:356-359(1991).  
RN [13]  
RP SEQUENCE OF 21-41, AND TISSUE SPECIFICITY.  
RC TISSUE=Semen;  
RX MEDLINE=95401076; PubMed=7671139;  
RA Okubo T., Tada T., Ochiai Y., Ueyama H., Eimoto T., Sasaki M.;  
RT "Human seminal plasma beta-microseminoprotein: its purification,  
RT characterization, and immunohistochemical localization.";

[illegible]



Query March 100.0%; Score 268; DB 1; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 8.5e-27;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SCVFIPNEGVGSDSTRKMDLKGKHPINSEWQNDNCETCTCYET 45  
 21 SCVFIPNEGVGSDSTRKMDLKGKHPINSEWQNDNCETCTCYET 65

RESULT 2  
 MSMB\_PAPAN STANDARD; PRT; 114 AA.

AC 028767;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Beta-microseminoprotein precursor (prostate secreted seminal plasma protein) (PSP-94).  
 GN MSMB OR PSP94.  
 OS Papio anubis (Olive baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Papio.  
 OC NCBI\_TaxID=9555;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RX MEDLINE=97316893; PubMed=9174167;  
 RA Xuan J.W., Wu D., Guo Y., Garde S., Shum D.T., Mikay M., Zhong R., Chan J.L.;  
 RL "Molecular cloning and gene expression analysis of PSP94 (prostate secretory protein of 94 amino acids) in primates.";  
 RL DNA Cell Biol. 16:627-638(1997).  
 CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).  
 CC -1- SIMILARITY: Belongs to the Beta-microseminoprotein family.  
 CC  
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 CC  
 DR EMBL: U49786; AAB62726.1; -  
 DR InterPro: IPR008735; PSP94.  
 DR Pfam: PF05825; PSP94; 1.  
 KW Signal.  
 FT SIGNAL 1 20 BY SIMILARITY.  
 FT CHAIN 21 114 BETA-MICROSEMINOPROTEIN.  
 FT DISULFID 22 38 BY SIMILARITY.  
 FT DISULFID 57 93 BY SIMILARITY.  
 FT DISULFID 60 69 OR 70 (BY SIMILARITY).  
 FT DISULFID 62 70 OR 69 (BY SIMILARITY).  
 FT DISULFID 84 107 BY SIMILARITY.  
 SQ SEQUENCE 114 AA; 13013 MW; A08C837ED81F98BD CRC64;

Query March 83.6%; Score 224; DB 1; Length 114;  
 Best Local Similarity 82.2%; Pred. No. 2.8e-21;  
 Matches 37; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

1 SCVFIPNEGVGSDSTRKMDLKGKHPINSEWQNDNCETCTCYET 45  
 21 SCVFIPNEGVGSDSTRKMDLKGKHPINSEWQNDNCETCTCYET 65

RESULT 3  
 MSMB\_PAPAN STANDARD; PRT; 114 AA.  
 AC 028767;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Beta-microseminoprotein precursor (prostate secreted seminal plasma protein) (PSP-94).  
 GN MSMB OR PSP94.  
 OS Papio anubis (Olive baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Papio.  
 OC NCBI\_TaxID=9555;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RX MEDLINE=97316893; PubMed=9174167;  
 RA Xuan J.W., Wu D., Guo Y., Garde S., Shum D.T., Mikay M., Zhong R., Chan J.L.;  
 RL "Molecular cloning and gene expression analysis of PSP94 (prostate secretory protein of 94 amino acids) in primates.";  
 RL DNA Cell Biol. 16:627-638(1997).  
 CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).  
 CC -1- SIMILARITY: Belongs to the Beta-microseminoprotein family.  
 CC  
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 CC  
 DR EMBL: U49786; AAB62726.1; -  
 DR InterPro: IPR008735; PSP94.  
 DR Pfam: PF05825; PSP94; 1.  
 KW Signal.  
 FT SIGNAL 1 20 BY SIMILARITY.  
 FT CHAIN 21 114 BETA-MICROSEMINOPROTEIN.  
 FT DISULFID 22 38 BY SIMILARITY.  
 FT DISULFID 57 93 BY SIMILARITY.  
 FT DISULFID 60 69 OR 70 (BY SIMILARITY).  
 FT DISULFID 62 70 OR 69 (BY SIMILARITY).  
 FT DISULFID 84 107 BY SIMILARITY.  
 SQ SEQUENCE 114 AA; 13013 MW; A08C837ED81F98BD CRC64;

DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Beta-microseminoprotein precursor (prostate secreted seminal plasma protein) (PSP-94).  
 GN MSMB.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.  
 OC NCBI\_TaxID=9544;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=91274357; PubMed=2054385;  
 RA Noler S., Mikay M., Chretien M.;  
 RL "Prostatic secretory protein PSP94: gene organization and promoter sequence in rhesus monkey and human.";  
 RL Biochim. Biophys. Acta 1089:247-249(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91244325; PubMed=2037304;  
 RA Noler S., St Louis D., Mikay M., Chretien M.;  
 RL "Rapid evolution of prostatic protein PSP94 suggested by sequence divergence between rhesus monkey and human cDNAs.";  
 RL Genomics 9:775-777(1991).  
 CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).  
 CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.  
 CC  
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 CC  
 DR EMBL: X57932; CAA41003.1; -  
 DR EMBL: X57933; CAA41003.1; JOINED.  
 DR EMBL: X57934; CAA41003.1; JOINED.  
 DR EMBL: X57935; CAA41003.1; JOINED.  
 DR EMBL: M92161; AAA56903.1; -  
 DR PIR: S16237; A54663.  
 DR InterPro: IPR008735; PSP94.  
 DR Pfam: PF05825; PSP94; 1.  
 KW Signal.  
 FT SIGNAL 1 20 BY SIMILARITY.  
 FT CHAIN 21 114 BETA-MICROSEMINOPROTEIN.  
 FT DISULFID 22 38 BY SIMILARITY.  
 FT DISULFID 57 93 BY SIMILARITY.  
 FT DISULFID 60 69 OR 70 (BY SIMILARITY).  
 FT DISULFID 62 70 OR 69 (BY SIMILARITY).  
 FT DISULFID 84 107 BY SIMILARITY.  
 SQ SEQUENCE 114 AA; 13079 MW; C074AB9948276C CRC64;

Query March 81.3%; Score 218; DB 1; Length 114;  
 Best Local Similarity 80.0%; Pred. No. 1.6e-20;  
 Matches 36; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

1 SCVFIPNEGVGSDSTRKMDLKGKHPINSEWQNDNCETCTCYET 45  
 21 SCVFIPNEGVGSDSTRKMDLKGKHPINSEWQNDNCETCTCYET 65

RESULT 4  
 MSMB\_PAPAN STANDARD; PRT; 114 AA.  
 AC 028767;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Beta-microseminoprotein precursor (prostate secreted seminal plasma protein) (PSP-94).  
 GN MSMB OR PSP94.  
 OS Papio anubis (Olive baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Papio.  
 OC NCBI\_TaxID=9555;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RX MEDLINE=97316893; PubMed=9174167;  
 RA Xuan J.W., Wu D., Guo Y., Garde S., Shum D.T., Mikay M., Zhong R., Chan J.L.;  
 RL "Molecular cloning and gene expression analysis of PSP94 (prostate secretory protein of 94 amino acids) in primates.";  
 RL DNA Cell Biol. 16:627-638(1997).  
 CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).  
 CC -1- SIMILARITY: Belongs to the Beta-microseminoprotein family.  
 CC  
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 CC  
 DR EMBL: U49786; AAB62726.1; -  
 DR InterPro: IPR008735; PSP94.  
 DR Pfam: PF05825; PSP94; 1.  
 KW Signal.  
 FT SIGNAL 1 20 BY SIMILARITY.  
 FT CHAIN 21 114 BETA-MICROSEMINOPROTEIN.  
 FT DISULFID 22 38 BY SIMILARITY.  
 FT DISULFID 57 93 BY SIMILARITY.  
 FT DISULFID 60 69 OR 70 (BY SIMILARITY).  
 FT DISULFID 62 70 OR 69 (BY SIMILARITY).  
 FT DISULFID 84 107 BY SIMILARITY.  
 SQ SEQUENCE 114 AA; 13013 MW; A08C837ED81F98BD CRC64;

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DE Beta-microseminoprotein J1 precursor (msp-j1).
GN MSPJ.
OS Saginus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99421644; PubMed=10491085;
RX Maekinen M., Valtonen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
beta-microseminoprotein."
RL Eur. J. Biochem. 264:407-414(1999).
CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ010155; CAB38123.1; -.
DR EMBL; AJ010156; CAB38123.1; JOINED.
DR GO; GO:0005576; C:extracellular; NAS.
DR InterPro; IPR008735; PSP94.
DR Pfam; PF05825; PSP94; 1.
DR Signal.
KW SIGNAL.
FT CHAIN 1 20 POTENTIAL.
FT SIGNAL 21 114 BETA-MICROSEMINOPROTEIN J1.
FT DISULFID 22 38 BY SIMILARITY.
FT DISULFID 57 93 BY SIMILARITY.
FT DISULFID 60 69 OR 70 (BY SIMILARITY).
FT DISULFID 62 70 OR 69 (BY SIMILARITY).
FT DISULFID 84 107 BY SIMILARITY.
SQ SEQUENCE 114 AA; 12746 MW; F3F05B013445BADA CXC64;

Query Match 72.8%; Score 195; DB 1; Length 114;
Best Local Similarity 70.5%; Freq. No. 1.2e-17;
Matches 31; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

OY 1 SCYFIPEGVPGDSTRKCMIDLKGNKHPINSEWQDNCECTCYE 44
DB 21 SCYILNDMIPGDSINECTDLKGNKHPINSKRIRDNDSCTCRE 64

RESULT 5
MSPA_SAGOE STANDARD; PRT; 112 AA.
AC 097936;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-microseminoprotein A1 precursor (msp-A1) (Fragment).
GN MSPA.
OS Saginus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99421644; PubMed=10491085;
RX Maekinen M., Valtonen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
beta-microseminoprotein."
RL Eur. J. Biochem. 264:407-414(1999).
CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
similarity).

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CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ010158; CAB38124.1; -.
DR EMBL; AJ010159; CAB38124.1; JOINED.
DR GO; GO:0005576; C:extracellular; TAS.
DR InterPro; IPR002400; GP_Cysknob.
DR InterPro; IPR008735; PSP94.
DR Pfam; PF05825; PSP94; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR SIGNAL.
KW SIGNAL.
FT CHAIN 1 19 BY SIMILARITY.
FT SIGNAL 20 112 BETA-MICROSEMINOPROTEIN A1.
FT DISULFID 21 37 BY SIMILARITY.
FT DISULFID 56 92 BY SIMILARITY.
FT DISULFID 59 68 OR 69 (BY SIMILARITY).
FT DISULFID 61 69 OR 68 (BY SIMILARITY).
FT DISULFID 83 106 BY SIMILARITY.
SQ SEQUENCE 112 AA; 12631 MW; DDA06BF0C5CD78B CXC64;

Query Match 70.9%; Score 190; DB 1; Length 112;
Best Local Similarity 65.9%; Freq. No. 4.9e-17;
Matches 29; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

OY 1 SCYFIPEGVPGDSTRKCMIDLKGNKHPINSEWQDNCECTCYE 44
DB 20 SCYILNDMIPGDSINECTDLKGNKHPINSKRIRDNDSCTCRE 63

RESULT 6
MSPA_SAGOE STANDARD; PRT; 114 AA.
AC 097935;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-microseminoprotein E1 precursor (msp-E1).
GN MSPA.
OS Saginus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99421644; PubMed=10491085;
RX Maekinen M., Valtonen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
beta-microseminoprotein."
RL Eur. J. Biochem. 264:407-414(1999).
CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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CC -----
DR EMBL; AJ010154; CAB38105.1; -.
DR GO; GO:0005576; C:extracellular; TAS.

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DR InterPro: IPR008735; PSP94.  
 DR Pfam: PF05825; PSP94; 1.  
 FT SIGNAL.  
 FT CHAIN 1 20 POTENTIAL.  
 FT DISULFID 21 114 BETA-MICROSEMINOPROTEIN E1.  
 FT DISULFID 22 38 BY SIMILARITY.  
 FT DISULFID 57 93 BY SIMILARITY.  
 FT DISULFID 60 69 OR 70 (BY SIMILARITY).  
 FT DISULFID 62 70 OR 69 (BY SIMILARITY).  
 FT DISULFID 84 107 BY SIMILARITY.  
 SQ SEQUENCE 114 AA; 12738 MW; 05E7A410125C94B2 CRC64;  
 Query Match 57.5%; Score 154; DB 1; Length 114;  
 Best Local Similarity 54.8%; Pred. No. 1.6e-12;  
 Matches 23; Conservative 11; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 SCYFIPNEGVPGDSTRKCMIDKGNKHPINSEWQDNCETCTC 42  
 Db 21 SCYVIRKIVPGETIKECTDLKGNKHPIDSRWRTEDELCAC 62  
 RESULT 7  
 MSMB\_PIG STANDARD; PRT; 111 AA.  
 ID MSMB\_PIG  
 AC 002826;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94) (T5507).  
 GN MSMB OR PSP94.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID:9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96117078; PubMed=8562060;  
 RA Tanaka T., Itahana K., Andoh N., Takeya T., Sato E.;  
 RT "Expression of prostatic secretory protein (PSP)-like protein in porcine corpus luteum: isolation and characterization of a new gene encoding PSP94-like protein."  
 RT Mol. Reprod. Dev. 42:149-156(1995).  
 RL [2]  
 RN SEQUENCE OF 21-111.  
 RP TISSUE=Seminal plasma;  
 RX MEDLINE=9416159; PubMed=8117114;  
 RA Fernlund P., Granberg L.B., Roepstorff P.;  
 RT "Amino acid sequence of beta-microseminoprotein from porcine seminal plasma."  
 RL Arch. Biochem. Biophys. 309:70-76(1994).  
 CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).  
 CC -1- TISSUE SPECIFICITY: CORPORA LUTEA, MOSTLY IN THE LUTEAL CELLS SURROUNDING BLOOD VESSELS.  
 CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.  
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 CC EMBL: S80724; AAB50711.1;  
 DR InterPro: IPR008735; PSP94.  
 DR Pfam: PF05825; PSP94; 1.  
 KW Signal. Pyroliadone carboxylic acid.  
 FT SIGNAL 1 20  
 FT CHAIN 21 111 BETA-MICROSEMINOPROTEIN.  
 FT DISULFID 22 35 BY SIMILARITY.

FT DISULFID 54 90 BY SIMILARITY.  
 FT DISULFID 57 66 OR 67 (BY SIMILARITY).  
 FT DISULFID 59 67 OR 66 (BY SIMILARITY).  
 FT DISULFID 81 104 BY SIMILARITY.  
 FT MOD RES 21 21 PYROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 111 AA; 12246 MW; ABR33A067A23765E CRC64;  
 Query Match 50.6%; Score 135.5; DB 1; Length 111;  
 Best Local Similarity 53.7%; Pred. No. 3.3e-10;  
 Matches 22; Conservative 6; Mismatches 10; Indels 3; Gaps 1;  
 QY 2 CYFIPNEGVPGDSTRKCMIDKGNKHPINSEWQDNCETCTC 42  
 Db 22 CYFIPNQL---KPNCCQLKGVSHPLNSVWTKNCEBCTC 59  
 RESULT 8  
 MSMB\_RAT STANDARD; PRT; 113 AA.  
 ID MSMB\_RAT  
 AC P97580;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94).  
 GN MSMB OR PSP94.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID:10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Prostate;  
 RX MEDLINE=96434955; PubMed=8837741;  
 RA Fernlund P., Granberg L.B., Larsson I.;  
 RT "Cloning of beta-microseminoprotein of the rat: a rapidly evolving mucosal surface protein."  
 RL Arch. Biochem. Biophys. 334:73-82(1996).  
 CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface. PRESENT IN THE SECRETIONS OF THE AIRWAYS, THE GASTROINTESTINAL AND THE UROGENITAL TRACTS.  
 CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.  
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 CC EMBL: U65486; AAB19102.1;  
 DR InterPro: IPR009041; PWD\_inhibitor.  
 DR InterPro: IPR008735; PSP94.  
 DR Pfam: PF05825; PSP94; 1.  
 KW Signal.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 113 BETA-MICROSEMINOPROTEIN.  
 FT DISULFID 22 38 BY SIMILARITY.  
 FT DISULFID 56 92 BY SIMILARITY.  
 FT DISULFID 59 68 OR 69 (BY SIMILARITY).  
 FT DISULFID 61 69 OR 68 (BY SIMILARITY).  
 FT DISULFID 83 106 BY SIMILARITY.  
 SQ SEQUENCE 113 AA; 12750 MW; 060246793AFA24B31 CRC64;  
 Query Match 33.8%; Score 90.5; DB 1; Length 113;  
 Best Local Similarity 41.7%; Pred. No. 0.00015;  
 Matches 15; Conservative 8; Mismatches 12; Indels 1; Gaps 1;  
 QY 10 VPGDSTRKCMIDKGNKHPINSEWQDNCETCTC 45

Db 30 LPNKSDECTVDGKHYLNTYMO-KNCEMCFCEKT 64

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RESULT 9
MSMB_MOUSE STANDARD; PRT; 113 AA.
ID MSMB_MOUSE 008540;
AC 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma
protein) (prostate secretory protein PSP94) (PSP-94).
GN MSMB OR PSP94.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1;
RA Xuan J.W., McKay M., Wu D., Guo Y., Chin J.L.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
similarity).
CC -! SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -! SIMILARITY: Belongs to the beta-microseminoprotein family.
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CC -----
CC DR EMBL; U99840; AAB49583.1; -.
CC DR MGI; MGI:97166; Msmb.
CC DR InterPro; IPR008735; PSP94.
CC DR Pfam; PF05825; PSP94; 1.
CC KW Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 113 BETA-MICROSEMINOPROTEIN.
FT DISULFID 22 38 BY SIMILARITY.
FT DISULFID 56 92 BY SIMILARITY.
FT DISULFID 59 68 OR 69 (BY SIMILARITY).
FT DISULFID 61 69 OR 68 (BY SIMILARITY).
FT DISULFID 83 106 BY SIMILARITY.
SQ SEQUENCE 113 AA; 12844 MW; 892DAD4BFE49379 CRC64;

Query Match 32.6%; Score 87.5; DB 1; Length 113;
Best Local Similarity 38.6%; Pred. No. 0.00035;
Matches 17; Conservative 6; Mismatches 20; Indels 1; Gaps 1;
QY 2 CYFINEGVPGDSTKCMDLKGNKHPINSEMOCTNCECTCYET 45
Db 22 CSENRELFPMQMSDDCMADONKRFHFNTPWK-KNCTWCSCDKT 64

RESULT 10
VWF_PIG STANDARD; PRT; 2482 AA.
ID VWF_PIG 028533;
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Von Willebrand factor precursor (VWF) (Fragment).
GN VWF OR P8VWF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]

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RP SEQUENCE FROM N.A.
RA Seaman W.T., Read M.S., Bellinger D.A., Nichols T.C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 397-553 FROM N.A.
RX MEDLINE=93356762; PubMed=8352759;
RA Laverne J.M., Piao Y.C., Ferreira V., Kerbiriou-Nabias D.,
RA Bahak B.R., Meyer D.;
RT "Primary structure of the factor VIII binding domain of human, porcine
and rabbit von Willebrand factor";
RL Biochem. Biophys. Res. Commun. 194:1019-1024 (1993).
CC -! FUNCTION: Important in the maintenance of homeostasis, it
participates in platelet-vessel wall interactions by forming a
noncovalent complex with coagulation factor VIII at the site of
vascular injury (By similarity).
CC -! SUBUNIT: Multimeric (By similarity).
CC -! PTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR
INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).
CC -! SIMILARITY: Contains 3 VWF domains.
CC -! SIMILARITY: Contains 1 C-terminal cysteine knot-like (CTCK) domain.
CC -! SIMILARITY: SOME TO SILKORM HEMOCYTIN.
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CC -----
CC DR EMBL; AF052036; AAC06229.1; -.
CC DR EMBL; S64541; AAB27829.2; -.
CC DR PIR; PNO563; PNO563.
CC DR HSSP; P04275; IATZ.
CC DR InterPro; IPR006207; Cys_knot.
CC DR InterPro; IPR006207; Cys_knot_C.
CC DR InterPro; IPR009041; PMF_inhibitor.
CC DR InterPro; IPR002919; TIL_Cystich.
CC DR InterPro; IPR002035; VWF_A.
CC DR InterPro; IPR001007; VWF_C.
CC DR InterPro; IPR001846; VWF_D.
CC DR Pfam; PF00007; Cys_knot; 1.
CC DR Pfam; PF01826; TIL; 3.
CC DR Pfam; PF00082; Vwf; 3.
CC DR Pfam; PF00093; Vwf; 3.
CC DR Pfam; PF00094; Vwf; 3.
CC DR PRINTS; PR00453; VWFADOMAIN.
CC DR SMART; SM00041; CT; 1.
CC DR SMART; SM00327; VWA; 3.
CC DR SMART; SM00214; VWC; 5.
CC DR SMART; SM00216; VWD; 3.
CC DR PROSITE; PS01185; CTCK_1; 1.
CC DR PROSITE; PS01225; CTCK_2; 1.
CC DR PROSITE; PS0234; VWF_A; 3.
CC DR PROSITE; PS01208; VWF_C; 1; 3.
CC DR PROSITE; PS0184; VWF_D; 3.
CC KW Blood coagulation; platelet; Glycoprotein; Extracellular matrix;
KW Plasma; Hemostasis; Repeat; Cell adhesion.
FT PROPEP 1 1 NON TER.
FT CHAIN 438 2482 BY SIMILARITY.
FT DOMAIN 62 215 VON WILLEBRAND FACTOR.
FT DOMAIN 438 461 VWF 2.
FT DOMAIN 462 507 AMINO-TERMINAL.
FT DOMAIN 500 527 E1.
FT DOMAIN 541 687 VWF 3.
FT DOMAIN 947 1127 VWF 1.
FT DOMAIN 1167 1334 VWF 2.
FT DOMAIN 1360 1540 VWF 3.
FT DOMAIN 1619 1771 VWF 4.
FT DOMAIN 1885 1930 E2.
FT DOMAIN 1924 1997 VWF 1.

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FT DOMAIN 2098 2164 VMFC 2.
FT DOMAIN 2249 2314 VMFC 3.
FT DOMAIN 2393 2481 CTCK.
FT SITE 2176 2178 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 441 482 BY SIMILARITY.
FT DISULFID 450 478 BY SIMILARITY.
FT DISULFID 484 495 BY SIMILARITY.
FT DISULFID 541 670 BY SIMILARITY.
FT DISULFID 563 705 BY SIMILARITY.
FT DISULFID 572 667 BY SIMILARITY.
FT DISULFID 588 595 BY SIMILARITY.
FT DISULFID 734 758 BY SIMILARITY.
FT DISULFID 745 785 BY SIMILARITY.
FT DISULFID 763 765 BY SIMILARITY.
FT DISULFID 827 839 BY SIMILARITY.
FT DISULFID 823 843 BY SIMILARITY.
FT DISULFID 800 804 BY SIMILARITY.
FT DISULFID 870 873 BY SIMILARITY.
FT DISULFID 908 911 BY SIMILARITY.
FT DISULFID 942 1128 BY SIMILARITY.
FT DISULFID 1338 1339 BY SIMILARITY.
FT DISULFID 1335 1541 BY SIMILARITY.
FT DISULFID 1548 1573 BY SIMILARITY.
FT DISULFID 1568 1609 OR 1611 (BY SIMILARITY).
FT DISULFID 1641 1792 BY SIMILARITY.
FT DISULFID 1619 1754 BY SIMILARITY.
FT DISULFID 1596 1757 BY SIMILARITY.
FT DISULFID 1662 1670 BY SIMILARITY.
FT DISULFID 2393 2443 BY SIMILARITY.
FT DISULFID 2408 2457 BY SIMILARITY.
FT DISULFID 2419 2473 BY SIMILARITY.
FT DISULFID 2423 2475 BY SIMILARITY.
FT DISULFID 2423 2475 BY SIMILARITY.
FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 905 905 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1184 1184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1243 1243 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1640 1640 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1892 1892 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1959 1959 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2026 2026 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2069 2069 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2215 2215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2254 2254 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2459 2459 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 2482 AA; 272394 MW; D499B7DDFBBCAEDD CXC64;

Query Match 27.2%; Score 73; DB 1; Length 2482;
Best Local Similarity 29.3%; Pred. No. 0.62;
Matches 17; Conservative 8; Mismatches 17; Indels 16; Gaps 2;

QY 1 SCYFIPNEG-----VPGDSTRKMDLGNKPKPISENQOTN--CECTC 42
DB 1895 SCGDHPSBEGCFPPHVMGLSSCVBACICQVDDGIRHQLFETWVPHQPCQICTC 1952

RESULT 11
ZAN HUMAN STANDARD; PRT; 2812 AA.
AC Q9Y493; 090218; 096185; 096186; 096187; 096189; 096190;
AC Q9BXN9; 09B283; 09B284; 09B285; 09B286; 09B287; 09B288;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Zonadhesin precursor.
GN ZAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catartini; Hominoidea; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).
RC TISSUE=Testis;

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RA Cheung T.L., Massler M.J., Cornwall G.A., Hardy D.M.;
RT "Multiple intra-species variants of human zonadhesin."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=99018118; PubMed=9799793;
RA Glockner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,
RA Tsui L.-C., Rosenthal A.;
RT "Large-scale sequencing of two regions in human chromosome 7q22:
RT analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci
RT reveals 17 genes."
RL Genome Res. 8:1060-1073(1998).
RN [3]
RP SEQUENCE OF 1810-2812 FROM N.A. (ISOFORM 1).
RX MEDLINE=21138439; PubMed=11239002;
RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RA Waller W., Koop B.F.;
RT "Comparative analysis of the gene-dense ACHE/TFR2 region on human
RT chromosome 7q22 with the orthologous region on mouse chromosome 5."
RL Nucleic Acids Res. 29:1352-1365(2001).
RN [4]
RP SEQUENCE OF 2375-2683 FROM N.A. (ISOFORM 7).
RC TISSUE=Testis;
RX MEDLINE=97271566; PubMed=9126492;
RA Gao Z., Hartung T., Garders D.L.;
RT "Chromosome localization of the mouse zonadhesin gene and the human
RT zonadhesin gene (ZAN)."
RL Genomics 41:119-122(1997).
RN [5]
RP FUNCTION: Birds in a species-specific manner to the zona pellucida
of the egg. May be involved in gamete recognition and/or
signaling.
CC - SUBUNIT: Probably forms covalent oligomers.
CC - SUBCELLULAR LOCATION: Type I membrane protein, exclusively on the
apical region of the sperm head (By similarity).
CC - ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=7;
CC Name=3;
CC IsoId=Q9Y493-1; Sequence=Displayed;
CC Name=1;
CC IsoId=Q9Y493-2; Sequence=VSP_001430, VSP_001431;
CC Name=2;
CC IsoId=Q9Y493-3; Sequence=VSP_001428, VSP_001429;
CC Name=4;
CC IsoId=Q9Y493-4; Sequence=VSP_001424, VSP_001425;
CC Name=5;
CC IsoId=Q9Y493-5; Sequence=VSP_001420, VSP_001421;
CC Name=6;
CC IsoId=Q9Y493-6; Sequence=VSP_001422, VSP_001423;
CC Name=7;
CC IsoId=Q9Y493-7; Sequence=VSP_001426, VSP_001427.
CC - TISSUE SPECIFICITY: In testis, primarily in haploid spermatis.
CC - DOMAIN: The NAM domains probably mediate sperm adhesion to the
zona pellucida.
CC - DOMAIN: During sperm migration through the reproductive tracts,
the mucin-like domain might inhibit inappropriate trapping of
spermatozoa or promoting adhesion to the oviductal isthmus.
CC - DOMAIN: The VMFD domain 2 may mediate covalent oligomerization (by
similarity to human intestinal mucin MUC2).
CC - SIMILARITY: Contains 3 NAM domains.
CC - SIMILARITY: Contains 1 EGF-like domain.
CC - CAUTION: Ref.2 sequence differs from that shown due to
transposition of a number of exons.
CC -----
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EMBL; M59850; NOT\_ANNOTATED\_CDS.  
Lectin; Transmembrane; Glycoprotein.  
FT TRANSMEM 1210 1235 POTENTIAL.  
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 218 218 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 361 361 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 452 452 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 643 643 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 874 874 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 976 976 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1122 1122 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1187 1187 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1197 1197 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARIANT 441 441 R -> K N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 1276 AA; 143239 MW; A6B90F11DC25B4 CRC64;

Query Match 25.0%; Score 67; DB 1; Length 1276;  
Best Local Similarity 31.7%; Pred. No. 1.7;  
Matches 13; Conservative 6; Mismatches 10; Indels 12; Gaps 1;

17 KQMDLKNKHPINSEMOYD-----CETCCYCT 45  
Db 1084 KQVESKSGDKITHKWEIDERSNANPKPNPCETACNQT 1124

RESULT 13  
ZAN\_PIG STANDARD; PRT; 2476 AA.  
AC Q28583;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Zonadhesin precursor.  
GN ZAN.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 823-830; 859-872; 883-890;  
RP 920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656;  
RP 1658-1667; 1777-1785 AND 1914-1921.  
RC SIRAIN-Weistman; TISSUE=Testis;  
RA MEDLINE=96064658; PubMed=7592795;  
RX Hardy D.M., Garbers D.L.;  
RT "A sperm membrane protein that binds in a species-specific manner to the egg extracellular matrix is homologous to von Willbrand factor".  
RL J. Biol. Chem. 270:26025-26028(1995).  
RT FUNCTION: Binds in a species-specific manner to the zona pellucida of the egg. May be involved in gamete recognition and/or signaling.  
CC -1- SUBUNIT: Probably forms covalent oligomers.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein, exclusively on the apical region of the sperm head (by similarity).  
CC -1- TISSUE SPECIFICITY: In testis, primarily in haploid spermatis.  
CC -1- Not in lung, liver, heart, spleen, brain, kidney, epididymis.  
CC -1- DOMAIN: The MAM domains probably mediate sperm adhesion to the zona pellucida.  
CC -1- DOMAIN: During sperm migration through the reproductive tracts,

the mucin-like domain might inhibit inappropriate trapping of spermatozoa or promoting adhesion to the oviductal isthmus.  
CC -1- DOMAIN: The VWFD domains 2 and 3 may mediate covalent oligomerization (By similarity to human intestinal mucin MUC3).  
CC -1- PTM: THE MAM DOMAINS AND THE MUCIN-LIKE DOMAINS ARE MISSING FROM THE ZONADHESIN THAT BINDS TO THE EGG EXTRACELLULAR MATRIX. PROCESSING MIGHT OCCUR DURING SPERM MATURATION AND/OR CAPACITATION.  
CC -1- SIMILARITY: Contains 2 MAM domains.  
CC -1- SIMILARITY: Contains 5 VWFD domains.  
CC -1- SIMILARITY: Contains 1 EGF-like domain.  
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EMBL; U40024; AAC48486.1; -  
DR PIR; T34022; T34022.  
DR HSP; P56682; 1CCV.  
DR InterPro; IPR006209; EGF\_1ike.  
DR InterPro; IPR006998; MAM\_domain.  
DR InterPro; IPR002919; TIL\_Cysrich.  
DR InterPro; IPR003328; TIF\_Cysrich.  
DR InterPro; IPR001007; VWF\_C.  
DR InterPro; IPR001846; VWF\_D.  
DR Pfam; PF00008; EGF\_1.  
DR Pfam; PF00629; MAM; 2.  
DR Pfam; PF01826; TIL; 5.  
DR Pfam; PF02345; TIF; 5.  
DR Pfam; PF00094; vwd; 4.  
DR SMART; SM00137; MAM; 1.  
DR SMART; SM00214; VWC; 2.  
DR SMART; SM00216; VWD; 4.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS50026; EGF\_3; 1.  
DR PROSITE; PS00740; MAM\_1; 1.  
DR PROSITE; PS50060; MAM\_2; 2.  
KW Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion; Repeat.  
FT SIGNAL 1 29  
FT CHAIN 30 2476  
FT DOMAIN 30 2418 ZONADHESIN.  
FT TRANSMEM 2419 2439 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 2440 2476 POTENTIAL.  
FT DOMAIN 31 144 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 147 312 MAM 1.  
FT DOMAIN 319 667 MAM 2.  
FT DOMAIN 668 799 53 X HEPTAPEPTIDE REPEATS (APPROXIMATE)  
FT DOMAIN 800 1184 (MUCIN-LIKE DOMAIN).  
FT DOMAIN 1185 1573 VWFD 1 (PARTIAL).  
FT DOMAIN 1574 1968 VWFD 2.  
FT DOMAIN 1969 2370 VWFD 3.  
FT DOMAIN 2371 2381 VWFD 4.  
FT DISULFID 2372 2390 VWFD 5.  
FT DISULFID 2392 2401 BY SIMILARITY.  
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 735 735 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 758 758 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 833 833 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 858 858 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1154 1154 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1329 1329 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1448 1448 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1544 1544 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1596 1596 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1654 1654 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1843 1843 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1965 1965 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2122 2122 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2165 2165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2178 2178 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2329 2329 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2359 2359 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 823 823 C -> V (IN REF. 1; AA SEQUENCE).  
 FT CONFLICT 923 923 S -> Y (IN REF. 1; AA SEQUENCE).  
 FT CONFLICT 965 965 W -> Y (IN REF. 1; AA SEQUENCE).  
 FT CONFLICT 1241 1241 S -> X (IN REF. 1; AA SEQUENCE).  
 SQ SEQUENCE 2476 AA; 270364 MW; A13B690375A6548C CRC64;

Query Match 25.0%; Score 67; DB 1; Length 2476;  
 Best Local Similarity 40.7%; Pred. No. 3.5;  
 Matches 11; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

QY 18 CMDLKGKHPINSEWQTDN--CETCTC 42  
 Db 1513 CTTORGSHYHVGESWYTDNCSRLCTC 1539

RESULT 14  
 SL17\_ENTH1 STANDARD; PRT; 1285 AA.

AC P23502;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE 170 kDa surface lectin precursor.  
 GN CEL-170/4.  
 OS Entamoeba histolytica.  
 OC Eukaryota; Entamoebidae; Entamoeba.  
 OX NCBI\_Taxid=5759;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 16-33.  
 RX MEDLINE=91156704; PubMed=2003392.  
 RA Tannich E., Ebert F., Horstmann R.D.;  
 RT "Primary structure of the 170-kDa surface lectin of pathogenic  
 RT Entamoeba histolytica.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:1849-1853(1991).  
 RN [2]  
 RP REVISIONS TO N-TERMINUS.  
 RA Tannich E., Nickel R., Ebert F., Horstmann R.D.;  
 RL Submitted (Aug-1991) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 16-30.  
 RX MEDLINE=89123408; PubMed=2536731;  
 RA Pectri W.A. Jr., Chapman M.D., Snodgrass T., Mann B.J., Broman J.,  
 RA Ravdin J.I.;  
 RT "Subunit structure of the galactose and N-acetyl-D-galactosamine-  
 RT inhibitable adherence lectin of Entamoeba histolytica";  
 RL J. Biol. Chem. 264:3007-3012(1989).  
 CC -1- FUNCTION: Mediates adherence of E. histolytica to colonic mucins,  
 CC an essential step for pathogenic tissue invasion.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- PTM: phosphorylated regions may have a role in signal  
 CC transduction.

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CC EMBL; M60498; AAA29106.1; -  
 DR EMBL; X61003; CAA43321.1; -  
 KW Signal: Lectin; Transmembrane; Repeat; Glycoprotein;  
 KW Phosphorylation.  
 FT SIGNAL 1 15  
 FT CHAIN 16 1285 170 kDa SURFACE LECTIN.

FT DOMAIN 16 1218 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1219 1247 POTENTIAL.  
 FT DOMAIN 1248 1285 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 378 1208 CYS-RICH.  
 FT DOMAIN 378 653 9 X APPROXIMATE TANDEM REPEATS.  
 FT REPEAT 378 407 1.  
 FT REPEAT 408 438 2.  
 FT REPEAT 439 464 3.  
 FT REPEAT 465 497 4.  
 FT REPEAT 498 525 5.  
 FT REPEAT 526 554 6.  
 FT REPEAT 555 584 7.  
 FT REPEAT 585 620 8.  
 FT REPEAT 621 653 9.  
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 651 651 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 882 882 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1196 1196 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1205 1205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 16 16 D -> G (IN REF. 3).  
 SQ SEQUENCE 1285 AA; 144410 MW; 64BB2DFD2AD8ECBA CRC64;

Query Match 24.6%; Score 66; DB 1; Length 1285;  
 Best Local Similarity 31.7%; Pred. No. 2.3; Mismatches 10; Indels 12; Gaps 1;  
 Matches 13; Conservative 6;

QY 17 KCMDLKGKHPINSEWQTDN-----CETCTCYET 45  
 Db 1092 KVESKSGDKTKTHMEIDTERSNIIDPKRPNCETATCDQT 1132

RESULT 15  
 VWF\_HUMAN STANDARD; PRT; 2813 AA.  
 ID VWF\_HUMAN  
 AC P04275;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Von Willebrand factor precursor (VWF).  
 GN VWF OR F8VWF.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=90062044; PubMed=2584182;  
 RA Mancuso D.J., Tukey E.A., Westfield L.A., Worral N.K.,  
 RA Shelton-Inioes B.B., Sorace J.M., Alevy Y.G., Sadler J.E.;  
 RT "Structure of the gene for human von Willebrand factor.";  
 RL J. Biol. Chem. 264:19514-19527(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=87016349; PubMed=3489923;  
 RA Bonthron D., Orr E.C., Mitsuoka L.M., Ginsburg D., Handin R.I.,  
 RA Orkin S.H.;  
 RT "Nucleotide sequence of pre-pro von Willebrand factor cDNA.";  
 RL Nucleic Acids Res. 14:7125-7128(1986).  
 RN [3]

CC SEQUENCE OF 1-120 FROM N.A., AND SEQUENCE OF 23-56.  
 CC TISSUE=Umbilical vein endothelial cells;  
 CC MEDLINE=87213253; PubMed=3495266;  
 RX Shelton-Inioes B.B., Broze G.J. Jr., Miletich J.P., Sadler J.E.;  
 RT "Evolution of human von Willebrand factor: cDNA sequence  
 RT polymorphisms, repeated domains, and relationship to von Willebrand  
 RT antigen II.";  
 RL Biochem. Biophys. Res. Commun. 144:657-665(1987).  
 RN [4]  
 RP SEQUENCE OF 1-1400 FROM N.A.



RX MEDLINE=87004550; PubMed=3019665;  
RA Verweij C.L., Diergaarde P.J., Hart M., Pannekoek H.;  
RT "Full-length von Willebrand factor (vWF) cDNA encodes a highly  
RT repetitive protein considerably larger than the mature vWF subunit.";  
RL EMO J. 5:1839-1847(1986).  
RN [5]  
RP ERDATUM.  
RA Verweij C.L., Diergaarde P.J., Hart M., Pannekoek H.;  
RL EMO J. 5:3074-3074(1986).  
RN [6]  
RP SEQUENCE OF 764-2813.  
RA Titani K., Kumar S., Takio K., Ericsson L.H., Wade R.D., Ashida K.,  
RA Walsh K.A., Choque M.W., Sadler J.E., Fujikawa K.;  
RT "Amino acid sequence of human von Willebrand factor.";  
RL Biochemistry 25:3171-3184(1986).  
RN [7]  
RP SEQUENCE OF 761-1424 FROM N.A.  
RA MEDLINE=86269894; PubMed=3524673;  
RA Titani K., Kumar S., Takio K., Ericsson L.H., Wade R.D., Ashida K.,  
RA Walsh K.A., Choque M.W., Sadler J.E., Fujikawa K.;  
RT "Amino acid sequence of human von Willebrand factor.";  
RL Biochemistry 25:3171-3184(1986).  
RN [8]  
RP SEQUENCE OF 764-873 AND 1289-2813 FROM N.A.  
RA MEDLINE=86016708; PubMed=2864688;  
RA Sadler J.E., Shelton-Inloes B.B., Sorace J.M., Harlan J.M.,  
RA Titani K., Davie E.W.;  
RT "Cloning and characterization of two cDNAs coding for human von  
RT Willebrand factor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:6394-6398(1985).  
RN [9]  
RP SEQUENCE OF 990-1947 FROM N.A.  
RA MEDLINE=91105089; PubMed=1988024;  
RA Mancuso D.J., Tuley E.A., Westfield L.A., Lester-Mancuso T.L.,  
RA Le Beau M., Sorace J.M., Sadler J.E.;  
RT "Human von Willebrand factor gene and pseudogene: structural analysis  
RT and differentiation by polymerase chain reaction.";  
RL Biochemistry 30:253-269(1991).  
RN [10]  
RP SEQUENCE OF 2731-2813 FROM N.A.  
RA MEDLINE=85269603; PubMed=3875078;  
RA Verweij C.L., de Vries C.J.M., Distel B., van Zonneveld A.-J.,  
RA Gaurs van Kessel A., van Mourik J.A., Pannekoek H.;  
RT "Construction of cDNA coding for human von Willebrand factor using  
RT antibody probes for colony-screening and mapping of the chromosomal  
RT gene.";  
RL Nucleic Acids Res. 13:4699-4717(1985).  
RN [11]  
RP SEQUENCE OF 1-177 FROM N.A.  
RA MEDLINE=8811704; PubMed=2828057;  
RA Bonthron D., Orlin S.H.;  
RT "The human von Willebrand factor gene. Structure of the 5' region.";  
RL Eur. J. Biochem. 171:51-57(1988).  
RN [12]  
RP SEQUENCE OF 2621-2813 FROM N.A.  
RA MEDLINE=85244588; PubMed=3874428;  
RA Ginsburg D., Handin R.I., Bonthron D.T., Donlon T.A., Bruns G.A.P.,  
RA Latt S.A., Orlin S.H.;  
RT "Human von Willebrand factor (vWF): isolation of complementary DNA  
RT (cDNA) clones and chromosomal localization.";  
RL Science 228:1401-1406(1985).  
RN [13]  
RP SEQUENCE OF 2731-2813 FROM N.A.  
RA MEDLINE=85201687; PubMed=3873280;  
RA Lynch D.C., Zimmerman T.S., Collins C.J., Brown M., Morin M.J.,  
RA Ling B.H., Livingston D.M.;  
RT "Molecular cloning of cDNA for human von Willebrand factor:  
RT authentication by a new method.";  
RL Cell 41:49-56(1985).  
RN [14]  
RP REVISIONS.  
RA Lynch D.C.;  
RL

RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.  
RN [15]  
RP SEQUENCE OF 2731-2813 FROM N.A.  
RA MEDLINE=87260814; PubMed=3496594;  
RA Collins C.J., Underdahl J.P., Levene R.B., Ravera C.P.,  
RA Morin M.J., Dombalagian M.J., Ricca G., Livingston D.M.,  
RA Lynch D.C.;  
RT "Molecular cloning of the human gene for von Willebrand factor and  
RT identification of the transcription initiation site.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:4393-4397(1987).  
RN [16]  
RP DISULFIDE BONDS.  
RA MEDLINE=88163465; PubMed=3502076;  
RA Marti T., Rosselet S.J., Titani K., Walsh K.A.;  
RT "Identification of disulfide-bridged substructures within human von  
RT Willebrand factor.";  
RL Biochemistry 26:8099-8109(1987).  
RN [17]  
RP STRUCTURE OF CARBOHYDRATES.  
RA MEDLINE=86274702; PubMed=3089784;  
RA Samor B., Michalek J.C., Debray H., Mazurier C., Goudeau M.,  
RA van Halbeek H., Vlieghart J.F.G., Montreuil J.;  
RT "Primary structure of a new tetraantennary glycan of the N-  
RT acetylglucosaminic type isolated from human factor VIII/von  
RT Willebrand factor.";  
RL Eur. J. Biochem. 158:295-298(1986).  
RN [18]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1261-1468.  
RA MEDLINE=98221174; PubMed=9553097;  
RA Emsley J., Cruz M., Handin R., Liddington R.;  
RT "Crystal structure of the von Willebrand factor A1 domain and  
RT implications for the binding of platelet glycoprotein Ib.";  
RL J. Biol. Chem. 273:10396-10401(1998).  
RN [19]  
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1685-1873.  
RA MEDLINE=97472999; PubMed=9331419;  
RA Huisinga E.G., Martijn van der Plas R., Kroon J., Sima J.J., Gros P.;  
RT "Crystal structure of the A3 domain of human von Willebrand factor:  
RT implications for collagen binding.";  
RL Structure 5:1147-1156(1997).  
RN [20]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1686-1872.  
RA MEDLINE=97460108; PubMed=9312128;  
RA Blenkowska J., Cruz M., Attomo A., Handin R., Liddington R.;  
RT "The von Willebrand factor A3 domain does not contain a metal ion-  
RT dependent adhesion site motif.";  
RL J. Biol. Chem. 272:25162-25167(1997).  
RN [21]  
RP VARIANTS TRP-1597 AND ASP-1607.  
RA MEDLINE=89264495; PubMed=2786201;  
RA Ginsburg D., Konkle B.A., Gill J.C., Montgomery R.R.,  
RA Bockenstedt P.L., Johnson T.A., Yang A.Y.;  
RT "Molecular basis of human von Willebrand disease: analysis of  
RT platelet von Willebrand factor mRNA.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:3723-3727(1989).  
RN [22]  
RP VARIANTS THR-1628.  
RA MEDLINE=91196734; PubMed=1673047;  
RA Iannuzzi M.C., Hidak N., Boehnke M., Bruck M.E., Hanna W.T.,  
RA Collins F.S., Ginsburg D.;  
RT "Analysis of the relationship of von Willebrand disease (vWD) and  
RT hereditary hemorrhagic telangiectasia and identification of a  
RT potential type IIA vWD mutation (I1686S to Thr)."  
RL Am. J. Hum. Genet. 48:757-763(1991).  
RN [23]  
RP VARIANTS NORMANDY-2 TRP-816 AND NORMANDY-3 GLN-854.  
RA MEDLINE=92001464; PubMed=1832934;  
RA Gaucher C., Mercier B., Jorieu S., Oufkir D., Mazurier C.;  
RT "Identification of two point mutations in von Willebrand factor  
RT gene of three families with the 'Normandy' variant of von Willebrand  
RT disease.";  
RL Br. J. Haematol. 78:506-514(1991).  
RN [24]

RP VARIANT CYS-1308.  
 RX MEDLINE=92104315; PubMed=1761120;  
 RA Donner M., Andersson A.-M., Kristoffersson A.-C., Nilsson I.M.,  
 Dahlback B., Holmberg L.;  
 RT "An Arg554->Cys545 substitution mutation of the von Willebrand  
 factor in type IIB von Willebrand's disease.";  
 RL Eur. J. Haematol. 47:342-345(1991).  
 RN [25]  
 RP VARIANTS TRP-1306; CYS-1308 AND PRO-1613.  
 RX MEDLINE=91185601; PubMed=2010538;  
 RA Randi A.M., Rabinowitz I., Mancuso D.J., Mannucci P.M., Sadler J.E.;  
 RT "Molecular basis of von Willebrand disease type IIB. Candidate  
 mutations cluster in one disulfide loop between proposed platelet  
 glycoprotein Ib binding sequences.";  
 RL J. Clin. Invest. 87:1220-1226(1991).  
 RN [26]  
 RP VARIANTS TRP-1306; CYS-1308; MET-1316; GLN-1341 AND HIS-1399.  
 RX MEDLINE=91185602; PubMed=1672694;

Query Match 24.6%; Score 66; DB 1; Length 2813;  
 Best Local Similarity 27.6%; Pred. No. 5.4;  
 Matches 16; Conservative 8; Mismatches 18; Indels 16; Gaps 2;

Cy 1 SCYFIPEG-----VPGDSTRKCMDLKGKHPINSEWQTN--CETCTC 42  
 Db 2226 SCGHPHSGCPCFPDKNWLESGCVPEACCTGCTGEGVGQFLAWVPDHPQCTC 2283

Search completed: March 11, 2004, 17:53:20  
 Job time : 9.34677 secs

GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: March 11, 2004, 18:06:28 ; Search time 4.1129 Seconds  
(without alignments)  
350.816 Million cell updates/sec

Title: US-09-977-406a-5

Perfect score: 15

Sequence: 1 EWQTDNCFCTCYET 15

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 36191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 78:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

# SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	114	2	A34567
2	6	40.0	366	2	JC7094
3	6	40.0	601	2	B96744
4	6	40.0	885	2	T32374
5	5	33.3	38	2	JN0613
6	5	33.3	38	2	S27242
7	5	33.3	83	2	S53116
8	5	33.3	91	2	S52089
9	5	33.3	114	2	A54653
10	5	33.3	119	1	S73864
11	5	33.3	130	2	G65019
12	5	33.3	167	2	C86241
13	5	33.3	210	2	A61679
14	5	33.3	246	2	A81679
15	5	33.3	295	2	S76790
16	5	33.3	301	2	T26546
17	5	33.3	319	1	I50370
18	5	33.3	332	1	C70905
19	5	33.3	334	2	D82803
20	5	33.3	340	1	B55973
21	5	33.3	347	2	A38453
22	5	33.3	349	1	AC0825
23	5	33.3	358	1	A55973
24	5	33.3	358	1	A55973
25	5	33.3	358	1	A55973
26	5	33.3	358	1	A55973
27	5	33.3	360	1	A55198
28	5	33.3	360	1	T06592
29	5	33.3	361	2	I50505

30	5	33.3	363	1	C55973	transcription fact
31	5	33.3	366	2	S66351	methionine adenosy
32	5	33.3	374	2	S41758	heat shock protein
33	5	33.3	374	2	C97058	molecular chaperon
34	5	33.3	390	2	S49491	methionine adenosy
35	5	33.3	390	2	S46540	methionine adenosy
36	5	33.3	390	2	G84785	probable s-adenosy
37	5	33.3	391	2	T43318	YN123W protein ho
38	5	33.3	393	2	U00410	methionine adenosy
39	5	33.3	393	2	JN0131	methionine adenosy
40	5	33.3	393	2	S38875	methionine adenosy
41	5	33.3	393	2	S46538	methionine adenosy
42	5	33.3	393	2	C86155	s-adenosylmethioni
43	5	33.3	394	2	T06180	methionine adenosy
44	5	33.3	396	2	T10710	methionine adenosy
45	5	33.3	397	2	S66352	methionine adenosy

## ALIGNMENTS

RESULT 1  
A34567  
beta-microseminoprotein precursor - human  
N:Alternate names: beta-inhibin; prostatic secretory protein; PSP-94; seminal plasma pr  
C:Species: Homo sapiens (man)  
C:Date: 13-Jul-1990 #sequence revision 13-Jul-1990 #text change 20-Aug-1999  
C:Accession: A34567; A26451; K29777; A30984; A60673; S16238; I52682  
R:Green, C.B.; Lin, W.Y.; Kwok, S.C.M.  
Biochem. Biophys. Res. Commun. 167, 1184-1190, 1990  
A:Title: Cloning and nucleotide sequence analysis of the human beta-microseminoprotein ;  
A:Reference number: A34567; MUID:90211299; PMID:2322265  
A:Accession: A34567  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-114 <GRS>  
A:Cross-References: GB:M5885; NID:G338414; PIDN:AAA36635.1; PID:G338415  
R:Akiyama, K.; Yoshioke, Y.; Schmid, K.; Offner, G.D.; Troxler, R.F.; Teuda, R.; Hara, I  
Biochim. Biophys. Acta 829, 288-294, 1985  
A:Title: The amino acid sequence of human beta-microseminoprotein..  
A:Reference number: A29777; MUID:8519974; PMID:3995056  
A:Accession: A29777  
A:Molecule type: protein  
A:Residues: 21-58, 'PT', 61-113 <AKI>  
R:Seidman, N.G.; Arpatli, N.T.; Rochemont, J.; Sheth, A.R.; Chretien, M.  
FEBS Lett. 175, 349-355, 1984  
A:Title: Complete amino acid sequence of human seminal plasma beta-inhibin. Prediction ;  
A:Reference number: A30984; MUID:85004133; PMID:6434350  
A:Accession: A30984  
A:Molecule type: protein  
A:Residues: 21-112, 'G', 114 <SEI>  
R:Reiber, H.; Andersen, C.; Murne, A.; Rannevik, G.; Lindstroem, C.; Lilja, H.; Fernlu  
Am. J. Pathol. 137, 593-604, 1990  
A:Title: Beta microseminoprotein is not a prostate-specific protein.  
A:Reference number: A60673; MUID:90379237; PMID:2205099  
A:Accession: A60673  
A:Molecule type: protein  
A:Residues: 21, 'X', 23-34 <WEI>  
A:Experimental source: gastric juice  
R:Nollet, S.; Moikay, M.; Chretien, M.  
Biochim. Biophys. Acta 1089, 247-249, 1991  
A:Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in  
A:Reference number: S16237; MUID:91274357; PMID:2054385  
A:Accession: S16238  
A:Molecule type: DNA

A:Residues: 1-114 <NOL>  
A:Cross-references: EMBL:X57928; NID:935760; PIDN:CAA41002.1; PID:9825707  
A>Note: the authors translated the codon ACT for residue 54 as Trp  
R:Lin, A.Y.; Bradner, R.C.; Vessella, R.L.  
A:Reference number: 74, 91-99, 1993  
A>Title: Decreased expression of prostatic secretory protein PSP94 in prostate cancer.  
A:Reference number: 152682; MUID:94115955; PMID:7506990  
A:Accession: 152682  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-114 <RES>  
A:Cross-references: GB:S67815; NID:9460568; PIDN:AAB29732.1; PID:9460569  
A:Comment: This protein is a component of seminal plasma as well as secretory fluids from  
C:Genetics:  
A:Gene: GDB:MSNB  
A:Cross-references: GDB:128042; OMIM:157145  
A:Map position: 10q11.2-10q11.2  
A:Insertions: 1/3; 37/1; 72/2  
C:Superfamily: seminal plasma protein  
C:Keywords: semen  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-114/Product: seminal plasma protein #status experimental <MAT>

Query Match 100.0%; Score 15; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 7.5e-11;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EMOTDNCCTCTCTCT 15  
51 EMOTDNCCTCTCTCT 65

RESULT 2  
JC7094  
nine-heme cytochrome c - Desulfovibrio desulfuricans  
C:Species: Desulfovibrio desulfuricans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000  
C:Accession: U07094  
R:Saraiva, L.M.; da Costa, P.N.; Legall, J.  
Biochem. Biophys. Res. Commun. 262, 629-634, 1999  
A>Title: Sequencing the gene encoding Desulfovibrio desulfuricans ATCC 27774 nine-heme c  
A:Reference number: JC7094; MUID:99400423; PMID:10471375  
A:Accession: JC7094  
A:Molecule type: DNA  
A:Residues: 1-326 <SAR>  
A:Cross-references: GB:AF186393; NID:95924394; PIDN:AMD56586.1; PID:95924395  
A:Experimental source: ATCC 27774  
C:Genetics:  
A:Gene: 9Hcc  
C:Keywords: electron transfer; heme; heme binding

Query Match 40.0%; Score 6; DB 2; Length 326;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 DNCCTC 10  
75 DNCCTC 80

RESULT 3  
B96744  
unknown protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: B96744  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso, J.; Chiu, C.W.; Chung, M.X.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, U.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, Rizzo, W.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: B96744  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-601 <STO>  
A:Cross-references: GB:AE005173; NID:911054407; PIDN:AA27794.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: P28P5.4  
A:Map position: 1

Query Match 40.0%; Score 6; DB 2; Length 601;  
Best Local Similarity 100.0%; Pred. No. 8.8;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

7 CECTTC 12  
514 CECTTC 519

RESULT 4  
T32374  
hypothetical protein K10F12.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 28-Jul-2000  
C:Accession: T32374  
R:Mohdman, P.; Beck, C.  
submitted to the EMBL Data Library, September 1997  
A:Description: The sequence of C. elegans cosmid K10F12.  
A:Reference number: 221157  
A:Accession: T32374  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-895 <WOH>  
A:Cross-references: EMBL:AF025462; PIDN:AAB71005.1; GSPDB:GN00021; CESP:K10F12.3  
A:Experimental source: strain Bristol N2; clone K10F12  
C:Genetics:  
A:Gene: CESP:K10F12.3  
A:Map position: 3  
A:Insertions: 46/1; 124/3; 165/1; 223/3; 282/3; 340/3; 381/1; 485/3; 516/2; 549/1; 6  
C:Superfamily: Yeast 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; 1 phosphodiesterase domain Y homology  
F:338-487/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X ho

Query Match 40.0%; Score 6; DB 2; Length 895;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 TDNCCT 9  
288 TDNCCT 293

RESULT 5  
JN0613  
defensin 4K - scorpion (leirus quinquestratus)  
N:Alternate names: antibacterial 4K peptide  
C:Species: Leirus quinquestratus hebraeus  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 03-Feb-1994  
C:Accession: JN0613  
R:Cociancich, S.; Goffion, M.; Bontems, F.; Bulier, P.; Bouet, F.; Menez, A.; Hoffmann, Biochem. Biophys. Res. Commun. 194, 17-22, 1993  
A>Title: Purification and characterization of a scorpion defensin, a 4kDa antibacterial  
A:Reference number: JN0613; MUID:93326112; PMID:8335834  
A:Accession: JN0613  
A:Molecule type: protein  
A:Residues: 1-38 <COO>  
A>Note: this protein is similar to scorpion toxins and insect defensins

Query Match 33.3%; Score 5; DB 2; Length 38;  
Best Local Similarity 100.0%; Pred. No. 15;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCTCY 13  
|||||  
Db 32 TCTCY 36

## RESULT 6

S27242

defensin - blue darter

C/Species: Aeschna cyanea (blue darter)

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 17-Mar-1999

C/Accession: S27242

R/Bulet, P.; Cociancich, S.; Reuland, M.; Sauber, F.; Bischoff, R.; Hegy, G.; van Dorssse

Eur. J. Biochem. 209, 977-984, 1992

A/Title: A novel insect defensin mediates the inducible antibacterial activity in larvae

A/Reference number: S27242; PMID:93049356; PMID:1425705

A/Accession: S27242

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-38 &lt;BLU&gt;

Query Match 33.3%; Score 5; DB 2; Length 38;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCTCY 13  
|||||  
Db 33 TCTCY 37

## RESULT 7

S53116

methionine adenosyltransferase (EC 2.5.1.6) - chickpea (fragment)

N/Alternate names: S-adenosylmethionine synthetase

C/Species: Cicer arietinum (chickpea, garbanzo)

C/Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 05-May-2000

C/Accession: S53116

R/Cervantes, E.

submitted to the EMBL Data Library, March 1995

A/Reference number: S53116

A/Accession: S53116

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-83 &lt;CEB&gt;

A/Cross-references: EMBL:X85252; NID:G1808591; PIDN:CA59508.1; PID:G732576

C/Superfamily: methionine adenosyltransferase

C/Keywords: S-adenosylmethionine; transferase

Query Match 33.3%; Score 5; DB 2; Length 83;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CECTC 11  
|||||  
Db 43 CECTC 47

## RESULT 8

S52089

transcription factor isl-2a (clone S3) - chinook salmon

N/Alternate names: insulin enhancer-binding protein isl-2a; isllet-2a protein

C/Species: Oncorhynchus tshawytscha (chinook salmon)

C/Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 15-Oct-1999

C/Accession: S52089

R/Gong, Z.; Hew, C.L.

Biochim. Biophys. Acta 1260, 349-354, 1995

A/Title: Several splicing variants of isl-1 like genes in the chinook salmon (Oncorhynchus

A/Reference number: S52089; PMID:95178560; PMID:7873614

A/Accession: S52089

A/Molecule type: mRNA

A/Residues: 1-91 &lt;CON&gt;

A/Cross-references: EMBL:X64882

A/Experimental source: clone S3

C/Genetics:

A/Gene: isl-2a

C/Superfamily: transcription factor isl-1; homeobox homology; LIM metal-binding repeat 1

C/Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati

F/3-56/Domain: LIM metal-binding repeat homology &lt;LIM&gt;

Query Match 33.3%; Score 5; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ETCCT 12  
|||||  
Db 40 ETCCT 44

## RESULT 9

A54663

seminal plasma protein PSP-94 precursor - rhesus macaque

N/Alternate names: prostatic secretory protein PSP94

C/Species: Macaca mulatta (rhesus macaque)

C/Date: 02-Jun-1995 #sequence\_revision 02-Jun-1995 #text\_change 20-Aug-1999

C/Accession: S16237; A54663

R/Nolet, S.; Mbikay, M.; Chretien, M.

Biochim. Biophys. Acta 1089, 247-249, 1991

A/Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence 1

A/Reference number: S16237; PMID:91274357; PMID:2054385

A/Accession: S16237

A/Molecule type: DNA

A/Residues: 1-114 &lt;NO2&gt;

A/Cross-references: EMBL:X57932; NID:G38094; PIDN:CAA41003.1; PID:G829152

A/Note: the authors translated the codon ACT for residue 54 as TTP

R/Nolet, S.; St-Louis, D.; Mbikay, M.; Chretien, M.

Genomics 9, 775-777, 1991

A/Title: Rapid evolution of prostatic protein PSP-94 suggested by sequence divergence b

A/Reference number: A54663; PMID:91244325; PMID:2037304

A/Accession: A54663

A/Molecule type: mRNA

A/Residues: 1-114 &lt;NO2&gt;

A/Cross-references: GB:M92161; NID:G342280; PIDN:AAA36903.1; PID:G342281

C/Genetics:

A/Introns: 1/3; 37/1; 72/2

C/Superfamily: seminal plasma protein

F/1-20/Domain: signal sequence #status predicted &lt;SIG&gt;

Query Match 33.3%; Score 5; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDNCE 8  
|||||  
Db 54 TDNCE 58

## RESULT 10

S73864

hypothetical protein H10 orf19 - Mycoplasma pneumoniae (strain ATCC 29342)

C/Species: Mycoplasma pneumoniae

A/Variety: ATCC 29342

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000

C/Accession: S73864

R/Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.

Nucleic Acids Res. 24, 4420-4449, 1996

A/Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae

A/Reference number: S73864; PMID:97105885; PMID:8948633

A/Accession: S73864

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-119 &lt;HIM&gt;

A/Cross-references: EMBL:AE000052; GB:U00089; NID:G1674223; PIDN:AAB96186.1; PID:G16742

C/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C/Genetics:

A/Genetic code: SGC3

## C:Superfamily: holo-ACP synthase

Query Match 33.3%; Score 5; DB 1; Length 119;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CTDC 7  
DB 21 CTDC 25

## RESULT 11

hypothetical protein b2448 - Escherichia coli (strain K-12)

C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C:Accession: G65019  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC  
A.; Rose, D.U.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: G65019  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-130 <BLAT>  
A:Cross-references: GB:AE000332; GB:U00096; NID:G1788789; PIDN:AA075501.1; PID:G1788790;  
A:Experimental source: strain K-12, substrain W61655  
C:Superfamily: Escherichia coli hypothetical protein b2448

Query Match 33.3%; Score 5; DB 2; Length 130;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDNC 8  
DB 43 TDNC 47

## RESULT 12

protein T16B5.9 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: C86241  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizlar, L.  
Nature 408, 815-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: C86241  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-167 <STO>  
A:Cross-references: GB:AE005172; NID:94874271; PIDN:AD31336.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: T16B5.9  
A:Map position: 1

Query Match 33.3%; Score 5; DB 2; Length 167;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TCYET 15  
DB 91 TCYET 95

## RESULT 13

transposase alx4082 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120  
A:Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C:Accession: AC2316  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Matsumoto, A.; Iriyach  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AC2316  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-210 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BA075781.1; PID:G17133217; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alx4082

Query Match 33.3%; Score 5; DB 2; Length 210;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQTD 5  
DB 111 EMQTD 115

## RESULT 14

conserved hypothetical protein TC0662 [imported] - Chlamydia muridarum (strain N199)

C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 11-May-2000  
C:Accession: AB1679  
R:Read, T.D.; Brumham, R.C.; Shan, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,  
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg  
Nucleic Acids Res. 28, 1397-1406, 2000  
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A:Reference number: AB1500; MUID:20150255; PMID:10684935  
A:Accession: AB1679  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-246 <TEB>  
A:Cross-references: GB:AE002334; GB:AE002160; NID:G7190690; PIDN:AA039485.1; PID:G71906  
A:Experimental source: strain N199 (MoPn)  
C:Genetics:  
A:Gene: TC0662

Query Match 33.3%; Score 5; DB 2; Length 246;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TCYET 15  
DB 198 TCYET 202

## RESULT 15

hypothetical protein - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 23-Dec-2002  
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.  
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud  
DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis  
s.  
A:Reference number: S74322; MUID:97061201; PMID:8905231

Fri Mar 12 09:42:16 2004

us-09-977-406a-5.olg.rpr

Page 5

A:Accession: S76790  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-295 <KAN>  
A:Cross-references: EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BA18702.1; PID:g165379  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Genetics:  
A:Start codon: GTG  
C:Superfamily: fructosamine kinase

Query Match 33.3%; Score 5; DB 2; Length 295;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 WOTDN 6  
Db 132 WOTDN 136

Search completed: March 11, 2004, 18:13:47  
Job time : 5.129 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2004, 18:06:28 ; Search time 17.5484 Seconds

(without alignments)  
350.816 Million cell updates/sec

Title: US-09-977-406a-58

Sequence: 1 EMOTDNCERTCTCYETETSCC.....YIVVEKKDKPKTCSVSEWII 64

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : PIR 78:\*\*

1: p1r1:\*\*  
2: p1r2:\*\*  
3: p1r3:\*\*  
4: p1r4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	114	2	A34567 beta-microseminopr
2	18	28.1	114	2	A54663 seminal plasma pro
3	7	10.9	91	2	S41663 beta-microseminopr
4	7	10.9	113	2	S26482 choriionic gonadotr
5	7	10.9	113	2	FC1244 lvanolyisin precurs
6	7	10.9	528	2	S22341 lvanolyisin precurs
7	7	10.9	529	2	A43505 lsteriolysin O pr
8	7	10.9	529	2	S24231 lsteriolysin O pr
9	7	10.9	529	2	AC1100 lsteriolysin O pr
10	7	10.9	530	2	S22340 seeligeriolysin
11	7	10.9	917	2	T22898 hypotnetical prote
12	7	9.4	129	2	B90228 hypotnetical prote
13	6	9.4	132	1	FZK11 fatty acid-binding
14	6	9.4	132	2	T03397 hypotnetical prote
15	6	9.4	137	2	T43245 probable actin-dep
16	6	9.4	146	2	F82418 cytochrome c554 VC
17	6	9.4	150	2	H64576 hypotnetical prote
18	6	9.4	151	2	E71051 hypotnetical prote
19	6	9.4	159	2	S48570 hypotnetical prote
20	6	9.4	183	2	F83858 hypotnetical prote
21	6	9.4	203	2	AF2598 conserved hypotnet
22	6	9.4	203	2	G97380 phn1 protein (impo
23	6	9.4	208	2	T33326 hypotnetical prote
24	6	9.4	266	2	S82713 hypotnetical prote
25	6	9.4	278	2	S64317 probable membrane
26	6	9.4	285	2	H69369 branched-chain ami
27	6	9.4	288	2	A70371 conserved hypotnet
28	6	9.4	304	2	AD1603 tRNA pseudouridine
29	6	9.4	304	2	AH1240 tRNA pseudouridine

30	6	9.4	311	1	BRBT sulfate-binding pr
31	6	9.4	319	2	T46145 hypotnetical prote
32	6	9.4	324	2	T24465 hypotnetical prote
33	6	9.4	326	2	HC7094 nine-heme cytocho
34	6	9.4	328	2	H71871 hypotnetical prote
35	6	9.4	328	2	B62924 cyptophanyl-tRNA
36	6	9.4	337	2	C71875 hypotnetical prote
37	6	9.4	343	1	DE51MP malate dehydrogena
38	6	9.4	356	2	T19715 hypotnetical prote
39	6	9.4	377	2	T32798 hypotnetical prote
40	6	9.4	379	2	A88066 protein R52.3 (lmp
41	6	9.4	384	2	T38544 probable expolyph
42	6	9.4	406	2	T24492 hypotnetical prote
43	6	9.4	425	2	C64516 hypotnetical prote
44	6	9.4	430	2	C64554 ATP-dependent nucl
45	6	9.4	437	2	H64865 probable sterol de

#### ALIGNMENTS

RESULT 1  
A34567  
beta-microseminoprotein precursor - human  
N:Alternate names: beta-inhibin; prostatic secretory protein; PSP-94; seminal plasma pro  
C:Species: Homo sapiens (man)  
C>Date: 13-Jul-1990 #sequence revision 13-Jul-1990 #text change 20-Aug-1999  
C/Accession: A34567; A26451; A29777; A30984; A60673; S16236; I52682  
R/Green, C.B.; Liu, W.Y.; Kwok, S.C.M.  
Biochem. Biophys. Res. Commun. 167, 1184-1190, 1990  
A>Title: Cloning and nucleotide sequence analysis of the human beta-microseminoprotein  
A:Reference number: A34567; MUID:90211299; PMID:232265  
A:Accession: A34567  
A>Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-114 <GRE>  
A:Cross-references: GB:M34376; NID:G514370; PIDN:AAA59871.1; PID:G514372  
R/Mikay, M.; Nole, S.; Fournier, S.; Benjannet, S.; Chapelaine, P.; Paradis, G.; Dub  
DNA 6, 23-29, 1987  
A>Title: Molecular cloning and sequence of the cDNA for a 94-amino-acid seminal plasma  
A:Reference number: A26451; MUID:87161231; PMID:382888  
A:Accession: A26451  
A:Molecule type: mRNA  
A:Residues: 1-114 <MBI>  
A:Cross-references: GB:M5885; NID:G338414; PIDN:AAA36635.1; PID:G338415  
R/Kiyama, K.; Yoshioke, Y.; Schmidt, K.; Offner, G.D.; Troxler, R.F.; Tsuda, R.; Hara, I  
Biochim. Biophys. Acta 828, 288-294, 1985  
A>Title: The amino acid sequence of human beta-microseminoprotein.  
A:Reference number: A29777; MUID:8519974; PMID:395056  
A:Accession: A29777  
A:Molecule type: protein  
A:Residues: 21-58, 'PT', 61-113 <AKI>  
R/Seidah, N.G.; Arhanti, N.J.; Rochemont, J.; Sheth, A.R.; Chretien, M.  
FEBS Lett. 175, 349-355, 1984  
A>Title: Complete amino acid sequence of human seminal plasma beta-inhibin. Prediction  
A:Reference number: A30984; MUID:85004133; PMID:643350  
A:Accession: A30984  
A:Molecule type: protein  
A:Residues: 21-112, 'G', 114 <SEI>  
R/Reiber, H.; Andersson, C.; Murne, A.; Rannevik, G.; Lindstroem, C.; Lilja, H.; Fernlur  
Am. J. Pathol. 137, 593-604, 1990  
A>Title: Beta microseminoprotein is not a prostate-specific protein.  
A:Reference number: A60673; MUID:90379237; PMID:2205099  
A:Accession: A60673  
A:Molecule type: protein  
A:Residues: 21, 'X', 23-34 <WBI>  
A:Experimental source: gastric juice  
R/Nolet, S.; Molay, M.; Chretien, M.  
Biochim. Biophys. Acta 1089, 247-249, 1991  
A>Title: Prostatic secretory protein PSP(94) : gene organization and promoter sequence in  
A:Reference number: S16237; MUID:91274357; PMID:2054385  
A:Accession: S16238  
A:Molecule type: DNA



Db 70 PKTCNV 76

## RESULT 6

S22341  
Ivanolysin precursor - *Listeria ivanovii*  
C:Species: *Listeria ivanovii*  
C>Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 21-Aug-1998  
C:Accession: S22341; S36683  
R:Haas, A.; Dumbsky, M.; Krefl, J.  
Biochim. Biophys. Acta 1130, 81-84, 1992  
A:Title: Listeriolysin genes: complete sequence of 110 from *Listeria ivanovii* and of 1ac  
A:Reference number: S22340; PMID:92182018; PMID:1543752  
A:Accession: S22341  
A:Molecule type: DNA  
A:Residues: 1-528 <HAS>  
A:Cross-references: EMBL:X60461  
A:Note: the authors translated the codon ACA for residue 331 as Val  
R:Krefl, J.  
submitted to the EMBL Data Library, July 1991  
A:Reference number: S36683  
A:Accession: S36683  
A:Molecule type: DNA  
A:Residues: 1-319, 'T', 321-528 <KRE>  
A:Cross-references: EMBL:X60461  
C:Genetics:  
A:Gene: 110  
C:Superfamily: dipeptide transport protein  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-528/Product: Ivanolysin #status predicted <MAT>

Query Match 10.9%; Score 7; DB 2; Length 528;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIVVEKK 51  
Db 97 YIVVEKK 103

## RESULT 7

A43505  
Listeriolysin O precursor - *Listeria monocytogenes*  
C:Species: *Listeria monocytogenes*  
C>Date: 21-Oct-1992 #sequence\_revision 21-Oct-1992 #text\_change 20-Aug-1999  
C:Accession: A43505; S05306; A47606; S12400; A61079  
R:Mengaud, J.; Vicente, M.F.; Chenevert, J.; Pereira, J.M.; Geoffroy, C.; Giacquel-sarrey  
Infect. Immun. 56, 766-772, 1988  
A:Title: Expression in *Escherichia coli* and sequence analysis of the listeriolysin O de  
A:Reference number: A43505; PMID:8153053; PMID:3126142  
A:Accession: A43505  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-529 <MEN>  
A:Cross-references: GB:M24199; NID:q149652; PIDN:AAA03018.1; PID:q149653  
A:Note: this sequence is derived from a strongly hemolytic strain, serotype 1/2c  
R:Domann, E.; Chakraborty, T.  
Nucleic Acids Res. 17, 6406, 1989  
A:Title: Nucleotide sequence of the listeriolysin gene from a *Listeria monocytogenes* ser  
A:Reference number: S05306; PMID:8936664; PMID:2505236  
A:Accession: S05306  
A:Molecule type: DNA  
A:Residues: 1-529 <DOM>  
A:Cross-references: EMBL:X15127; NID:q44106; PIDN:CAA33223.1; PID:g44107  
A:Experimental source: strain EGD  
A:Note: this sequence is derived from a weakly hemolytic strain, serotype 1/2a  
R:Mengaud, J.; Chenevert, J.; Geoffroy, C.; Galliard, J.L.; Cossart, P.  
Infect. Immun. 55, 3225-3227, 1987  
A:Title: Identification of the structural gene encoding the SH-activated hemolysin of *Li*  
A:Reference number: A47606; PMID:88057627; PMID:2824384  
A:Accession: A47606  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 413-480 <ME2>  
A:Cross-references: GB:M29171

R:Michel, E.; Reich, K.A.; Favier, R.; Berche, P.; Cossart, P.  
Mol. Microbiol. 4, 2167-2178, 1990  
A:Title: Attenuated mutants of the intracellular bacterium *Listeria monocytogenes* obtai  
A:Reference number: S12400; PMID:91211627; PMID:1965218  
A:Accession: S12400  
A:Molecule type: DNA  
A:Residues: 483-493 <MIC>  
A:Experimental source: strain 1028, serotype 1/2c  
C:Genetics:  
A:Gene: hlyA; 115A  
C:Superfamily: dipeptide transport protein  
C:Keywords: virulence factor  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-529/Product: listeriolysin O #status predicted <MAT>

Query Match 10.9%; Score 7; DB 2; Length 529;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIVVEKK 51  
Db 98 YIVVEKK 104

## RESULT 8

S24231  
Listeriolysin precursor - *Listeria monocytogenes* (strain 12067)  
C:Species: *Listeria monocytogenes*  
A:Variety: strain 12067  
C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Aug-1999  
C:Accession: S24231  
R:Rasmussen, O.F.; Beck, T.; Olsen, J.E.; Doms, L.; Rossen, L.  
Infect. Immun. 59, 3945-3951, 1991  
A:Title: *Listeria monocytogenes* isolates can be classified into two major types accordi  
A:Reference number: S24230; PMID:92040062; PMID:1937753  
A:Accession: S24231  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-529 <RAS>  
A:Cross-references: EMBL:X60035; NID:q44110; PIDN:CAA42639.1; PID:g44112  
A:Experimental source: strain 12067, serotype 4b  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
C:Genetics:  
A:Gene: 115A  
C:Superfamily: dipeptide transport protein  
C:Keywords: virulence factor  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-529/Product: listeriolysin #status predicted <MAT>

Query Match 10.9%; Score 7; DB 2; Length 529;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIVVEKK 51  
Db 98 YIVVEKK 104

## RESULT 9

AC1100  
Listeriolysin O precursor [imported] - *Listeria monocytogenes* (strain EGD-e)  
C:Species: *Listeria monocytogenes*  
C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 17-May-2002  
C:Accession: AC1100  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Biocker  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fschl, H.  
Science 294, 849-852, 2001  
A:Authors: Krefl, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Me  
ok, C.; Schuener, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,  
A:Title: Comparative genomics of *Listeria* species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AC1100

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-529 <GLA>

A:Cross-references: GB:NC\_003210; PIDN:CAD00729.1; PID:g16409567; GSPDB:GN00177

A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: hly

C:Superfamily: dipeptide transport protein

Query Match 10.9%; Score 7; DB 2; Length 529;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIVVEKK 51

Db 98 YIVVEKK 104

#### RESULT 10

S22340

seeligeriolysin - *Listeria seeligeri*

C:Species: *Listeria seeligeri*

C>Date: 22-Nov-1993 #sequence\_revision 01-Dec-1995 #text\_change 20-Aug-1999

C:Accession: S22340

R:Haas, A.; Dumsky, M.; Kref, J.

Biochim. Biophys. Acta 1130, 81-84, 1992

A>Title: Listeriolysin genes: complete sequence of llo from *Listeria ivanovii* and of lsc

A:Reference number: S22340; MUID:92182018; PMID:1543752

A:Accession: S22340

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-530 <HAA>

A:Cross-references: EMBL:X60462; NID:944144; PIDN:CAA42996.1; PID:944145

A>Note: the authors translated the codon GCC for residue 287 as Pro

C:Superfamily: dipeptide transport protein

Query Match 10.9%; Score 7; DB 2; Length 530;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIVVEKK 51

Db 99 YIVVEKK 105

#### RESULT 11

T22898

hypothetical protein F58B3.5 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 06-Jan-2003

C:Accession: T22898

R:Harris, B.

submitted to the EMBL Data Library, May 1996

A:Reference number: Z19633

A:Accession: T22898

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-917 <WIL>

A:Cross-references: EMBL:Z73427; PIDN:CAA97803.1; GSPDB:GN00022; CESP:F58B3.5

A:Experimental source: clone F58B3

C:Genetics:

A:Gene: CESP:F58B3.5

A:Map position: 4

A:introns: 27/2; 135/2; 620/1; 655/1; 874/3

C:Superfamily: methionyl-tRNA synthetase, dimer-forming

Query Match 10.9%; Score 7; DB 2; Length 917;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 VEKKDPK 54

Db 20 VEKKDPK 26

#### RESULT 12

B90228

hypothetical protein SSO0783 [imported] - *Sulfolobus solfataricus*

C:Species: *Sulfolobus solfataricus*

C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001

C:Accession: B90228

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweez, M.J.; Chan

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.

aret, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A>Description: *Sulfolobus solfataricus* complete genome.

A:Reference number: A99139

A:Accession: B90228

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-129 <KUR>

A:Cross-references: GB:AF006641; NID:g13813959; PIDN:AAK41081.1; GSPDB:GN00155

C:Genetics:

A:Gene: SSO0783

Query Match 9.4%; Score 6; DB 2; Length 129;

Best Local Similarity 100.0%; Pred. No. 48;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 IYVEKK 51

Db 121 IYVEKK 126

#### RESULT 13

P2RRT1

fatty acid-binding protein, intestinal - rat

N:Alternate names: FABP

C:Species: *Rattus norvegicus* (Norway rat)

C>Date: 17-Dec-1982 #sequence\_revision 21-Feb-1997 #text\_change 22-Jun-1999

C:Accession: I65761; A03147

R:Gordon, J.I.; Lowe, U.B.

Chem. Phys. Lipids 38, 137-158, 1985

A>Title: Analyzing the structures, functions and evolution of two abundant gastrointestinal

A:Reference number: I65761; MUID:86053743; PMID:3840724

A:Accession: I65761

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-132 <RES>

A:Cross-references: GB:M35992; NID:9204087; PIDN:AAA41141.1; PID:9204088

R:Alpers, D.H.; Strauss, A.W.; Ockner, R.K.; Bass, N.M.; Gordon, J.I.

Proc. Natl. Acad. Sci. U.S.A. 81, 313-317, 1984

A>Title: Cloning of a cDNA encoding rat intestinal fatty acid binding protein.

A:Reference number: A03147; MUID:84119477; PMID:6582489

A:Accession: A03147

A:Molecule type: mRNA

A:Residues: 1-9; 'Y', 'I', 'L', '84-132 <ALP>

A:Cross-references: GB:X01180; NID:9204081; PIDN:AAA41138.1; PID:9204082

C:Superfamily: myelin P2 protein

C:Keywords: blocked amino end; intestine; lipid binding

F;2/Modified site: blocked amino end (Ala) (in mature form) (probably acetylated) #stat

F;127/Binding site: fatty acid (Arg) #status predicted

Query Match 9.4%; Score 6; DB 1; Length 132;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 RIFKKE 41

Db 127 RIFKKE 132

#### RESULT 14

T03397

hypothetical protein - maize (fragment)

C/Species: Zea mays (maize)  
C/Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 29-Oct-1999  
C/Accession: T03397  
R/Alba, M.M.; Vinti, G.; Messagne, R.; Pages, M.  
submitted to the EMBL Data Library, April 1997  
A/Reference number: Z14927  
A/Accession: T03397  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-132 <ALB>  
A/Cross-references: EMBL:Y12762; NID:e1045993; PDB:CAA73301.1; PID:e314311  
A/Experimental source: strain L.W64-A

# Query Match

Best Local Similarity 9.4%; Score 6; DB 2; Length 132;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 VSTPVG 28  
Db 101 VSTPVG 106

# RESULT 15

T43245

Probable actin-depolymerizing factor - fission yeast (Schizosaccharomyces pombe)

C/Species: Schizosaccharomyces pombe

C/Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 18-Feb-2000

C/Accession: T43245; T38120

R/Kawamukai, M.

submitted to the EMBL Data Library, December 1996

A/Description: S. pombe cDNA for actin depolymerizing factor.

A/Reference number: Z22362

A/Accession: T43245

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-137 <KAW>

A/Cross-references: EMBL:D89939; PDB:BAI1039.1

R/Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, August 1996

A/Reference number: Z21771

A/Accession: T38120

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-137 <CON>

A/Cross-references: EMBL:Z98600; PDB:CAH11258.1; GSPDB:GN00066; SPDB:SPAC20G4.06c

A/Experimental source: strain 972h-; cosmid C20G4

C/Genetics:

A/Gene: SPAC20G4.06c

A/Map position: 1

A/Introns: 1/3; 37/1

A/Note: adf1

C/Superfamily: cofilin

C/Keywords: actin binding

# Query Match

Best Local Similarity 9.4%; Score 6; DB 2; Length 137;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 IYVEKK 51  
Db 39 IYVEKK 44

Search completed: March 11, 2004, 18:13:49  
Job time : 19.5484 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2004, 17:57:02 ; Search time 11.871 Seconds  
(without alignments)  
280.726 Million cell updates/sec

Title: US-09-977-406A-58

Perfect score: 64  
Sequence: 1 EMQIDNCETCTCTETETSCC.....YIVVERKDKKTCVSEWII 64

Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size: 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	100.0	114	1 MSMB_HUMAN	P08118 homo sapien
2	18	28.1	114	1 MSMB_MACMU	P25142 macaca mula
3	15	23.4	114	1 MSPU_SAGOE	O97949 saguinus ce
4	13	20.3	112	1 MSPA_SAGOE	O97936 saguinus ce
5	9	14.1	114	1 MSMB_PAPAN	Q28767 papio anubi
6	9	14.1	114	1 MSPE_SAGOE	O97935 saguinus ce
7	7	10.9	111	1 MSMB_PIG	O02826 sus scrofa
8	7	10.9	111	1 CGHR_XANMA	P37125 xanthomias
9	7	10.9	528	1 TACY_LISIV	F31831 listeria lv
10	7	10.9	529	1 TACY_LISMO	F13128 listeria mo
11	7	10.9	530	1 TACY_LISSE	P31830 listeria se
12	7	10.9	917	1 SYM_CABEL	O20970 caenorhabdi
13	6	9.4	113	1 MSMB_MOUSE	O08540 mus muscula
14	6	9.4	127	1 RK20_SPTOL	P28803 spinacia cl
15	6	9.4	131	1 FABI_RAT	P02653 ratius norv
16	6	9.4	137	1 COPI_SCHPO	P78929 schizosacch
17	6	9.4	159	1 YHSE_YEAST	P38832 saccharomyc
18	6	9.4	158	1 RUVA_STRP8	O8n237 streptococc
19	6	9.4	198	1 RUVA_STRP8	O99xm9 streptococc
20	6	9.4	277	1 Y4OR_RHISN	P55603 rhicobium s
21	6	9.4	278	1 YGII_YEAST	P51227 saccharomyc
22	6	9.4	304	1 TRUB_LISIN	O92c26 listeria in
23	6	9.4	304	1 TRUB_LISMO	O8y7f3 listeria in
24	6	9.4	326	1 CYC9_DSDE	O91m68 desulfocvibr
25	6	9.4	329	1 CYC9_SALTY	P02906 salmonella
26	6	9.4	333	1 SYM_UREPA	O99qws ureaplasma
27	6	9.4	342	1 MDHF_YEAST	P32419 saccharomyc
28	6	9.4	401	1 CGBI_ORYJA	O9d930 crytias jay
29	6	9.4	447	1 EF12_DAUCA	P34803 daucus caro
30	6	9.4	447	1 EF1A_MAIZE	O64937 oryza sativ
31	6	9.4	447	1 EF1A_ORYSA	O41011 pisum sativ
32	6	9.4	447	1 EF1A_PEA	P25698 glycine max
33	6	9.4	447	1 EF1A_SOYBN	

## ALIGNMENTS

RESULT 1	ID	MSMB_HUMAN	STANDARD	PRT	114 AA.
AC	P08118	P11999	Q3125	Q9UC59	
DT	01-AUG-1988	(Rel. 08, Created)			
DT	01-AUG-1988	(Rel. 08, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94) (Seminal plasma beta-inhibin) (Immunoglobulin binding factor) (IGBF) (PN44).				
GN	MSMB OR PRSP.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid:9606;				
RN	[1]	Taxid:9606;			
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=87161231; PubMed=3829888;				
RA	Madikay M., Nolet S., Fournier S., Chappela P.,				
RA	Paradis G., Dube J.Y., Tremblay R., Lazure C., Seidah N.G.,				
RA	Chretien M.;				
RT	Molecular cloning and sequence of the cDNA for a 94-amino-acid				
RT	seminal plasma protein secreted by the human prostate.;				
RL	DNA 6:23-29(1987).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91274357; PubMed=2054385;				
RA	Nolet S., Madikay M., Chretien M.;				
RT	"Prostatic secretory protein PSP94: gene organization and promoter				
RT	sequence in rhesus monkey and human.;"				
RL	Biochim. Biophys. Acta 1089:247-249(1991).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90211299; PubMed=2322265;				
RA	Green C.B., Liu W.Y., Kwok S.C.M.;				
RT	"Cloning and nucleotide sequence analysis of the human beta-				
RT	microseminoprotein gene.;"				
RL	Biochem. Biophys. Res. Commun. 167:1184-1190(1990).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90073664; PubMed=2590204;				
RA	Lundvall A., Lindstrom C., Weiber H., Abrahamson P.-A., Lilja H.,				
RT	"Molecular cloning of a small prostate protein, known as beta-				
RT	microseminoprotein, PSP94 or beta-inhibin, and demonstration of				
RT	transcripts in non-genital tissues.;"				
RL	Biochem. Biophys. Res. Commun. 164:1310-1315(1989).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Prostate;				
RX	MEDLINE=94115555; PubMed=7506990;				
RA	Liu A.Y., Branner R.C., Vessella R.L.;				
RT	"Decreased expression of prostatic secretory protein PSP94 in				
RT	prostate cancer.;"				
RL	Cancer Lett. 74:91-99(1993).				
RN	[6]				

34	6	9.4	447	1	EF1A_VICRA	O24534 vicia faba
35	6	9.4	447	1	EF1A_WHEAT	O03033 triticum ae
36	6	9.4	449	1	EF11_DAUCA	P29521 daucus caro
37	6	9.4	449	1	EF1A_MANES	O49169 manihot esc
38	6	9.4	459	1	MURD_LACPL	O88w80 lactobacill
39	6	9.4	481	1	MTN3_MOUSE	O35701 mus musculu
40	6	9.4	482	1	YSR2_CABEL	O09950 caenorhabdi
41	6	9.4	486	1	MTN3_HUMAN	O15232 homo sapien
42	6	9.4	487	1	HEP_DROME	O23977 dirosophila
43	6	9.4	488	1	SYF_BORBU	O51363 borrelia bu
44	6	9.4	494	1	CPAA_RABIT	O05555 oryctolagus
45	6	9.4	494	1	CPAB_RABIT	O05556 oryctolagus

RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.  
 RC TISSUE=Prostate; PubMed=7566962;  
 RX MEDLINE=96032566; PubMed=7566962;  
 RA Xian J.W., Chin J.L., Guo Y., Chambers A.F., Finkelstein M.A.,  
 RA Clarke M.W.;  
 RT "Alternative splicing of PSP94 (prostatic secretory protein of 94  
 RT amino acids) mRNA in prostate tissue.";  
 RL Oncogene 11:1041-1047(1995).  
 RN [17]  
 RP SEQUENCE FROM N.A.  
 RA Balaji-Gupta M., Clarke M.W.;  
 RT "Prostate specific protein (PSP94) expression in a human endometrial  
 RT cell line (KME).";  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 RN [18]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate; PubMed=12477932;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,  
 RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Ramey U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smillius D.E.,  
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [19]  
 RP SEQUENCE OF 2-72 FROM N.A.  
 RX MEDLINE=99421644; PubMed=10491085;  
 RA Maekinen M., Vaittonen-Andre C., Lundwall A.;  
 RT "New world, but not old world, monkeys carry several genes encoding  
 RT beta-microseminoprotein.";  
 RL Eur. J. Biochem. 264:407-414(1999).  
 RN [10]  
 RP SEQUENCE OF 21-113.  
 RX MEDLINE=85199974; PubMed=3995056;  
 RA Akiyama K., Yoshioka Y., Schmidt K., Offner G.D., Troxler R.F.,  
 RA Tsuda R., Hara M.;  
 RT "The amino acid sequence of human beta-microseminoprotein.";  
 RL Biochim. Biophys. Acta 823:286-294(1985).  
 RN [11]  
 RP SEQUENCE OF 21-114.  
 RX MEDLINE=85004133; PubMed=6434350;  
 RA Seidat N.G., Arbatli N.J., Rochemont J., Sheth A.R., Chretien M.;  
 RT "Complete amino acid sequence of human seminal plasma beta-inhibin.  
 RT Prediction of post Glu-Arg cleavage as a maturation site.";  
 RL FEBS Lett. 175:349-355(1984).  
 RN [12]  
 RP SEQUENCE OF 21-50 AND 113-114.  
 RX MEDLINE=92028964; PubMed=1930232;  
 RA Liang Z.G., Kamada M., Koide S.S.;  
 RT "Structural identity of immunoglobulin binding factor and prostatic  
 RT secretory protein of human seminal plasma.";  
 RL Biochem. Biophys. Res. Commun. 180:356-359(1991).  
 RN [13]  
 RP SEQUENCE OF 21-41, AND TISSUE SPECIFICITY.  
 RC TISSUE=Semen;  
 RX MEDLINE=95401076; PubMed=7671139;  
 RA Okubo I., Tada T., Ochitai Y., Ueyama H., Shimoto T., Sasaki M.;  
 RT "Human seminal plasma beta-microseminoprotein: its purification,  
 RT characterization, and immunohistochemical localization.";

RL Int. J. Biochem. Cell Biol. 27:603-611(1995).  
 RN [14]  
 RP SEQUENCE OF 21-32.  
 RX MEDLINE=21648993; PubMed=11788998;  
 RA Gharouri B., Stahlboom B., Tagesson C., Lindahl M.;  
 RT "Newly identified proteins in human nasal lavage fluid from  
 RT non-smokers and smokers using two-dimensional gel electrophoresis and  
 RT peptide mass fingerprinting.";  
 RL Proteomics 2:112-120(2002).  
 CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells.  
 CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface.  
 CC -1- ALTERNATIVE PRODUCTS: Secreted. Sperm surface.  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=PSP94;  
 CC IsoId=P08118-1; Sequence=Displayed;  
 CC Name=PSP57;  
 CC IsoId=P08118-2; Sequence=VSP\_003275, VSP\_003276;  
 CC -1- TISSUE SPECIFICITY: Strongly expressed in prostate, liver, kidney,  
 CC breast and penis. Also expressed in pancreas, esophagus, stomach,  
 CC duodenum, colon, trachea, lung, salivary glands and fallopian  
 CC tube. PSP94 is expressed in lung and breast, whereas PSP57 is  
 CC found in kidney and bladder.  
 CC -1- MISCELLANEOUS: SPECIFIC RECEPTORS FOR THIS PROTEIN ARE FOUND ON  
 CC SPERMATOZOIA AND IN THE PROSTATE.  
 CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.  
 CC -----  
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 CC -----  
 DR EMBL, M34376; AAA59871.1; JOINED.  
 DR EMBL, M34373; AAA59871.1; JOINED.  
 DR EMBL, M34374; AAA59871.1; JOINED.  
 DR EMBL, M34375; AAA59871.1; JOINED.  
 DR EMBL, M15885; AAA36635.1; JOINED.  
 DR EMBL, X57928; CAA41002.1; JOINED.  
 DR EMBL, X57929; CAA41002.1; JOINED.  
 DR EMBL, X57930; CAA41002.1; JOINED.  
 DR EMBL, X57931; CAA41002.1; JOINED.  
 DR EMBL, S67815; AAA29732.1; JOINED.  
 DR EMBL, U22178; AAA83556.1; JOINED.  
 DR EMBL, U78976; AAB37355.1; JOINED.  
 DR EMBL, BC005257; AAH05257.1; JOINED.  
 DR EMBL, A013356; CAB39325.1; JOINED.  
 DR PIR, A34567; A34567.  
 DR PIR, G01730; G01730.  
 DR Genew; HGNC:7372; MSMB.  
 DR MIM: 157145; --  
 DR GO; GO:0005615; Cytoplasmic space; TAS.  
 DR GO; GO:0005634; Cytoplasm; TAS.  
 DR InterPro; IPR008735; PSP94.  
 DR Pfam; PF05825; PSP94, 1.  
 KW Signal; Polymorphism; Alternative splicing.  
 FT CHAIN 1 20  
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 FT DISULFID 22 38 BY SIMILARITY.  
 FT DISULFID 23 93 BY SIMILARITY.  
 FT DISULFID 57 93 BY SIMILARITY.  
 FT DISULFID 60 69 OR 70 (BY SIMILARITY).  
 FT DISULFID 62 70 OR 69 (BY SIMILARITY).  
 FT DISULFID 84 107 BY SIMILARITY.  
 FT VARSPLIC 37 77 KMDLGNKHPINSMDNCECTCYETSCCTIVSTPV  
 FT -> MELHLMVMTKAKSSRRRTASISWMBRRDGRKRVLS  
 FT VNG (in isoform PSP57).  
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 FT /FTID=VSP\_003276.  
 FT /FTID=VSP\_003276.  
 FT L -> S (in dbSNP:1804776).  
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 FT I -> M (in dbSNP:1804778).  
 FT VARIANT 78 114  
 FT VARIANT 17 17  
 FT VARIANT 25 25



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SQ SEQUENCE 114 AA; 13079 MW; C0/4AEB984B276C CRC64;
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 CORFKEDCKIVVEKK 51
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ID MSPT SAGOE STANDARD; PRT; 114 AA.
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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-microseminoprotein J1 precursor (msp-J1).
GN MSPJ.
OS Saginus oedipus (cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginini.
OX NCBI_TaxID=9490;
RN [1]
RP MEDLINE=99421644; Pubmed=10491085;
RX Maekinen M., Vaitonen-Andre C., Lundwall A.;
RA "New world, but not old world, monkeys carry several genes encoding
RT beta-microseminoprotein."
RL Eur. J. Biochem. 264:407-414(1999).
CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
-----
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-----
DR EMBL, AJ010155; CAB38123.1; JOINED.
DR EMBL, AJ010156; CAB38123.1; JOINED.
DR GO, GO:0005576; CAB38123.1; JOINED.
DR InterPro; IPR008735; PSP94.
DR Pfam; PF05825; PSP94; 1.
KM SIGNAL.
FT CHAIN 1 20 POTENTIAL.
FT FT 21 114 BETA-MICROSEMINOPROTEIN J1.
FT DISUFID 22 38 BY SIMILARITY.
FT DISUFID 57 93 BY SIMILARITY.
FT DISUFID 60 69 OR 70 (BY SIMILARITY).
FT DISUFID 62 70 OR 69 (BY SIMILARITY).
FT DISUFID 84 107 BY SIMILARITY.
SC SEQUENCE 114 AA; 12746 MW; F3F05BD013445BMD4 CRC64;

Query Match 23.4%; Score 15; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 EISCTLVSPVGYD 30
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AC 097936;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-microseminoprotein J1 precursor (msp-J1).
GN MSPJ.
OS Saginus oedipus (cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginini.
OX NCBI_TaxID=9490;
RN [1]
RP MEDLINE=99421644; Pubmed=10491085;
RX Maekinen M., Vaitonen-Andre C., Lundwall A.;
RA "New world, but not old world, monkeys carry several genes encoding
RT beta-microseminoprotein."
RL Eur. J. Biochem. 264:407-414(1999).
CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-microseminoprotein A1 precursor (msp-A1) (Fragment).
GN MSPA.
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99421644; PubMed=10491085;
RA Meekinen M., Valtanen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
RT beta-microseminoprotein."
RL Eur. J. Biochem. 264:407-414(1999).
CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AJ010158; CAB38124.1; -.
CC EMBL: AJ010159; CAB38124.1; JOINED.
CC GO: GO:0005576; C:extracellular; TAS.
CC InterPro: IPR002400; GRCYSKNOT.
CC Pfam: PF05825; PSP94.
CC PRINTS: PR00438; GRCYSKNOT.
KM Signal.
FT NON TER 1 19
FT SIGNAL 20 112 BY SIMILARITY.
FT CHAIN 21 37 BETA-MICROSEMINOPROTEIN A1.
FT DISULFID 56 92 BY SIMILARITY.
FT DISULFID 59 68 BY SIMILARITY.
FT DISULFID 61 69 OR 69 (BY SIMILARITY).
FT DISULFID 83 106 OR 68 (BY SIMILARITY).
FT DISULFID 83 106 BY SIMILARITY.
SQ SEQUENCE 112 AA; 12631 MW; DDA06BFC1CSCD78B CRC64;

Query Match 20.3%; Score 13; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 EDCXIVVERK 53
DB 90 EDCXIVVERK 102

RESULT 5
MSMB_PAPAN STANDARD; PRT; 114 AA.
AC Q28767;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma
DE protein) (Prostate secretory protein PSP94) (PSP-94).
GN MSMB OR PSP94.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.

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```

RC TISSUE=Prostate; PubMed=9174167;
RX MEDLINE=97316893;
RA Xuan J.W., Wu D., Guo Y., Garde S., Shum D.T., Mikiy M., Zhong R.,
RA Chin J.L.;
RT "Molecular cloning and gene expression analysis of PSP94 (prostate
RT secretory protein of 94 amino acids) in primates."
RL DNA Cell Biol. 16:627-638(1997).
CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U49786; AA62726.1; -.
CC InterPro: IPR008735; PSP94.
CC Pfam: PF05825; PSP94.
KM Signal.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 114 BETA-MICROSEMINOPROTEIN.
FT DISULFID 22 38 BY SIMILARITY.
FT DISULFID 57 93 BY SIMILARITY.
FT DISULFID 60 69 OR 70 (BY SIMILARITY).
FT DISULFID 62 70 OR 69 (BY SIMILARITY).
FT DISULFID 84 107 BY SIMILARITY.
SQ SEQUENCE 114 AA; 13013 MW; A08C837ED81P98BD CRC64;

Query Match 14.1%; Score 9; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 43 CXIVVERK 51
DB 93 CXIVVERK 101

RESULT 6
MSPE_SAGOE STANDARD; PRT; 114 AA.
AC Q97935;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-microseminoprotein E1 precursor (msp-E1).
GN MSPE.
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99421644; PubMed=10491085;
RA Meekinen M., Valtanen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
RT beta-microseminoprotein."
RL Eur. J. Biochem. 264:407-414(1999).
CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Ilyanolsin precursor (Thiol-activated cytolysin).  
 GN ILO.  
 OS Listeria ivanovii.  
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.  
 CX NCBI\_TaxID=1638;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19119;  
 RX MEDLINE=92182018; PubMed=1543752;  
 RA Haas A., Dumbsky M., Kreft J.;  
 RT "Ilyanolsin genes: complete sequence of ilo from Listeria ivanovii  
 and of ilo from Listeria seeligeri";  
 RL Biochim. Biophys. Acta 1150:81-84 (1992).  
 CC -1- FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL  
 CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION.  
 CC CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO  
 CC EUKARYOTIC CELL MEMBRANES.  
 CC -1- SIMILARITY: Belongs to the thiol-activated cytolysin family.  
 CC -----  
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 CC -----  
 DR EMBL; X60461; CAA42995.2; -.  
 DR PIR; S22341; S22341.  
 DR HSSP; P19995; IPRO.  
 DR InterPro; IPR001869; Thiol\_cytolysin.  
 DR Pfam; PF01289; Thiol\_cytolysin; 1.  
 DR PRINTS; PR01400; TACTYOLYSIN.  
 DR PRODOM; PD007062; Thiol\_cytolysin; 1.  
 DR PROSITE; PS00481; THIOI\_CYTOLYSINS; 1.  
 KW Cytolysis; Hemolysis; Toxin; Lipid-binding; signal.  
 FT SIGNAL 1 23  
 FT CHAIN 1 528 IVANOLYSIN.  
 FT ACCT SITE 483 483 BINDING TO CHOLESTEROL (BY SIMILARITY).  
 SO SEQUENCE 528 AA; 58542 MW; D133BEC1A8C51A65 CRC64;  
 Query Match 10.9%; Score 7; DB 1; Length 528;  
 Best Local Similarity 100.0%; Pred. No. 5.2;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 45 YIVVEKK 51  
 DB 97 YIVVEKK 103  
 RESULT 10  
 TACTY\_LISMO STANDARD; PRT; 529 AA.  
 ID TACTY\_LISMO  
 AC P13128; Q48747; Q57096; Q57206;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Listeriolysin O precursor (Thiol-activated cytolysin).  
 GN HLY OR LISA OR HLYA OR LMO0202.  
 OS Listeria monocytogenes.  
 CC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.  
 CX NCBI\_TaxID=1639;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EGD / Serovar 1/2a;  
 RX MEDLINE=89366684; PubMed=2505236;  
 RA Domann E., Chakraborty T.;  
 RT "Nucleotide sequence of the listeriolysin gene from a Listeria  
 RT monocytogenes serotype 1/2a strain";  
 RL Nucleic Acids Res. 17:6406-6406 (1989).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88153053; PubMed=3126142;  
 RA Mengaud J., Viscide M.-F., Chenevert J., Pereira J.M., Geoffroy C.,  
 RA Gicquel-Sanzey B., Baguerio F., Perez-Diaz J.-C., Cossart P.;  
 RT "Expression in *Escherichia coli* and sequence analysis of the  
 RT listeriolysin O determinant of Listeria monocytogenes";  
 RL Infect. Immun. 56:766-772 (1988).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=12067;  
 RX MEDLINE=92040062; PubMed=1937753;  
 RA Rasmussen O.F., Beck T., Olsen J.E., Dons L., Rossen L.;  
 RT "Listeria monocytogenes isolates can be classified into two major  
 RT types according to the sequence of the listeriolysin gene";  
 RL Infect. Immun. 59:3945-3951 (1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=F2365 / Serotype 4b, F5782 / Serotype 4b,  
 RC F4233 / Serotype 1/2b, and F6789 / Serotype 1/2b;  
 RX MEDLINE=98210071; PubMed=9541569;  
 RA Vines A., Swaminathan B.;  
 RT "Identification and characterization of nucleotide sequence  
 RT differences in three virulence-associated genes of Listeria  
 RT monocytogenes strains representing clinically important serotypes";  
 RL Curr. Microbiol. 36:309-318 (1998).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EGD-e / Serovar 1/2a;  
 RX MEDLINE=21537279; PubMed=11679669;  
 RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,  
 RA Baguerio F., Brangeul L., Blocher H., Brandt P., Chakraborty T.,  
 RA Charbit A., Chetouani F., Couve E., de Darvar A., Dehoux P.,  
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,  
 RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,  
 RA Gautier L., Geisel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,  
 RA Jones L.M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurupat G.,  
 RA Madeno E., Maitournam A., Mata Vicente J., Ng E., Nedjati H.,  
 RA Nordisk G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,  
 RA Remmel B., Rose M., Schlutener T., Simoes N., Tierrez A.,  
 RA Vazquez-Boland J.-A., Voss H., Wehlund J., Cossart P.;  
 RT "Comparative genomics of Listeria species";  
 RL Science 294:649-652 (2001)  
 CC -1- FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL  
 CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION.  
 CC CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO  
 CC EUKARYOTIC CELL MEMBRANES.  
 CC -1- SIMILARITY: Belongs to the thiol-activated cytolysin family.  
 CC -----  
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 CC -----  
 DR EMBL; X15127; CAA33223.1; -.  
 DR EMBL; M24199; AAA03018.1; -.  
 DR EMBL; X60035; CAA42639.1; -.  
 DR EMBL; U25443; AAA69525.1; -.  
 DR EMBL; U25446; AAA69528.1; ALT INIT.  
 DR EMBL; U25449; AAA69531.1; ALT\_INIT.  
 DR EMBL; U25452; AAA69534.1; -.  
 DR EMBL; AL591974; CAD00729.1; -.  
 DR PIR; A43505; A43505.  
 DR PIR; A43100; A43100.  
 DR PIR; S24231; S24231.  
 DR HSSP; P19995; IPRO.  
 DR Listerist; LMO00202;  
 DR InterPro; IPR001869; Thiol\_cytolysin.  
 DR Pfam; PF01289; Thiol\_cytolysin; 1.  
 DR PRINTS; PR01400; TACTYOLYSIN.



RESULT 13  
MSMB\_MOUSE STANDARD; PRT; 113 AA.  
ID MSMB\_MOUSE  
AC O08540; 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Beta-microseminoprotein precursor (prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94).  
GN MSMB OR PSP94.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
ON NCI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CD-1;  
RA Xuan J.W., Mdkay M., Wu D., Guo Y., Chin J.L.;  
RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
RL  
CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).  
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.  
CC  
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CC  
CC EMBL; U09840; AAB49683.1; -.  
CC DR MGD; MGI:97166; Msmdb.  
CC DR InterPro; IPR008735; PSP94.  
CC DR Pfam; PFO5825; PSP94; 1.  
CC KW Signal.  
CC FT SIGNAL 1 20 POTENTIAL.  
CC FT CHAIN 21 113 BETA-MICROSEMINOPROTEIN.  
CC FT DISULFID 22 113 BY SIMILARITY.  
CC FT DISULFID 56 92 BY SIMILARITY.  
CC FT DISULFID 59 68 OR 69 (BY SIMILARITY).  
CC FT DISULFID 61 69 OR 68 (BY SIMILARITY).  
CC FT DISULFID 83 106 BY SIMILARITY.  
CC SQ SEQUENCE 113 AA; 12844 MW; 892DAAD4BFE9379 CRC64;  
Query Match 9.4%; Score 6; DB 1; Length 113;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 29 YDXDNC 34  
DB 78 YDXDNC 83

RESULT 14  
RK20\_SPIOI STANDARD; PRT; 127 AA.  
ID RK20\_SPIOI  
AC P28803; Q9M3K6; 01-DEC-1992 (Rel. 24, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Chloroplast 50S ribosomal protein L20.  
GN RPL20.  
OS Spinacia oleracea (Spinach).  
OC Chloroplast; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Spinacia.  
ON NCI\_TaxID=3562;  
RN  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV.  
RA Schmidt J., Herfurth E., Subramanian A.R.;  
RT Purification and characterization of seven chloroplast ribosomal proteins: evidence that organellar ribosomal protein genes are functional and that NH2-terminal processing occurs via multiple pathways in chloroplasts.  
RT Plant Mol. Biol. 20:459-465 (1992).  
CC -1- FUNCTION: This protein binds directly to 23S ribosomal RNA and is necessary for the in vitro assembly process of the 50S ribosomal subunit. It is not involved in the protein synthesizing functions of that subunit (By similarity).  
CC -1- SIMILARITY: Belongs to the L20P family of ribosomal proteins.  
CC  
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CC  
CC EMBL; AJ400848; CAB88751.1; -.  
CC DR PIR; S26228; S26228.  
CC DR HAMAP; MF\_00382; -; 1.  
CC DR InterPro; IPR005813; Ribosomal\_L20.  
CC DR InterPro; IPR005812; Ribosomal\_L20b/O.  
CC DR Pfam; PFO0453; Ribosomal\_L20; 1.  
CC DR PRINTS; PR00062; Ribosomal\_L20.  
CC DR ProDom; PD002389; L20; 1.  
CC DR TIGRFAMs; TIGR01032; rplL bact; 1.  
CC DR PROSITE; PS00937; RIBOSOMAL\_L20; 1.  
CC KW Ribosomal protein; rRNA-binding; Chloroplast.  
CC FT INIT\_MET 0  
CC FT CONFLICT 15 15 K -> E (IN REF. 2).  
CC SQ SEQUENCE 127 AA; 15557 MW; E0F49508C9C6CEC0 CRC64;  
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Best Local Similarity 100.0%; Pred. No. 19;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 39 KXEDCK 44  
DB 116 KXEDCK 121

RESULT 15  
FABI\_RAT STANDARD; PRT; 131 AA.  
ID FABI\_RAT  
AC P02693; 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Fatty acid-binding protein, intestinal (I-FABP) (FABPI).  
GN FABP2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
ON NCI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=84119477; PubMed=6582489;  
RX

RA Alpers D.H., Strauss A.W., Ockner R.K., Bass N.W., Gordon J.I.;  
 RT "Cloning of a cDNA encoding rat intestinal fatty acid binding  
 RL protein.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 81:313-317(1984).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86053743; PubMed=3840724;  
 RA Gordon J.I., Lowe J.B.;  
 RT "Analyzing the structures, functions and evolution of two abundant  
 RT gastrointestinal fatty acid binding proteins with recombinant DNA and  
 RL computational techniques.";  
 RN Chem. Phys. Lipids 38:137-158(1985).  
 [3]  
 RP SEQUENCE OF 1-79 FROM N.A.  
 RX MEDLINE=88058967; PubMed=2824476;  
 RA Sweetser D.A., Birkemaler E.H., Klisak I.J., Zollman S.,  
 RA Sparkes R.S., Mohandas T., Lusis A.J., Gordon J.I.;  
 RT "The human and rodent intestinal fatty acid binding protein genes. A  
 RT comparative analysis of their structure, expression, and linkage  
 RL relationships.";  
 RN J. Biol. Chem. 262:16060-16071(1987).  
 [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=89362478; PubMed=2671390;  
 RA Sacchettini J.C., Gordon J.I., Banaszak L.J.;  
 RT "Crystal structure of rat intestinal fatty acid-binding protein.  
 RT Refinement and analysis of the Escherichia coli-derived protein with  
 RL bound palmitate.";  
 RN J. Mol. Biol. 208:327-339(1989).  
 [5]  
 RP X-RAY CRYSTALLOGRAPHY (1.96 ANGSTROMS).  
 RX MEDLINE=90046570; PubMed=2682622;  
 RA Sacchettini J.C., Gordon J.I., Banaszak L.J.;  
 RT "Refined apoprotein structure of rat intestinal fatty acid binding  
 RL protein produced in Escherichia coli.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 86:7736-7740(1989).  
 [6]  
 RP X-RAY CRYSTALLOGRAPHY (1.19 ANGSTROMS).  
 RX MEDLINE=92156174; PubMed=1740465;  
 RA Scapin G., Gordon J.I., Sacchettini J.C.;  
 RT "Refinement of the structure of recombinant rat intestinal fatty  
 RL acid-binding apoprotein at 1.2-A resolution.";  
 RN J. Biol. Chem. 267:4253-4269(1992).  
 [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
 RX MEDLINE=20158726; PubMed=10692339;  
 RA Ropson I.J., Yowler B.C., Dalesio P.M., Banaszak L., Thompson J.;  
 RT "Properties and crystal structure of a beta-barrel folding mutant.";  
 RN Biophys. J. 78:1551-1560(2000).  
 [8]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=97178830; PubMed=9063893;  
 RA Hodgeson M.E., Cistola D.P.;  
 RT "Discrete backbone disorder in the nuclear magnetic resonance  
 RT structure of apo intestinal fatty acid-binding protein: implications  
 RL for the mechanism of ligand entry.";  
 RN Biochemistry 36:1450-1460(1997).  
 CC -1- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR  
 CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-CoA ESTERS.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to the fatty-acid binding protein (FABP)  
 CC family.  
 CC -----  
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 CC -----  
 CC DR EMBL; K01180; AAA41138.1; -  
 CC EMBL; M35992; AAA41141.1; -

DR EMBL; M18080; AAA41133.1; -  
 DR PIR; I65761; F2RTI.  
 DR PDB; 1IFB; 15-JAN-92.  
 DR PDB; 2IFB; 30-APR-94.  
 DR PDB; 1IFC; 31-JAN-94.  
 DR PDB; 1ICM; 31-JAN-94.  
 DR PDB; 1ICN; 31-JAN-94.  
 DR PDB; 1AEL; 01-APR-97.  
 DR PDB; 1URE; 12-MAR-97.  
 DR PDB; 1A57; 27-MAY-98.  
 DR PDB; 1DC9; 20-MAR-00.  
 DR InterPro; IPR000463; Fatty acid BP.  
 DR InterPro; IPR000566; Lipocin\_cytfabp.  
 DR Pfam; PF00061; lipocalin; 1.  
 DR PRINTS; PR00178; FATTYACIDBP.  
 DR PROSITE; PS00214; FABP; 1.  
 KW Transport; Lipid-binding; Acetylation; 3D-structure.  
 FT INIT MET 0  
 FT MOD RES 1  
 FT CONFLICT 1  
 FT STRAND 82  
 FT HELIX 4  
 FT TURN 12  
 FT HELIX 14  
 FT TURN 22  
 FT HELIX 25  
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 FT STRAND 119  
 FT TURN 120  
 FT STRAND 121  
 FT TURN 122  
 FT STRAND 131  
 SQ SEQUENCE 131 AA; 14993 MW; A60D8170868E571E CRC64;

Query Match 9.4%; Score 6; DB 1; Length 131;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 36 RIFKE 41  
 DB 126 RIFKE 131

Search completed: March 11, 2004, 18:11:10  
 Job time: 12.871 secs

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OM protein - protein search, using sw model

Run on: March 11, 2004, 18:08:03 ; Search time 15.2419 seconds  
(without alignments)  
152.420 Million cell updates/sec

Title: US-09-977-406a-88

Perfect score: 45  
Sequence: 1 SCFIPNEGVPDSTRKCMD.....HPINSEWQDNECTCTCYET 45

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size: 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

1: Issued Patents AA:\*  
2: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep.\*  
3: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep.\*  
4: /cgn2\_6/prodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/2/iaa/PCtUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/2/iaa/backfilest1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	17	37.8	17	1	US-07-899-535A-3
3	6	13.3	241	2	US-08-460-309-17
4	6	13.3	241	2	US-08-125-077-17
5	6	13.3	433	4	US-09-489-039A-9744
6	6	13.3	454	4	US-09-107-532A-4860
7	6	13.3	454	4	US-09-134-000C-6535
8	6	13.3	479	4	US-09-552-991A-19246
9	6	13.3	509	4	US-09-252-991A-27888
10	6	13.3	536	4	US-09-653-274-10
11	6	13.3	877	2	US-08-407-875-2
12	6	13.3	877	2	US-09-126-280-2
13	6	13.3	877	4	US-09-277-858-2
14	6	13.3	929	4	US-09-254-594-3
15	6	13.3	929	4	US-09-254-594-6
16	6	13.3	1115	2	US-08-568-459A-2
17	6	13.3	1115	2	US-08-487-826B-2
18	6	13.3	1115	2	US-09-210-288-2
19	6	13.3	1115	6	5198347-6
20	6	13.3	3088	4	US-09-562-702A-8
21	6	13.3	3088	4	US-09-562-702A-4
22	6	13.3	3110	4	US-09-562-702A-2
23	6	13.3	3110	4	US-09-562-702A-6
24	6	13.3	3110	4	US-09-562-702A-7
25	6	13.3	3110	4	US-09-562-702A-8
26	6	13.3	3111	2	US-08-460-309-4
27	6	13.3	3111	2	US-08-125-077-4

28	5	11.1	5	4	US-09-101-272G-70	Sequence 70, Appl
29	5	11.1	6	1	US-07-791-213D-35	Sequence 35, Appl
30	5	11.1	6	1	US-08-293-150A-35	Sequence 35, Appl
31	5	11.1	6	4	US-09-101-272G-69	Sequence 69, Appl
32	5	11.1	7	1	US-07-791-213D-34	Sequence 34, Appl
33	5	11.1	7	1	US-08-293-150A-34	Sequence 34, Appl
34	5	11.1	8	1	US-09-101-272G-68	Sequence 68, Appl
35	5	11.1	8	1	US-07-791-213D-33	Sequence 33, Appl
36	5	11.1	8	1	US-08-293-150A-33	Sequence 33, Appl
37	5	11.1	9	1	US-09-101-272G-67	Sequence 67, Appl
38	5	11.1	9	1	US-07-791-213D-32	Sequence 32, Appl
39	5	11.1	9	1	US-08-293-150A-32	Sequence 32, Appl
40	5	11.1	9	4	US-08-481-968A-24	Sequence 24, Appl
41	5	11.1	9	4	US-08-154-712B-24	Sequence 24, Appl
42	5	11.1	9	4	US-09-101-272G-66	Sequence 66, Appl
43	5	11.1	10	1	US-07-791-213D-31	Sequence 31, Appl
44	5	11.1	10	1	US-08-293-150A-31	Sequence 31, Appl
45	5	11.1	10	4	US-09-101-272G-65	Sequence 65, Appl

#### ALIGNMENTS

RESULT 1  
US-07-899-535A-1  
; Sequence 1, Application US/07899535A  
; Patent No. 5428011  
; GENERAL INFORMATION:  
; APPLICANT: Sheth, Anil R.  
; APPLICANT: Garde, Seema  
; TITLE OF INVENTION: Pharmaceutical Preparations For  
; TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate  
; TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Mr. George Loud  
; STREET: 2001 Jefferson Davis Highway, Suite 306  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/899,535A  
; FILING DATE: 16-JUN-1992  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Loud, George A.  
; REGISTRATION NUMBER: 25,814  
; REFERENCE/DOCKET NUMBER: S&B-A835  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-415-0960  
; TELEFAX: 703-415-0962  
; TELEX: 24 8614  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 94 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; US-07-899-535A-1

Query Match 100.0%; Score 45; DB 1; Length 94;  
Best Local Similarity 100.0%; Pred. NO. 1.4e-40;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SCYFIPNEGVPDSTRKMDLKGNKHPINSEWQTDNCECTCTCYET 45  
DB 1 SCYFIPNEGVPDSTRKMDLKGNKHPINSEWQTDNCECTCTCYET 45

RESULT 2  
US-07-899-535A-3

Sequence 3, Application US/07899535A  
Patent No. 5428011

## GENERAL INFORMATION:

APPLICANT: Sheth, Anil R.

APPLICANT: Garde, Seema

TITLE OF INVENTION: Pharmaceutical Preparations For  
Inhibiting Tumours Associated With Prostate

TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mr. George Loud

STREET: 2001 Jefferson Davis Highway, Suite 306

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/899,535A

FILING DATE: 16-JUN-1992

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Loud, George A.

REGISTRATION NUMBER: 25,814

REFERENCE/DOCKET NUMBER: S&amp;B-A835

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-415-0960

TELEFAX: 703-415-0962

TELEX: 24 8614

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYDROTHERMAL: NO

US-07-899-535A-3

Query Match

Best Local Similarity 100.0%; Score 17; DB 1; Length 17;  
Pred. No. 1,5e-11;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SCYFIPNEGVPDSTRK 17

DB 1 SCYFIPNEGVPDSTRK 17

RESULT 3  
US-08-460-309-17

Sequence 17, Application US/08460309  
Patent No. 5837496

## GENERAL INFORMATION:

APPLICANT: Ernyvall, Eva

APPLICANT: Leivo, Ilmo

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin  
Fragments and Uses Thereof

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California  
COUNTRY: USA  
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,309

FILING DATE: 08/125,077

APPLICATION NUMBER: US PCT/US 94/10730

FILING DATE: 22-SEP-1993

APPLICATION NUMBER: US 07/472,319

FILING DATE: 21-SEP-1994

APPLICATION NUMBER: US 07/919,951

FILING DATE: 27-JUL-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LA 9721

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-8949

TELEFAX: (619) 535-9001

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-460-309-17

Query Match

Best Local Similarity 100.0%; Score 6; DB 2; Length 241;  
Pred. No. 56;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 NCETCT 41

DB 103 NCETCT 108

RESULT 4  
US-08-125-077-17

Sequence 17, Application US/08125077  
Patent No. 5872231 5840863

## GENERAL INFORMATION:

APPLICANT: Ernyvall, Eva

APPLICANT: Leivo, Ilmo

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin  
Fragments and Uses Thereof

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/125,077

FILING DATE: 22-SEP-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/US 94/10730  
FILING DATE: 21-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/472,319  
FILING DATE: 30-JAN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/919,951  
FILING DATE: 27-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LA 9721  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-125-077-17

Query Match 13.3%; Score 6; DB 2; Length 241;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 NCETCT 41  
Db 103 NCETCT 108

RESULT 5  
US-09-489-039A-9744  
Sequence 9744, Application US/03489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 9744  
LENGTH: 433  
TYPE: PRT  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-9744

Query Match 13.3%; Score 6; DB 4; Length 433;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KGNKHP 27  
Db 264 KGNKHP 269

RESULT 6  
US-09-107-532A-4860  
Sequence 4860, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSER: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street

CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Arinello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 4860:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 454 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...454  
SEQUENCE DESCRIPTION: SEQ ID NO: 4860:  
US-09-107-532A-4860

Query Match 13.3%; Score 6; DB 4; Length 454;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DLKGNK 25  
Db 222 DLKGNK 227

RESULT 7  
US-09-134-000C-6535  
Sequence 6535, Application US/09134000C  
Patent No. 6617156  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 032796-032  
CURRENT APPLICATION NUMBER: US/09/134,000C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/055,778  
PRIOR FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 6812  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6535  
LENGTH: 454  
TYPE: PRT  
ORGANISM: Enterococcus faecalis  
US-09-134-000C-6535

Query Match 13.3%; Score 6; DB 4; Length 454;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DLGNKX 25  
| | | | |  
Db 222 DLGNKX 227

RESULT 8  
US-09-252-991A-19246  
; Sequence 19246, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 19246  
; LENGTH: 479  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-19246

Query Match 13.3%; Score 6; DB 4; Length 479;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PGDSTR 16  
| | | | |  
Db 19 PGDSTR 24

RESULT 9  
US-09-252-991A-27888  
; Sequence 27888, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 27888  
; LENGTH: 503  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-27888

Query Match 13.3%; Score 6; DB 4; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NEGVPG 12  
| | | | |  
Db 123 NEGVPG 128

RESULT 10  
US-09-252-991A-23445  
; Sequence 23445, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.

QY 7 NEGVPG 12  
| | | | |  
Db 351 NEGVPG 356

RESULT 11  
US-09-653-274-10  
; Sequence 10, Application US/09653274  
; Patent No. 6635742  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, Bryan J  
; APPLICANT: Yeung, George Y  
; APPLICANT: Arterburn, Matthew C  
; APPLICANT: Mize, Nancy K  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Dimanac, Radjole T  
; TITLE OF INVENTION: Methods and Materials Relating to Semaphorin-Like  
; FILE REFERENCE: HYS-23  
; CURRENT APPLICATION NUMBER: US/09/653,274  
; CURRENT FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: 09/491,404  
; PRIOR FILING DATE: 2000-01-10  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 536  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-653-274-10

Query Match 13.3%; Score 6; DB 4; Length 536;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VPQDST 15  
| | | | |  
Db 280 VPQDST 285

RESULT 12  
US-08-407-875-2  
; Sequence 2, Application US/08407875  
; Patent No. 5912122  
; GENERAL INFORMATION:  
; APPLICANT: Dagset, Lorie  
; APPLICANT: Lu, Chin-Chun  
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
; SUBTYPE METAB, NUCLEIC ACIDS ENCODING SAME AND USES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/407,875  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9921  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 877 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-407-875-2

Query Match 13.3%; Score 6; DB 2; Length 877;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 DSTRKC 18  
Db 378 DSTRKC 383

RESULT 13  
US-09-126-280-2  
Sequence 2, Application US/09126280  
Patent No. 6103524  
GENERAL INFORMATION:  
APPLICANT: Wu, Su  
APPLICANT: Belagade, Rama M  
TITLE OF INVENTION: Metabotropic Glutamate Receptor Protein and Nucleic  
Acid  
FILE REFERENCE: Sequence List  
Patent No. 6103524  
CURRENT APPLICATION NUMBER: US/09/126,280  
CURRENT FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 877  
TYPE: PRT  
ORGANISM: Human  
US-09-126-280-2

Query Match 13.3%; Score 6; DB 3; Length 877;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 DSTRKC 18  
Db 378 DSTRKC 383

RESULT 14  
US-09-277-858-2  
Sequence 2, Application US/09277858  
Patent No. 6362316

GENERAL INFORMATION:  
APPLICANT: Dagget, Lorrie  
Lu, Chin-Chun  
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTOR  
SUBTYPE MGLUR6, NUCLEIC ACIDS ENCODING SAME AND USES  
THEREOF

NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/277,858  
FILING DATE: 26-Mar-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/407,875  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9921  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 877 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-277-858-2

Query Match 13.3%; Score 6; DB 4; Length 877;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 DSTRKC 18  
Db 378 DSTRKC 383

RESULT 15  
US-09-254-594-3  
Sequence 3, Application US/09254594  
Patent No. 6566094  
GENERAL INFORMATION:  
APPLICANT: KIMURA, Toru  
APPLICANT: KIKUCHI, Kaoru  
TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y  
FILE REFERENCE: 0020-4527P  
CURRENT APPLICATION NUMBER: US/09/254,594  
CURRENT FILING DATE: 1999-05-11  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 3  
LENGTH: 929  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1..7)  
OTHER INFORMATION: Tissue Type: Brain  
NAME/KEY: misc\_feature

LOCATION: ()..()  
; OTHER INFORMATION: Identification Method: P for resulting peptide  
US-09-254-594-3

Query March 13.3%; Score 6; DB 4; Length 929;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VPGDST 15  
|||  
Db 289 VPGDST 294

Search completed: March 11, 2004, 18:14:43  
Job time : 16.2419 secs

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CM protein - protein search, using sw model

Run on: March 11, 2004, 18:06:28 ; Search time 12.3387 Seconds  
(without alignments)  
350.816 Million cell updates/sec

Title: US-09-977-406a-88  
Perfect score: 45  
Sequence: 1 SCYFIPNEGVPDSTRKMD.....HPINSEWQTDNCECTCYET 45  
Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 283366 segs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: PIR 78.\*  
1: p1r1.\*  
2: p1r2.\*  
3: p1r3.\*  
4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	114	2	A34567 beta-microseminopr
2	16	35.6	77	2	G01730 PSP57 - human
3	11	24.4	114	2	A54663 seminal plasma pro
4	7	15.6	93	2	AF0776 conserved hypothet
5	7	15.6	502	2	D70806 probable fadhl7 pr
6	6	13.3	91	2	S41563 beta-microseminopr
7	6	13.3	105	2	PC4046 hypothetrical 105 p
8	6	13.3	160	2	H86662 chiol. peroxidase (
9	6	13.3	215	2	T41423 hypothetrical prote
10	6	13.3	226	2	T49719 hypothetrical prote
11	6	13.3	239	2	D71187 probable ribosom
12	6	13.3	324	2	AF1379 hypothetrical prote
13	6	13.3	326	2	TC7094 nine-heme cytochro
14	6	13.3	405	2	D96614 hypothetrical prote
15	6	13.3	458	2	S41593 translation elonga
16	6	13.3	458	2	A34561 translation elonga
17	6	13.3	460	2	S43861 translation elonga
18	6	13.3	468	2	T50982 origin recognition
19	6	13.3	485	2	C83598 hypothetrical prote
20	6	13.3	487	2	B71677 histidine kinase s
21	6	13.3	497	2	G97738 histidine kinase s
22	6	13.3	525	2	T34556 helicase - fission
23	6	13.3	570	2	T38489 unknown protein (l
24	6	13.3	601	2	B96744 phosphonolpyruvat
25	6	13.3	803	2	E82392 metabotropic gluta
26	6	13.3	871	2	A46742 hypothetrical prote
27	6	13.3	881	2	T33810 hypothetrical prote
28	6	13.3	895	2	T32374 hypothetrical prote
29	6	13.3	900	2	C96842

30	6	13.3	960	2	S54461 hypothetrical prote
31	6	13.3	966	2	G68189 hypothetrical prote
32	6	13.3	1070	2	T30848 Duffy receptor - p
33	6	13.3	1140	2	T24213 hypothetrical prote
34	6	13.3	1295	2	A32901 gld1 protein precu
35	6	13.3	1460	2	T00095 hypothetrical prote
36	6	13.3	1496	2	T19833 hypothetrical prote
37	6	13.3	1696	2	T23617 hypothetrical prote
38	6	13.3	3328	2	T30835 breast cancer tumo
39	6	13.3	3329	2	T42205 breast cancer susc
40	6	13.3	3329	2	T30904 breast cancer tumo
41	5	11.1	18	2	T11312 protein gp45.1 - p
42	5	11.1	20	2	S00492 hemocyanin chain I
43	5	11.1	35	2	G60529 hemocyanin M3' - c
44	5	11.1	36	2	A38728 pyruvate decarboxy
45	5	11.1	38	2	UN0613 defensin 4K - scor

## ALIGNMENTS

## RESULT 1

A34567 beta-microseminoprotein precursor - human  
N:Alternate names: beta-inhibin; prostatic secretory protein; PSP-94; seminal plasma pro  
C:Species: Homo sapiens (man)  
C:Date: 13-Jul-1990 #sequence revision 13-Jul-1990 #text change 20-Aug-1999  
C:Accession: A34567; A26451; A29777; A30984; A60673; S16238; I52682  
R:Green, C.B.; Liu, W.Y.; Kwok, S.C.M.  
Biochem. Biophys. Res. Commun. 167, 1184-1190, 1990  
A:Title: Cloning and nucleotide sequence analysis of the human beta-microseminoprotein;  
A:Reference number: A34567; MUID:90211299; PMID:2322265  
A:Accession: A34567  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-114 <GRE>  
A:Cross-references: GB:M4376; NID:G514370; PIDN:AAA59671.1; PID:G514372  
R:Widlay, M.; Nole, S.; Fournier, S.; Benjannet, S.; Chapelaine, P.; Paradis, G.; Dub  
DNA 6, 23-29, 1987  
A:Title: Molecular cloning and sequence of the cDNA for a 94-amino-acid seminal plasma I  
A:Reference number: A26451; MUID:87161231; PMID:3829888  
A:Accession: A26451  
A:Molecule type: mRNA  
A:Residues: 1-114 <MBI>  
A:Cross-references: GB:M45885; NID:G338414; PIDN:AAA36635.1; PID:G338415  
R:Akiyama, K.; Yoshioke, Y.; Schmid, K.; Offner, G.D.; Troxler, R.F.; Teuda, R.; Hara, I  
Biochim. Biophys. Acta 829, 288-294, 1985  
A:Title: The amino acid sequence of human beta-microseminoprotein.  
A:Reference number: A29777; MUID:8519974; PMID:3995056  
A:Accession: A29777  
A:Molecule type: Protein  
A:Residues: 21-58; PT, 61-113 <AKI>  
R:Seidman, N.G.; Arpatli, N.U.; Rochemont, J.; Sheth, A.R.; Chretien, M.  
FEBS Lett. 175, 349-355, 1984  
A:Title: Complete amino acid sequence of human seminal plasma beta-inhibin. Prediction  
A:Reference number: A30984; MUID:85004133; PMID:6434350  
A:Accession: A30984  
A:Molecule type: Protein  
A:Residues: 21-112; G, 114 <SEI>  
R:Weilber, H.; Anderson, C.; Murne, A.; Ramevik, G.; Lindstroem, C.; Lilja, H.; Fernlur  
Am. J. Pathol. 137, 593-604, 1990  
A:Title: Beta microseminoprotein is not a prostate-specific protein.  
A:Reference number: A60673; MUID:90379237; PMID:2205099  
A:Accession: A60673  
A:Molecule type: Protein  
A:Residues: 21, 'X', 23-34 <WEI>  
A:Experimental source: gastric juice  
R:Nollet, S.; Mikay, M.; Chretien, M.  
Biochim. Biophys. Acta 1089, 247-249, 1991  
A:Title: Prostatic secretory protein (PSP-94): gene organization and promoter sequence in  
A:Reference number: S16237; MUID:91274357; PMID:2054385  
A:Accession: S16238  
A:Molecule type: DNA

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A:Residues: 1-114 <NOL>  
 A:Cross-references: EMBL:X57928; NID:G35760; PIDN:CAA1002.1; PID:9825707  
 A:Note: the authors translated the codon ACT for residue 54 as Trp  
 R:Lit, A.Y.; Brader, R.C.; Vessella, R.L.  
 Cancer Lett. 74, 91-99, 1993  
 A:Title: Decreased expression of prostatic secretory protein PSP94 in prostate cancer.  
 A:Reference number: 152682; MUID:94115955; PMID:7506990  
 A:Accession: 152682  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-114 <RES>  
 A:Cross-references: GB:567815; NID:9460568; PIDN:AA29732.1; PID:9460569  
 A:Comment: This protein is a component of seminal plasma as well as secretory fluids from  
 C:Genetics:  
 A:Gene: GDB:MSMB  
 A:Cross-references: GDB:128042; OMIM:157145  
 A:Map position: 10q11.2-10q11.2  
 A:Introns: 1/3; 37/1; 72/2  
 C:Superfamily: seminal plasma protein  
 C:Keywords: semen  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-114/Product: seminal plasma protein #status experimental <MAT>

Query Match 100.0%; Score 45; DB 2; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 4,1e-42;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SCVFIPNEGVGDSIRKCMPLKGNKHPINSEWOTNCECTCYET 45  
 DB 21 SCVFIPNEGVGDSIRKCMPLKGNKHPINSEWOTNCECTCYET 65

RESULT 2  
 G01730  
 PSP57 - human  
 C:Species: Homo sapiens (man)  
 C:Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 20-Aug-1999  
 C:Accession: G01730  
 R:Xuan, J.W.; Chiu, J.L.; Guo, Y.; Chambers, A.F.; Finkelman, M.A.; Clarke, M.W.  
 submitted to the EMBL Data Library, March 1995  
 A:Reference number: G08240  
 A:Accession: G01730  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-77 <XUA>  
 A:Cross-references: EMBL:U22178; NID:9885984; PIDN:AAA83556.1; PID:9885985  
 C:Superfamily: seminal plasma protein

Query Match 35.6%; Score 16; DB 2; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 1,5e-10;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SCVFIPNEGVGDSIR 16  
 DB 21 SCVFIPNEGVGDSIR 36

RESULT 3  
 A54663  
 seminal plasma protein PSP-94 precursor - rhesus macaque  
 N:Alternate names: prostatic secretory protein PSP94  
 C:Species: Macaca mulatta (rhesus macaque)  
 C:Date: 02-Jun-1995 #sequence\_revision 02-Jun-1995 #text\_change 20-Aug-1999  
 C:Accession: S16237; A54663  
 R:Nolet, S.; Mbikay, M.; Chretien, M.  
 Biochim. Biophys. Acta 1089, 247-249, 1991  
 A:Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in  
 A:Reference number: S16237; MUID:91274357; PMID:2054385  
 A:Accession: S16237  
 A:Molecule type: DNA  
 A:Residues: 1-114 <NO2>  
 A:Cross-references: EMBL:X57932; NID:G38094; PINN:CAA1003.1; PID:9829152  
 A:Note: the authors translated the codon ACT for residue 54 as Trp

R:Nolet, S.; St-Louis, D.; Mbikay, M.; Chretien, M.  
 Genomics 9, 775-777, 1991  
 A:Title: Rapid evolution of prostatic protein PSP-94 suggested by sequence divergence between  
 A:Reference number: A54663; MUID:91244325; PMID:2037304  
 A:Accession: A54663  
 A:Molecule type: mRNA  
 A:Residues: 1-114 <NOL>  
 A:Cross-references: GB:M02161; NID:9342280; PIDN:AAA36903.1; PID:9342281  
 C:Genetics:  
 A:Introns: 1/3; 37/1; 72/2  
 C:Superfamily: seminal plasma protein  
 F:1-20/Domain: signal sequence #status predicted <SIG>

Query Match 24.4%; Score 11; DB 2; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 6,4e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DLKGNKHPINS 30  
 DB 40 DLKGNKHPINS 50

RESULT 4  
 AF0776  
 conserved hypothetical protein STY2382 [imported] - Salmonella enterica subsp. enterica  
 C:Species: Salmonella enterica subsp. enterica serovar Typhi  
 A:Note: this species has also been called Salmonella typhi  
 C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C:Accession: AF0776  
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher  
 th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar  
 , S.; Moule, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001  
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.  
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero  
 A:Reference number: AB0502; MUID:21534947; PMID:11677608  
 A:Accession: AF0776  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-93 <PAR>  
 A:Cross-references: GB:AU513382; PIDN:CA02532.1; PID:916503393; GSPDB:GN00176  
 C:Genetics:  
 A:Gene: STY2382

Query Match 15.6%; Score 7; DB 2; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 VPGDSTR 16  
 DB 79 VPGDSTR 85

RESULT 5  
 D70806  
 probable faad17 protein - Mycobacterium tuberculosis (strain H37RV)  
 C:Species: Mycobacterium tuberculosis  
 C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 18-Aug-2000  
 C:Accession: D70806  
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,  
 ; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentile, S.; Hamlin, N.; Holroyd, S.  
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
 Nature 393, 537-544, 1998  
 A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A:Reference number: A70500; MUID:98295987; PMID:9634230  
 A:Accession: D70806  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-502 <COU>  
 A:Cross-references: GB:AL022022; GB:AL123456; NID:93261554; PIDN:CAA17743.1; PID:9292444  
 A:Experimental source: strain H37RV  
 C:Genetics:



A:Gene: fadD17  
C:Superfamily: 4-conumarate-CoA ligase; acetate-CoA ligase homology  
F:51-486/Domain: acetate-CoA ligase homology <ACTL>

Query Match  
Best Local Similarity 15.6%; Score 7; DB 2; Length 502;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NEGVPGD 13  
DB 272 NEGVPGD 278

RESULT 6  
S41663  
beta-microseminoprotein - pig  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C/Accession: S41663  
R.Fernlund, P.; Granberg, L.B.; Roepstorff, P.  
Arch. Biochem. Biophys. 309, 70-76, 1994  
A/Title: Amino acid sequence of beta-microseminoprotein from porcine seminal plasma.  
A/Reference number: S41663; MUID:94161559; PMID:8117114  
A/Accession: S41663  
A/Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-91 <FER>  
C:Superfamily: seminal plasma protein

Query Match  
Best Local Similarity 13.3%; Score 6; DB 2; Length 91;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CYFIPN 7  
DB 2 CYFIPN 7

RESULT 7  
PC4046  
hypothetical 105 protein - Pseudomonas putida (fragment)  
C/Species: Pseudomonas putida  
C/Date: 04-Oct-1995 #sequence\_revision 10-Nov-1995 #text\_change 20-Jun-2000  
C/Accession: PC4046  
R.Jinoue, H.; Inagaki, K.; Sugimoto, M.; Esaki, N.; Soda, K.; Tanaka, H.  
J. Biochem. 117, 1120-1125, 1995  
A/Title: Structural analysis of the L-methionine gamma-lyase gene from Pseudomonas putida  
A/Reference number: J04174; MUID:96172583; PMID:8586629  
A/Accession: PC4046  
A:Molecule type: DNA  
A:Residues: 1-105 <TNO>  
A:Cross-references: GB:D88554; DBJ:D30039; NID:g1813427; PIDN:BA13643.1; PID:g1813428  
C/Comment: This protein shows homology with pyruvate dehydrogenase (lipoamide), and may  
C:Superfamily: pyruvate dehydrogenase (lipoamide); thiamin pyrophosphate-binding domain

Query Match  
Best Local Similarity 13.3%; Score 6; DB 2; Length 105;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GYVPGD 14  
DB 12 GYVPGD 17

RESULT 8  
H86662  
thiol peroxidase (EC 1.11.1.1-) [imported] - Lactococcus lactis subsp. lactis (strain IL1  
C/Species: Lactococcus lactis subsp. lactis  
C/Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C/Accession: H86662  
R.Bolotin, A.; Winkler, P.; Mauger, S.; Jallion, O.; Malarme, K.; Welssenbach, J.; Ehrli  
Genome Res. 11, 731-753, 2001  
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss

A/Reference number: A86625; MUID:21235186; PMID:11337471

A/Accession: H86662  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-160 <STO>  
A:Cross-references: GB:AE005176; PID:g12723168; PIDN:AAK04402.1; GSPDB:GN00146  
A:Experimental source: strain IL1403  
C/Genetics: tpx  
C:Superfamily: thioredoxin peroxidase  
C:Keywords: oxidoreductase

Query Match  
Best Local Similarity 13.3%; Score 6; DB 2; Length 160;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DKGK 25  
DB 30 DKGK 35

RESULT 9  
T41423  
hypothetical protein SPCC576.13 - fission yeast (Schizosaccharomyces pombe)  
C/Species: Schizosaccharomyces pombe  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C/Accession: T41423  
R.Wood, V.; Raundream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.  
submitted to the EMBL Data Library, September 1998  
A/Reference number: Z21954  
A/Accession: T41423  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-215 <WOO>  
A:Cross-references: EMBL:AL031798; PIDN:CAA21192.1; GSPDB:GN00068; SPDB:SPCC576.13  
A:Experimental source: strain 972h-, cosmid c576  
C/Genetics: tpx  
A:Gene: SPDB:SPCC576.13  
A/Map position: 3

Query Match  
Best Local Similarity 13.3%; Score 6; DB 2; Length 215;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VPGDST 15  
DB 20 VPGDST 25

RESULT 10  
T49719  
hypothetical protein B23J21.320 [imported] - Neurospora crassa  
C/Species: Neurospora crassa  
C/Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 18-Aug-2000  
C/Accession: T49719  
R.Schulze, U.; Altm, V.; Hohnes, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura,  
submitted to the Protein Sequence Database, May 2000  
A/Reference number: Z25022  
A/Accession: T49719  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-226 <SCH>  
A:Cross-references: EMBL:AL356172; GSPDB:GN00116; NCSP:B23J21.320  
A:Experimental source: BAC clone B23J21, strain OR74A  
C/Genetics: tpx  
A:Gene: NCSP:B23J21.320  
A/Map position: 6  
A/Introns: 90/1  
C:Superfamily: Neurospora crassa hypothetical protein B23J21.320

Query Match  
Best Local Similarity 13.3%; Score 6; DB 2; Length 226;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



C:Genetics:  
A:Gene: TER  
C:Superfamily: translation elongation factor Tu; translation elongation factor Tu homoid  
C:Keywords: GTP binding; methylated amino acid; nucleotide binding; P-loop; protein bios  
F:8-156/Domain: translation elongation factor Tu homology <ERTU>  
F:14-21/Region: nucleotide-binding motif A (P-loop)  
F:153-156/Region: GTP-binding NKXD motif  
F:330/Modified site: N6-methyllysine (Lys) #status predicted  
F:770/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted  
F:316/Modified site: N6,N6-dimethyllysine (Lys) #status predicted  
F:390/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 13.3%; Score 6; DB 2; Length 458;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGVPGD 13  
| | | | |  
| | | | |  
Db 299 EGVPGD 304

Search completed: March 11, 2004, 18:13:51  
Job time : 14.3387 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2004, 17:57:02 ; Search time 8.34677 Seconds  
(without alignments)  
280.726 Million cell updates/sec

Title: US-09-977-406a-88

Perfect score: 45  
Sequence: 1 SCYFIPNEGVPDSTRKMD.....HPINSEWQDNCETCTCYET 45

Scoring table: OLIGO  
Gapex 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size: 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	114	1 MSMB_HUMAN	P08118 homo sapien
2	11	24.4	114	1 MSMB_MACMU	P25142 macaca mula
3	11	24.4	114	1 MSMB_PAPAN	O28767 papio anubi
4	11	24.4	114	1 MSPJ_SAGOE	O97949 saguinus oe
5	8	17.8	112	1 MSPA_SAGOE	O97936 saguinus oe
6	8	17.8	114	1 MSPJ_SAGOE	O97935 saguinus oe
7	7	15.6	211	1 V33P_ADB40	P11805 human adeno
8	6	13.3	111	1 MSMB_PIG	O02826 sus scrofa
9	6	13.3	159	1 YQOO_CLOPE	O8x85 clostridium
10	6	13.3	223	1 EMBP_MOUSE	O61878 mus musculu
11	6	13.3	239	1 RL2_EYRHO	O59421 pyrococcus
12	6	13.3	301	1 SCOT_HUMAN	C73880 homo sapien
13	6	13.3	326	1 CYC9_DESDE	O97860 desulfovibr
14	6	13.3	458	1 BFIA_ASHGO	P41752 ashya goss
15	6	13.3	458	1 BFIA_CANAL	P16017 candida alb
16	6	13.3	459	1 MURD_LACPL	O88v80 lactobacill
17	6	13.3	460	1 BFIA_PODAN	O01520 podospora a
18	6	13.3	461	1 BFIA_PODCU	O01765 podospora c
19	6	13.3	499	1 YLII_MYCHO	P43055 mycoplasma
20	6	13.3	871	1 MGR6_RAT	P35349 rattus norv
21	6	13.3	877	1 MGR6_HUMAN	O15303 homo sapien
22	6	13.3	923	1 HXK3_HUMAN	P52790 homo sapien
23	6	13.3	930	1 SM6C_HUMAN	O9h3t2 homo sapien
24	6	13.3	931	1 SM6C_MOUSE	O9wrm3 mus musculu
25	6	13.3	960	1 SM6C_RAT	O9wrl3 rattus norv
26	6	13.3	960	1 YMK6_YEAST	O04279 saccharomyc
27	6	13.3	1070	1 PVDR_PLAVS	P22290 plasmodium
28	6	13.3	1295	1 GLP1_CAEL	P13508 caenorhabd
29	6	13.3	3110	1 LMA2_HUMAN	P24043 homo sapien
30	6	13.3	3329	1 BRCC_MOUSE	P97929 mus musculu
31	5	11.1	20	1 HCVA_PANJA	P82310 panulitius j
32	5	11.1	35	1 HCVA_CHEDE	P83173 cheirax deest
33	5	11.1	37	1 DEF4_ANDAU	P56686 androctonus

## ALIGNMENTS

RESULT 1	MSMB_HUMAN	STANDARD;	PRT;	114 AA.
ID	MSMB_HUMAN	P08118; P11999; Q13125; Q9UC59;		
AC	P08118; P11999; Q13125; Q9UC59;			
DT	01-AUG-1988 (Rel. 08, Created)			
DT	01-AUG-1988 (Rel. 08, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94) (Seminal plasma beta-inhibin) (Immunoglobulin binding factor) (IGBF) (PN44).			
DE	MSMB OR PSPP.			
GN	Homo sapiens (Human)			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid:9606;			
RN	[1] SEQUENCE FROM N.A.			
RX	MEDLINE=87161231; PubMed=3829888;			
RA	Molloy M., Nolet S., Fournier S., Benjannet S., Chapdelaine P., Paradis G., Dube J.Y., Tremblay R., Lazare C., Seidah N.G., Chretien M.;			
RT	"Molecular cloning and sequence of the cDNA for a 94-amino-acid seminal plasma protein secreted by the human prostate.";			
RL	DNA 6:23-29 (1987).			
RN	[2] SEQUENCE FROM N.A.			
RX	MEDLINE=91274357; PubMed=2054385;			
RA	Nolet S., Molloy M., Chretien M.;			
RT	"Prostatic secretory protein PSP94: gene organization and promoter sequence in rhesus monkey and human.";			
RL	Biochim. Biophys. Acta 1089:247-249 (1991).			
RN	[3] SEQUENCE FROM N.A.			
RX	MEDLINE=90211299; PubMed=2322265;			
RA	Green C.B., Liu W.Y., Kwok S.C.M.;			
RT	"Cloning and nucleotide sequence analysis of the human beta-microseminoprotein gene.";			
RL	Biochem. Biophys. Res. Commun. 167:1184-1190 (1990).			
RN	[4] SEQUENCE FROM N.A.			
RX	MEDLINE=90073664; PubMed=2590204;			
RA	Uvabaek M., Lindstroem C., Weider H., Abrahamsson P.-A., Lilja H., Lundwall A.;			
RT	"Molecular cloning of a small prostate protein, known as beta-microseminoprotein, PSP94 or beta-inhibin, and demonstration of transcripts in non-genital tissues.";			
RL	Biochem. Biophys. Res. Commun. 164:1310-1315 (1989).			
RN	[5] SEQUENCE FROM N.A.			
RP	TISSUE=Prostate;			
RC	MEDLINE=94115955; PubMed=7506990;			
RA	Liu A.Y., Brainer R.C., Vessella R.L.;			
RT	"Decreased expression of prostatic secretory protein PSP94 in prostate cancer.";			
RL	Cancer Lett. 74:91-99 (1993).			
RN	[6]			

34	5	11.1	38	1	DEF4_LEIHO	P41965 leirus qui
35	5	11.1	38	1	DEF1_AESCY	P80154 aescna cya
36	5	11.1	72	1	IFI_TREPA	O83135 treponema p
37	5	11.1	74	1	DEF1_DERVA	O86415 dermacentor
38	5	11.1	96	1	SP5G_BACME	P28016 bacillus me
39	5	11.1	97	1	SP5G_BACSU	P28015 bacillus su
40	5	11.1	98	1	RL3E_METTH	O27127 methanobact
41	5	11.1	105	1	YMK8_YEAST	O03759 saccharomyc
42	5	11.1	107	1	FTSL_HAEIN	P45058 haemophilus
43	5	11.1	109	1	GLB8_CERLA	O76243 cerebratulu
44	5	11.1	111	1	RL18_THERH	P80320 thermus the
45	5	11.1	113	1	CYC_EWEMI	P38091 emeticella

RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.  
RC TISSUE=Prostate;  
RX MEDLINE=9603256; PubMed=7566962;  
RA Xian J.W., Chin J.L., Guo Y., Chambers A.F., Finkelstein M.A.,  
RA Clarke M.W.,  
RT "Alternative splicing of PSP94 (prostatic secretory protein of 94  
RT amino acids) mRNA in prostate tissue.",  
RL Oncogene 11:1041-1047(1995).  
RP SEQUENCE FROM N.A.  
RA Bajaj-Gupta M., Clarke M.W.;  
RT "Prostate specific protein (PSP94) expression in a human endometrial  
RT cell line (KLE).";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RX MEDLINE=22398257; PubMed=12477932;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
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RA Paley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Greenwood J., Schmitz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Scherch A., Schein J.E., Jones S.J.W., Maira W.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.",  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RP SEQUENCE OF 2-72 FROM N.A.  
RX MEDLINE=99421644; PubMed=10491085;  
RA Maekinen M., Valtonen-Andre C., Lundwall A.;  
RT "New world, but not old world, monkeys carry several genes encoding  
RT beta-microseminoprotein.",  
RL Eur. J. Biochem. 264:407-414(1999).  
RP SEQUENCE OF 21-113.  
RX MEDLINE=85199974; PubMed=3995056;  
RA Akiyama K., Yoshioke Y., Schmid K., Offner G.D., Troxler R.F.,  
RA Tsuda R., Hara M.;  
RT "The amino acid sequence of human beta-microseminoprotein.",  
RL Biochim. Biophys. Acta 829:288-294(1985).  
RP SEQUENCE OF 21-114.  
RX MEDLINE=85004133; PubMed=6434350;  
RA Seidah N.G., Arbach N.J., Rochement J., Sheeh A.R., Chretien M.,  
RT "Complete amino acid sequence of human seminal plasma beta-inhibin.  
RT Prediction of post Glu-Arg cleavage as a maturation site.",  
RL FEBS Lett. 175:349-355(1984).  
RP SEQUENCE OF 21-50 AND 113-114.  
RX MEDLINE=92028964; PubMed=1930232;  
RA Liang Z.G., Kamada M., Koide S.S.;  
RT "Structural identity of immunoglobulin binding factor and prostatic  
RT secretory protein of human seminal plasma.",  
RL Biochem. Biophys. Res. Commun. 180:356-359(1991).  
RP SEQUENCE OF 21-41, AND TISSUE SPECIFICITY.  
RC TISSUE=Semen;  
RX MEDLINE=95401076; PubMed=7671139;  
RA Okubo I., Tada T., Ochiai T., Ueyama H., Shimoto T., Sasaki M.;  
RT "Human seminal plasma beta-microseminoprotein: its purification,  
RT characterization, and immunohistochemical localization.",  
RL Int. J. Biochem. Cell Biol. 27:603-611(1995).  
RP SEQUENCE OF 21-32.  
RX MEDLINE=21648993; PubMed=11788998;  
RA Ghatouari B., Stahlbom B., Tageson C., Lindehl M.;  
RT "Newly identified proteins in human nasal lavage fluid from  
RT non-smokers and smokers using two-dimensional gel electrophoresis and  
RT peptide mass fingerprinting.",  
RL Proteomics 2:112-120(2002).  
RP FUNCTION: Inhibits the secretion of FSH by pituitary cells.  
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=PSP94;  
CC IsoId=P08118-1; Sequence=Displayed;  
CC Name=PSP57;  
CC IsoId=P08118-2; Sequence=VSP\_003275, VSP\_003276;  
CC -1- TISSUE SPECIFICITY: Strongly expressed in prostate, liver, kidney,  
CC breast and penis. Also expressed in pancreas, esophagus, stomach,  
CC duodenum, colon, trachea, lung, salivary glands and fallopian  
CC tube. PSP94 is expressed in lung and breast, whereas PSP57 is  
CC found in kidney and bladder.  
CC -1- MISCELLANEOUS: SPECIFIC RECEPTORS FOR THIS PROTEIN ARE FOUND ON  
CC SPERMATOZOA AND IN THE PROSTATE.  
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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CC EMBL: X58158; CAA41002.1; JOINED.  
CC EMBL: X58159; CAA41002.1; JOINED.  
CC EMBL: X58160; CAA41002.1; JOINED.  
CC EMBL: X58161; CAA41002.1; JOINED.  
CC EMBL: X58162; CAA41002.1; JOINED.  
CC EMBL: X58163; CAA41002.1; JOINED.  
CC EMBL: X58164; CAA41002.1; JOINED.  
CC EMBL: X58165; CAA41002.1; JOINED.  
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CC EMBL: X58169; CAA41002.1; JOINED.  
CC EMBL: X58170; CAA41002.1; JOINED.  
CC EMBL: X58171; CAA41002.1; JOINED.  
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CC EMBL: X58177; CAA41002.1; JOINED.  
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CC EMBL: X58183; CAA41002.1; JOINED.  
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CC EMBL: X58186; CAA41002.1; JOINED.  
CC EMBL: X58187; CAA41002.1; JOINED.  
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CC EMBL: X58189; CAA41002.1; JOINED.  
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CC EMBL: X58193; CAA41002.1; JOINED.  
CC EMBL: X58194; CAA41002.1; JOINED.  
CC EMBL: X58195; CAA41002.1; JOINED.  
CC EMBL: X58196; CAA41002.1; JOINED.  
CC EMBL: X58197; CAA41002.1; JOINED.  
CC EMBL: X58198; CAA41002.1; JOINED.  
CC EMBL: X58199; CAA41002.1; JOINED.  
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CC EMBL: X58210; CAA41002.1; JOINED.  
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CC EMBL: X58218; CAA41002.1; JOINED.  
CC EMBL: X58219; CAA41002.1; JOINED.  
CC EMBL: X58220; CAA41002.1; JOINED.  
CC EMBL: X58221; CAA41002.1; JOINED.  
CC EMBL: X58222; CAA41002.1; JOINED.  
CC EMBL: X58223; CAA41002.1; JOINED.  
CC EMBL: X58224; CAA41002.1; JOINED.  
CC EMBL: X58225; CAA41002.1; JOINED.  
CC EMBL: X58226; CAA41002.1; JOINED.  
CC EMBL: X58227; CAA41002.1; JOINED.  
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CC EMBL: X58229; CAA41002.1; JOINED.  
CC EMBL: X58230; CAA41002.1; JOINED.  
CC EMBL: X58231; CAA41002.1; JOINED.  
CC EMBL: X58232; CAA41002.1; JOINED.  
CC EMBL: X58233; CAA41002.1; JOINED.  
CC EMBL: X58234; CAA41002.1; JOINED.  
CC EMBL: X58235; CAA41002.1; JOINED.  
CC EMBL: X58236; CAA41002.1; JOINED.  
CC EMBL: X58237; CAA41002.1; JOINED.  
CC EMBL: X58238; CAA41002.1; JOINED.  
CC EMBL: X58239; CAA41002.1; JOINED.  
CC EMBL: X58240; CAA41002.1; JOINED.  
CC EMBL: X58241; CAA41002.1; JOINED.  
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CC EMBL: X58246; CAA41002.1; JOINED.  
CC EMBL: X58247; CAA41002.1; JOINED.  
CC EMBL: X58248; CAA41002.1; JOINED.  
CC EMBL: X58249; CAA41002.1; JOINED.  
CC EMBL: X58250; CAA41002.1; JOINED.  
CC EMBL: X58251; CAA41002.1; JOINED.  
CC EMBL: X58252; CAA41002.1; JOINED.  
CC EMBL: X58253; CAA41002.1; JOINED.  
CC EMBL: X58254; CAA41002.1; JOINED.  
CC EMBL: X58255; CAA41002.1; JOINED.  
CC EMBL: X58256; CAA41002.1; JOINED.  
CC EMBL: X58257; CAA41002.1; JOINED.  
CC EMBL: X58258; CAA41002.1; JOINED.  
CC EMBL: X58259; CAA41002.1; JOINED.  
CC EMBL: X58260; CAA41002.1; JOINED.  
CC EMBL: X58261; CAA41002.1; JOINED.  
CC EMBL: X58262; CAA41002.1; JOINED.  
CC EMBL: X58263; CAA41002.1; JOINED.  
CC EMBL: X58264; CAA41002.1; JOINED.  
CC EMBL: X58265; CAA41002.1; JOINED.  
CC EMBL: X58266; CAA41002.1; JOINED.  
CC EMBL: X58267; CAA41002.1; JOINED.  
CC EMBL: X58268; CAA41002.1; JOINED.  
CC EMBL: X58269; CAA41002.1; JOINED.  
CC EMBL: X58270; CAA41002.1; JOINED.  
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CC EMBL: X58273; CAA41002.1; JOINED.  
CC EMBL: X58274; CAA41002.1; JOINED.  
CC EMBL: X58275; CAA41002.1; JOINED.  
CC EMBL: X58276; CAA41002.1; JOINED.  
CC EMBL: X58277; CAA41002.1; JOINED.  
CC EMBL: X58278; CAA41002.1; JOINED.  
CC EMBL: X58279; CAA41002.1; JOINED.  
CC EMBL: X58280; CAA41002.1; JOINED.  
CC EMBL: X58281; CAA41002.1; JOINED.  
CC EMBL: X58282; CAA41002.1; JOINED.  
CC E

Query Match 100.0%; Score 45; DB 1; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 2, 1e-41;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCFFIPNEGVGSDTRKMDLKNKHPINSEWQTDNCETCTCYET 45  
 DB 21 SCFFIPNEGVGSDTRKMDLKNKHPINSEWQTDNCETCTCYET 65

## RESULT 2

MSMB\_MACMU STANDARD; PRT; 114 AA.  
 ID MSMB\_MACMU  
 AC P25142;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94).  
 GN Macaca mulatta (Rhesus macaque).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecidae; Macaca.  
 OC NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=91274357; Pubmed=2054385;  
 RA Noler S., Mlikay M., Chretien M.;  
 RT "Prostatic secretory protein PSP94: gene organization and promoter sequence in rhesus monkey and human.";  
 RL Biochim. Biophys. Acta 1089:247-249(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91244325; Pubmed=2037304;  
 RA Noler S., St Louis D., Mlikay M., Chretien M.;  
 RT "Rapid evolution of prostatic protein PSP94 suggested by sequence divergence between rhesus monkey and human cDNAs.";  
 RL Genomics 9:775-777(1991).  
 CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).  
 CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.

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 CC EMBL; X57932; CAA41003.1; -;  
 CC EMBL; X57933; CAA41003.1; JOINED.  
 CC EMBL; X57934; CAA41003.1; JOINED.  
 CC EMBL; X57935; CAA41003.1; JOINED.  
 CC EMBL; M92161; AAA36903.1; -;  
 CC PIR; S16237; A54663.  
 CC InterPro; IPR008735; PSP94.  
 CC Pfam; PF05825; PSP94; 1.  
 CC Signal.  
 CC CHAIN 1 20 BY SIMILARITY.  
 CC FT CHAIN 21 114 BETA-MICROSEMINOPROTEIN.  
 CC FT DISULFID 22 38 BY SIMILARITY.  
 CC FT DISULFID 57 93 BY SIMILARITY.  
 CC FT DISULFID 60 69 OR 70 (BY SIMILARITY).  
 CC FT DISULFID 62 70 OR 69 (BY SIMILARITY).  
 CC FT DISULFID 84 107 BY SIMILARITY.  
 CC SEQUENCE 114 AA; 13079 MW; C07A4EB9984B276C CRC64;

Query Match 24.4%; Score 11; DB 1; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 4, 9e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DLKGNKHPINS 30  
 DB 40 DLKGNKHPINS 50

## RESULT 3

MSMB\_PAPAN STANDARD; PRT; 114 AA.  
 ID MSMB\_PAPAN  
 AC Q28767;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94).  
 GN MSMB OR PSP94.  
 OS Papio anubis (Olive baboon).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecidae; Papio.  
 OC NCBI\_TaxID=9555;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=prostate;  
 RX MEDLINE=97316893; Pubmed=9174167;  
 RA Xuan J.W., Wu D., Guo Y., Garde S., Shum D.T., Mlikay M., Zhong R., Chin J.L.;  
 RT "Molecular cloning and gene expression analysis of PSP94 (prostate secretory protein of 94 amino acids) in primates.";  
 RL DNA Cell Biol. 16:627-638(1997).  
 CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).  
 CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.

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 CC EMBL; U49786; AAB62726.1; -;  
 CC InterPro; IPR008735; PSP94.  
 CC Pfam; PF05825; PSP94; 1.  
 CC Signal.  
 CC CHAIN 1 20 BY SIMILARITY.  
 CC FT CHAIN 21 114 BETA-MICROSEMINOPROTEIN.  
 CC FT DISULFID 22 38 BY SIMILARITY.  
 CC FT DISULFID 57 93 BY SIMILARITY.  
 CC FT DISULFID 60 69 OR 70 (BY SIMILARITY).  
 CC FT DISULFID 62 70 OR 69 (BY SIMILARITY).  
 CC FT DISULFID 84 107 BY SIMILARITY.  
 CC SEQUENCE 114 AA; 13013 MW; A08C637ED81E98ED CRC64;

Query Match 24.4%; Score 11; DB 1; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 4, 9e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DLKGNKHPINS 30  
 DB 40 DLKGNKHPINS 50

## RESULT 4

MSPT\_SAGOE STANDARD; PRT; 114 AA.  
 ID MSPT\_SAGOE  
 AC O97949;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

```

DE Beta-microseminoprotein J1 precursor (msp-J1).
GN MSBJ.
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99421644; PubMed=10491085;
RA Maekinen M., Valtonen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
RT beta-microseminoprotein."
RL Eur. J. Biochem. 264:407-414(1999).
CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By
CC similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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CC -----
DR EMBL; AJ010155; CAB38123.1; JOINED.
DR EMBL; AJ010156; CAB38123.1; JOINED.
DR EMBL; AJ010157; CAB38123.1; JOINED.
DR GO; GO:0005576; C:extracellular; NAS.
DR InterPro; IPR008735; PSP94.
DR Pfam; PF05825; PSP94; 1.
KW Signal.
FT SIGNAL. 1 20 POTENTIAL.
FT CHAIN 21 114 BETA-MICROSEMINOPROTEIN J1.
FT DISULFID 22 38 BY SIMILARITY.
FT DISULFID 57 93 BY SIMILARITY.
FT DISULFID 60 69 OR 70 (BY SIMILARITY).
FT DISULFID 62 70 OR 69 (BY SIMILARITY).
FT DISULFID 84 107 BY SIMILARITY.
SQ SEQUENCE 114 AA; 12746 MW; F3F05B013445B44 CRC64;

Query Match 24.4%; Score 11; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DLKGNKHPINS 30
DB 40 DLKGNKHPINS 50

RESULT 5
MSPE_SAGOE STANDARD: PRT; 112 AA.
ID MSPA_SAGOE
AC 097936;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-microseminoprotein A1 precursor (msp-A1) (Fragment).
GN MSPE.
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99421644; PubMed=10491085;
RA Maekinen M., Valtonen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
RT beta-microseminoprotein."
RL Eur. J. Biochem. 264:407-414(1999).
CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
CC similarity).

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CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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CC -----
DR EMBL; AJ010158; CAB38124.1; JOINED.
DR EMBL; AJ010159; CAB38124.1; JOINED.
DR GO; GO:0005576; C:extracellular; TAS.
DR InterPro; IPR002400; GF_CYSKNOT.
DR InterPro; IPR008735; PSP94.
DR Pfam; PF05825; PSP94; 1.
DR PRINTS; PR00438; GFCYSKNOT.
KW Signal.
FT SIGNAL. 1 19 BY SIMILARITY.
FT NON TER <1 19 BETA-MICROSEMINOPROTEIN A1.
FT CHAIN 20 112 BY SIMILARITY.
FT DISULFID 21 37 BY SIMILARITY.
FT DISULFID 56 92 BY SIMILARITY.
FT DISULFID 59 68 OR 69 (BY SIMILARITY).
FT DISULFID 61 69 OR 68 (BY SIMILARITY).
FT DISULFID 83 106 BY SIMILARITY.
SQ SEQUENCE 112 AA; 12631 MW; DOA06F0C15CD78B CRC64;

Query Match 17.8%; Score 8; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DLKGNKHP 27
DB 39 DLKGNKHP 46

RESULT 6
MSPE_SAGOE STANDARD: PRT; 114 AA.
ID MSPA_SAGOE
AC 097935;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-microseminoprotein E1 precursor (msp-E1).
GN MSPE.
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99421644; PubMed=10491085;
RA Maekinen M., Valtonen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
RT beta-microseminoprotein."
RL Eur. J. Biochem. 264:407-414(1999).
CC -1- FUNCTION: Inhibits the secretion of FSH by pituitary cells (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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CC -----
DR EMBL; AJ010154; CAB38105.1; JOINED.
DR GO; GO:0005576; C:extracellular; TAS.

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GN CPE2600.
OS Clostridium perfringens.
OS Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
CC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -1- SIMILARITY: Belongs to the UPE0247 family.
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CC -----
DR EMBL: AP003194; BAB82306.1;
DR HAMAP: MF00658; -.
DR InterPro: IPR003742; DUF163.
DR Pfam: PF02590; DUF163; 1.
DR TIGRFAMs: TIGR00246; TIGR00246; 1.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 159 AA; 18473 MW; 346CC442A085378 CRC64;

Query Match 13.3%; Score 6; DB 1; Length 159;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 MDLKN 24
Db 76 MDLKN 81

RESULT 10
EMBP_MOUSE STANDARD; PRT; 223 AA.
ID EMBP_MOUSE
AC Q61878;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Eosinophil granule major basic protein precursor (MBP) (Proteoglycan
DE 2, bone marrow).
DE P023 OR MBP-1.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=CBA/J; TISSUE=Liver;
RX MEDLINE=95403975; PubMed=7673718;
RA Larson K.A., Horton M.A., Madden B.J., Gleich G.J., Lee N.A.,
RA Lee J.J.;
RT "The identification and cloning of a murine major basic protein gene
RT expressed in eosinophils."
RL J. Immunol. 155:3002-3012(1995).
CC -1- FUNCTION: Cytotoxin and helminthotoxin. MBP also induces
CC noncytolytic histamine release from basophils. It is involved in
CC antiparasitic defense mechanisms and immune hypersensitivity
CC reactions (By similarity).
CC -1- SUBCELLULAR LOCATION: Matrix of eosinophil's large specific
CC granule (crystalloid core) (By similarity).
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
DR EMBL: LA5768; AAA83027.1;
DR HSPSP; P13727; ITHU.
DR WGD; WGI:103284; Prg2.
DR InterPro: IPR002352; EmaJor_baslc.
DR InterPro: IPR001304; Lactin_C.
DR Pfam: PF00059; Lactin c; 1.
DR PRINTS: PR00770; EMOJORBASICP.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
DR Eosinophil; Signal; Immune response; Antibiotic; Lactin.
FT SIGNAL 1 16
FT PROPEP 17 106
FT CHAIN 107 223
FT DOMAIN 124 223
FT DISULFD 126 221
FT DISULFD 198 213
FT DISULFD 198 213
SQ SEQUENCE 223 AA; 24255 MW; 7D6BD946DCEADAD00 CRC64;

Query Match 13.3%; Score 6; DB 1; Length 223;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGVPGD 13
Db 69 EGVPGD 74

RESULT 11
RL2_PYRO ID RL2_PYRO STANDARD; PRT; 239 AA.
AC O59421;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L2P.
DE RPL2P OR PHL775.
GN Pyrococcus horikoshii.
OS Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
CC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Hatake Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuza H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Res. 5:55-76(1998).
CC -1- SIMILARITY: Belongs to the L2P family of ribosomal proteins.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF000007; BAA30891.1;
DR PIR; D71187; D71187.

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DR HSPSP; P04257; 1RL2.  
 DR InterPro: IPR008994; Nucleic acid\_OR.  
 DR InterPro: IPR002171; Ribosomal\_L2.  
 DR InterPro: IPR008991; Transl\_CH3\_Like.  
 DR Pfam: PF03947; Ribosomal\_L2; 1.  
 DR Pfam: PF03947; Ribosomal\_L2; 1.  
 DR PROSITE: PS00467; RIBOSOMAL\_L2; FALSE\_NEG.  
 DR Ribosomal protein: Complete proteome.  
 KM SEQUENCE 239 AA; 26142 MW; 594B009C5AC63D11 CRC64;  
 SC SEQUENCE 239 AA; 26142 MW; 594B009C5AC63D11 CRC64;  
 Query Match 13.3%; Score 6; DB 1; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 8 EGVPGD 13  
 112 EGVPGD 117  
 RESULT 12  
 ID SCOL\_HUMAN STANDARD; PRT; 301 AA.  
 AC 075860;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE SCOL protein homolog, mitochondrial precursor.  
 GN SCOL OR SCOD1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99097350; PubMed=9878253;  
 RA Petruzzella V., Tiranti V., Fernandez P., Ianna P., Carrozzo R.,  
 RA Zeviani M.,  
 RT Identification and characterization of human cDNAs specific to BCS1,  
 RT PPT112, SCOL, COX15, and COX11, five genes involved in the formation  
 RT and function of the mitochondrial respiratory chain.";  
 RL Genomics 54:494-504(1998).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20484188; PubMed=11027508;  
 RA Horvath R., Lochmuller H., Stucka R., Yao J., Shoubridge E.A.,  
 RA Kim S.-H., Gerbitz K.-D., Jaksch M.,  
 RT Characterization of human SCOL and COX17 genes in mitochondrial  
 RT cytochrome-c-oxidase deficiency.";  
 RL Biochem. Biophys. Res. Commun. 276:530-533(2000).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Adrenal gland;  
 RA Peng Y., Li Y., Tu Y., Xu S., Han Z., Fu G., Chen Z.;  
 RT "A novel gene expressed in human adrenal gland.";  
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Uterus;  
 RA MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marisla K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Plange C.,  
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mallory S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarnarone P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Foley J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein U.E., Jones S.J.W., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [5]  
 RP SEQUENCE OF 112-301 FROM N.A.  
 RA Mei G., Yu W., Gibbs R.A.;  
 RN Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP REVIEW ON COX DEFICIENCY.  
 RX MEDLINE=21462247; PubMed=11579424;  
 RA Shoubridge E.A.;  
 RT "Cytochrome c oxidase deficiency.";  
 RL Am. J. Med. Genet. 106:46-52(2001).  
 [7]  
 RP VARIANT COX DEFICIENCY LEU-174.  
 RX MEDLINE=20489854; PubMed=11013136;  
 RA Valnot I., Osmond S., Gigarel N., Menaye B., Amiel J.,  
 RA Cormier-Daire V., Munlich A., Bonnefont J.-P., Rustin P., Rotig A.;  
 RT "Mutations of the SCOL gene in mitochondrial cytochrome c oxidase  
 RT deficiency with neonatal-onset hepatic failure and encephalopathy.";  
 RL Am. J. Hum. Genet. 67:1104-1109(2000).  
 CC -1- FUNCTION: Thought to play a role in either mitochondrial copper  
 CC transport or insertion of copper into the active site of COX.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN TISSUES  
 CC CHARACTERIZED BY HIGH RATES OF OXIDATIVE PHOSPHORYLATION (OXPHOS),  
 CC INCLUDING MUSCLE, HEART, AND BRAIN.  
 CC -1- DISEASE: Defects in SCOL are a cause of cytochrome c oxidase  
 CC deficiency (COX deficiency) [MIM:20110]. COX deficiency is a  
 CC clinically heterogeneous disorder. The clinical features are  
 CC ranging from isolated myopathy to severe multisystem disease, with  
 CC onset from infancy to adulthood.  
 CC -1- SIMILARITY: Belongs to the SCOL/2 family.  
 CC -----  
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 CC -----  
 DR EMBL, AF026852; AAD08641.1; -;  
 DR EMBL, AF295386; AAG33836.1; -;  
 DR EMBL, AF295381; AAG33836.1; JOINED.  
 DR EMBL, AF295382; AAG33836.1; JOINED.  
 DR EMBL, AF295383; AAG33836.1; JOINED.  
 DR EMBL, AF295384; AAG33836.1; JOINED.  
 DR EMBL, AF295385; AAG33836.1; JOINED.  
 DR EMBL, AF183424; AAG09693.1; -;  
 DR EMBL, BC015504; AAH15504.1; -;  
 DR EMBL, AF131816; AAD20051.1; -;  
 DR GeneW, HGNC:10603; SCOL.  
 DR MIM; 603644; -;  
 DR MIM; 220110; -;  
 DR GO; GO:0005739; C:mitochondrion; TAS.  
 DR GO; GO:0008535; P:cytochrome c oxidase biogenesis; TAS.  
 DR GO; GO:0006091; P:energy pathways; TAS.  
 DR InterPro: IPR003782; SCOL\_Senc.  
 DR Pfam; PF02630; SCOL\_Senc; 1.  
 KW Mitochondrion; Transit peptide; Copper; Chaperone; Disease mutation;  
 KW Polymorphism.  
 FT TRANSIT 1 ?  
 FT CHAIN ? 301 MITOCHONDRION (POTENTIAL).  
 FT METIL 169 169 SCOL PROTEIN HOMOLOG.  
 FT METIL 173 173 COPPER (POTENTIAL).  
 FT VARIANT 58 58 COPPER (POTENTIAL).  
 FT VARIANT 58 58 P->S (in dbSNP:1802083).  
 FT VARIANT 174 174 /FTId=VAR\_014537.  
 FT VARIANT 174 174 P->L (in COX deficiency).  
 FT /FTId=VAR\_012109.

SQ SEQUENCE 301 AA; 33814 MW; C4A0F35A1741894F CRC64;  
 Query Match 13.3%; Score 6; DB 1; Length 301;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PGDSTR 16  
 11 PGDSTR 16  
 DB 81 PGDSTR 86

RESULT 13  
 ID CYC9\_DESDE STANDARD; PRT; 326 AA.  
 AC OPEN68;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Nine-heme cytochrome c precursor (9Hcc).  
 OS Desulfovibrio desulfuricans.  
 CC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;  
 CC Desulfovibrionaceae; Desulfovibrio.  
 CC NCBI\_TaxID=876;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 27774;  
 RC MEDLINE=99400423; PubMed=10471375;  
 RA Saraiva L.M., da Costa P.N., Legall J.  
 RT "Sequencing the gene encoding Desulfovibrio desulfuricans ATCC 27774  
 RT nine-heme cytochrome c."  
 RL Biochem. Biophys. Res. Commun. 262:629-634(1999).  
 [2]  
 RP SEQUENCE FROM N.A. AND X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
 RC STRAIN=ATCC 27774;  
 RC MEDLINE=20025508; PubMed=10555582;  
 RA Matias P.M., Saraiva L.M., Soares C.M., Coelho A.V., Legall J.,  
 RA Carrondo M.A.;  
 RT "Nine-heme cytochrome c from Desulfovibrio desulfuricans ATCC 27774:  
 RT primary sequence determination, crystallographic refinement at 1.8 Å  
 RT and modelling studies of its interaction with the tetrahaem cytochrome  
 RT c3."  
 RL J. Biol. Inorg. Chem. 4:478-494(1999).  
 [3]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
 RC STRAIN=ATCC 27774;  
 RC MEDLINE=99148120; PubMed=10368280;  
 RA Matias P.M., Coelho R., Pereira I.A.C., Coelho A.V., Thompson A.W.,  
 RA Sliker L., Legall J., Carrondo M.A.;  
 RT "The primary and three-dimensional structures of a nine-heme  
 RT cytochrome c from Desulfovibrio desulfuricans ATCC 27774 reveal a new  
 RT member of the Hmc family."  
 RL Structure 7:119-130(1999).  
 CC -1- FUNCTION: MAY FORM PART OF A TRANSMEMBRANE REDOX COMPLEX THROUGH  
 CC WHICH ELECTRONS ARE TRANSFERRED TO THE CYTOPLASM FOR REDUCTION OF  
 CC SULFATE.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- SUBCELLULAR LOCATION: Periplasmic.  
 CC -1- PTM: BINDS 9 HEME GROUPS. ARRANGED INTO TWO TETRAHEME CLUSTERS AND  
 CC THE EXTRA HEME 4 IS LOCATED ASYMMETRICALLY BETWEEN THE TWO  
 CC REGIONS.  
 CC -1- SIMILARITY: Contains 9 cytochrome c domains.  
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 CC EMBL; AF166393; AAD56586.1; -  
 CC PIR; JC7094; JC7094.  
 CC PDB; 19HC; 01-DEC-99.

DR InterPro: IPR002322; Cyt CIII.  
 DR InterPro: IPR000345; CytC\_heme\_B5.  
 DR Pfam: PF02085; Cytochrome\_CIII\_1.  
 DR PRINTS; PRO0609; CYTOCHROME\_C3.  
 DR PROSITE; PS00190; CYTOCHROME\_C; 9.  
 KW Electon transport; Heme; Periplasmic; Signal; Repeat; 3d-structure.

FT SIGNAL 1 30  
 FT CHAIN 31 326  
 FT METAL 67 70  
 FT METAL 70 70  
 FT METAL 77 77  
 FT METAL 80 80  
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 FT METAL 141 141  
 FT METAL 144 144  
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 FT METAL 157 157  
 FT METAL 160 160  
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 FT METAL 227 227  
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 FT METAL 275 275  
 FT METAL 294 294  
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 FT METAL 301 301  
 FT METAL 314 314  
 FT METAL 317 317  
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 FT METAL 318 318  
 SQ SEQUENCE 326 AA; 35025 MW; 2E7025ADDF250E3 CRC64;  
 Query Match 13.3%; Score 6; DB 1; Length 326;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 DNCERC 40  
 35 DNCERC 40  
 DB 75 DNCERC 80

RESULT 14  
 ID EPIA\_ASHGO STANDARD; PRT; 458 AA.  
 AC P41752;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Elongation factor 1-alpha (EF-1-alpha).  
 GN TER.  
 OS Ashbya gossypii (Yeast) (Eremothecium gossypii).  
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Eremothecium.  
 CC NCBI\_TaxID=33169;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 10895;  
 RC MEDLINE=94150459; PubMed=8107673;  
 RA Steiner S., Philippsen P.;

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RT "Sequence and promoter analysis of the highly expressed TER gene of
RL the filamentous fungus Aschya gossypii."
CC Mol. Gen. Genet. 242:263-271(1994).
CC -1- FUNCTION: This protein promotes the GTP-dependent binding of
CC aminoacyl-tRNA to the A-site of ribosomes during protein
CC biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-Tu/EF-1A subfamily.
CC -----
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CC -----
CC EMBL; X73978; CAA52157.1; -.
CC PIR; S41593; S41593.
CC HSSP; P07157; 1A1P.
CC InterPro; IPR004539; EF1_alpha.
CC InterPro; IPR000795; EF_GTPbind.
CC InterPro; IPR004160; EFTU_Cterm.
CC InterPro; IPR004161; EFTU_D2.
CC InterPro; IPR009001; Elong_init_C.
CC InterPro; IPR009000; Translat_factor.
CC Pfam; PR00009; GTP_EFTU; 1.
CC Pfam; PR03144; GTP_EFTU_D2; 1.
CC Pfam; PR03143; GTP_EFTU_D3; 1.
CC PRINTS; PR00315; ELONGATNFACT.
CC TIGRFAMs; TIGR00483; EF-1_alpha; 1.
CC PROSITE; PS00301; EFACITOR_GTP; 1.
CC Elongation factor; Protein biosynthesis; GTP-binding.
CC FT NP_BIND 14 21 GTP (BY SIMILARITY).
CC FT NP_BIND 91 95 GTP (BY SIMILARITY).
CC FT NP_BIND 153 156 GTP (BY SIMILARITY).
CC SEQUENCE 458 AA; 49925 MW; 66C7CA7AB72D39F CRC64;
SQ
Query Match 13.3%; Score 6; DB 1; Length 458;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 EGVPGD 13
DB 299 EGVPGD 304

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CC EF-Tu/EF-1A subfamily.
CC -----
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CC -----
CC EMBL; M29334; AAA34339.1; -.
CC EMBL; M29335; AAA34340.1; -.
CC PIR; A35154; A35154.
CC HSSP; P07157; 1A1P.
CC InterPro; IPR004539; EF1_alpha.
CC InterPro; IPR000795; EF_GTPbind.
CC InterPro; IPR004160; EFTU_Cterm.
CC InterPro; IPR004161; EFTU_D2.
CC InterPro; IPR009001; Elong_init_C.
CC InterPro; IPR009000; Translat_factor.
CC Pfam; PR00009; GTP_EFTU; 1.
CC Pfam; PR03144; GTP_EFTU_D2; 1.
CC Pfam; PR03143; GTP_EFTU_D3; 1.
CC PRINTS; PR00315; ELONGATNFACT.
CC TIGRFAMs; TIGR00483; EF-1_alpha; 1.
CC PROSITE; PS00301; EFACITOR_GTP; 1.
CC Elongation factor; Protein biosynthesis; GTP-binding;
CC Multigene family.
CC FT NP_BIND 14 21 GTP (BY SIMILARITY).
CC FT NP_BIND 91 95 GTP (BY SIMILARITY).
CC FT NP_BIND 153 156 GTP (BY SIMILARITY).
CC SEQUENCE 458 AA; 50012 MW; C737C498FE923B09 CRC64;
SQ
Query Match 13.3%; Score 6; DB 1; Length 458;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 EGVPGD 13
DB 299 EGVPGD 304

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Search completed: March 11, 2004, 18:11:12  
Job time : 10.3468 secs

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## OM protein - protein search, using sw model

Run on: March 11, 2004, 18:08:03 ; Search time 21.6774 Seconds

(without alignments)  
152.420 Million cell updates/sec

Title: US-09-977-406A-58

Perfect score: 64

Sequence: 1 EWQIDNCETCTCTETETISCC.....YIVVEKKDPKKTGSEVEMII 64

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size: 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

1: Issued Patents AA: \*  
2: /cgn2\_6/prodata/2/1aa/5A COMB.pep: \*  
3: /cgn2\_6/prodata/2/1aa/5B COMB.pep: \*  
4: /cgn2\_6/prodata/2/1aa/6A COMB.pep: \*  
5: /cgn2\_6/prodata/2/1aa/6B COMB.pep: \*  
6: /cgn2\_6/prodata/2/1aa/BACKFILE1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	94	1	US-07-899-535A-1
2	26	40.6	28	1	US-07-899-535A-4
3	7	10.9	10	1	US-07-899-535A-2
4	7	10.9	626	4	US-09-485-717-2
5	6	9.4	40	4	US-09-065-383-30
6	6	9.4	104	4	US-08-858-207A-428
7	6	9.4	114	4	US-09-252-991A-25178
8	6	9.4	222	4	US-09-384-162-8
9	6	9.4	241	2	US-08-460-309-17
10	6	9.4	241	2	US-08-125-077-17
11	6	9.4	265	4	US-09-543-681A-6305
12	6	9.4	353	4	US-09-328-352-5693
13	6	9.4	333	3	US-08-888-429A-21
14	6	9.4	333	3	US-09-593-653-21
15	6	9.4	425	4	US-09-634-955B-19
16	6	9.4	453	4	US-09-328-152-4181
17	6	9.4	481	4	US-09-914-259-36
18	6	9.4	486	4	US-09-914-259-35
19	6	9.4	486	4	US-09-914-259-35
20	6	9.4	487	4	US-09-206-166-6
21	6	9.4	489	4	US-09-328-352-5330
22	6	9.4	488	3	US-09-232-468A-18
23	6	9.4	488	3	US-09-232-468A-24
24	6	9.4	488	3	US-08-686-968C-231
25	6	9.4	488	4	US-09-784-984B-52
26	6	9.4	488	4	US-09-784-984B-54
27	6	9.4	512	1	US-07-779-890-4

28	6	9.4	512	1	US-07-779-890-4	Sequence 4, Appli
29	6	9.4	512	2	US-09-008-962-4	Sequence 4, Appli
30	6	9.4	512	2	US-08-675-507-4	Sequence 4, Appli
31	6	9.4	512	3	US-09-213-205-4	Sequence 4, Appli
32	6	9.4	512	5	PCR-US93-05640-4	Sequence 4, Appli
33	6	9.4	518	4	US-09-065-383-27	Sequence 27, Appli
34	6	9.4	533	4	US-09-489-039A-7511	Sequence 7511, Ap
35	6	9.4	538	4	US-09-252-991A-30706	Sequence 30706, A
36	6	9.4	700	2	US-08-568-459A-10	Sequence 10, Appli
37	6	9.4	700	2	US-08-487-826B-10	Sequence 10, Appli
38	6	9.4	700	4	US-09-210-288-10	Sequence 10, Appli
39	6	9.4	771	4	US-09-214-916A-2	Sequence 2, Appli
40	6	9.4	771	4	US-09-214-916A-4	Sequence 4, Appli
41	6	9.4	774	3	US-08-902-632-2	Sequence 2, Appli
42	6	9.4	774	3	US-09-073-354-1	Sequence 1, Appli
43	6	9.4	774	3	US-08-656-005A-1	Sequence 1, Appli
44	6	9.4	774	3	US-09-073-259-1	Sequence 1, Appli
45	6	9.4	774	3	US-09-363-095-1	Sequence 1, Appli

## ALIGNMENTS

RESULT 1  
US-07-899-535A-1  
Sequence 1, Application US/07899535A  
Patent No. 5428011  
GENERAL INFORMATION:  
APPLICANT: Snelh, Anil R.  
APPLICANT: Garde, Seema  
TITLE OF INVENTION: Pharmaceutical Preparations For  
TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate  
TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Mr. George Loud  
STREET: 2001 Jefferson Davis Highway, Suite 306  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/07/899, 535A  
APPLICATION NUMBER: US/07/899, 535A  
CLASSIFICATION: 514  
FILING DATE: 16-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Loud, George A.  
REGISTRATION NUMBER: 25, 814  
REFERENCE/DOCKET NUMBER: S&B-A835  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-415-0960  
TELEFAX: 703-415-0962  
TELEX: 24 8614  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 94 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
US-07-899-535A-1  
Query Match 100.0%; Score 64; DB 1; Length 94;  
Best Local Similarity 100.0%; Pred. No. 8.8e-63;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWOJNCEJCTCYETETISCTIVSTPYGDKNCKORIFKKEDCKYIVKEDPKTCVS 60  
DB 31 EWOJNCEJCTCYETETISCTIVSTPYGDKNCKORIFKKEDCKYIVKEDPKTCVS 90  
QY 61 EMI 64  
DB 91 EMI 94

## RESULT 2

US-07-899-535A-4  
Sequence 4, Application US/07899535A  
Patent No. 5428011

## GENERAL INFORMATION:

APPLICANT: Sheth, Anil R.  
APPLICANT: Garde, Seema  
TITLE OF INVENTION: Pharmaceutical Preparations For  
TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate  
TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mr. George Loud  
STREET: 2001 Jefferson Davis Highway, Suite 306  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/899,535A  
FILING DATE: 16-JUN-1992  
CLASSIFICATION: 514

## ATTORNEY/AGENT INFORMATION:

NAME: Loud, George A.  
REGISTRATION NUMBER: 25,814  
REFERENCE/DOCKET NUMBER: S&B-A835  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-415-0960  
TELEFAX: 703-415-0962

## INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO

US-07-899-535A-4

Query Match 40.6%; Score 26; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1,2e-21;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 IFKKEDCKYIVKEDPKTCVSEW 62  
DB 1 IFKKEDCKYIVKEDPKTCVSEW 26

## RESULT 3

US-07-899-535A-2  
Sequence 2, Application US/07899535A  
Patent No. 5428011

## GENERAL INFORMATION:

APPLICANT: Sheth, Anil R.  
APPLICANT: Garde, Seema  
TITLE OF INVENTION: Pharmaceutical Preparations For  
TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate

TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mr. George Loud  
STREET: 2001 Jefferson Davis Highway, Suite 306  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/899,535A  
FILING DATE: 16-JUN-1992  
CLASSIFICATION: 514

## ATTORNEY/AGENT INFORMATION:

NAME: Loud, George A.  
REGISTRATION NUMBER: 25,814  
REFERENCE/DOCKET NUMBER: S&B-A835  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-415-0960  
TELEFAX: 703-415-0962

## INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO

US-07-899-535A-2

Query Match 10.9%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 TCVSEW 62  
DB 2 TCVSEW 8

## RESULT 4

US-09-485-717-2

Sequence 2, Application US/09485717

Patent No. 6673353

## GENERAL INFORMATION:

APPLICANT: Kaufmann, Stefan  
APPLICANT: Hess, Jrgen  
TITLE OF INVENTION: Tuberculosis Vaccine  
FILE REFERENCE: 16862PUS  
CURRENT APPLICATION NUMBER: US/09/485,717  
CURRENT FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: EP 97114614.7  
PRIOR FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: PCT/EP98-05109  
PRIOR FILING DATE: 1998-08-12  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 626

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: recombinant

US-09-485-717-2

Query Match 10.9%; Score 7; DB 4; Length 626;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



OY 45 YIVEK 51  
Db 143 YIVEK 149

## RESULT 5

US-09-065-383-30  
; Sequence 30, Application US/09065383  
; Patent No. 6391543  
; GENERAL INFORMATION:  
; APPLICANT: BILLING-MEDEL, PATRICIA  
; APPLICANT: COHEN, MAURICE  
; APPLICANT: COLPITS, TRACEY L.  
; APPLICANT: FRIEDMAN, PAULA N.  
; APPLICANT: GORDON, JULIAN  
; APPLICANT: GRANADOS, EDWARD N.  
; APPLICANT: HODGES, STEVEN C.  
; APPLICANT: KLAS, MICHAEL R.  
; APPLICANT: KRATOCHVIL, JON D.  
; APPLICANT: ROBERTS-RAP, LISA  
; APPLICANT: RUSSELL, JOHN C.  
; APPLICANT: STROUPE, STEPHEN D.  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/065,383  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/842,385  
; FILING DATE: 23-APR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 6084.US.P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6391543e  
; US-09-065-383-30

## Query Match

Best Local Similarity 9.4%; Score 6; DB 4; Length 40;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 48 VEKXP 53  
Db 4 VEKXP 9

## RESULT 6

US-08-858-207A-428  
; Sequence 428, Application US/08858207A

; Patent No. 6348328

; GENERAL INFORMATION:  
; APPLICANT: Black, Michael  
; APPLICANT: Hodgson, John  
; APPLICANT: Knowles, David  
; APPLICANT: Nicholas, Richard  
; APPLICANT: Stodola, Robert  
; TITLE OF INVENTION: No. 6348328e1 Compounds  
; NUMBER OF SEQUENCES: 552  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/858,207A  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/017670  
; FILING DATE: 14-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gimm, Edward R.  
; REGISTRATION NUMBER: 38,891  
; REFERENCE/DOCKET NUMBER: P50475  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-4478  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 428:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 104 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6348328e  
; US-08-858-207A-428

## Query Match

Best Local Similarity 9.4%; Score 6; DB 4; Length 104;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 27 VGYDXD 32  
Db 47 VGYDXD 52

## RESULT 7

US-09-252-991A-25178  
; Sequence 25178, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 25178  
; LENGTH: 114  
; TYPE: PRT

ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-25178

Query Match 9.4%; Score 6; DB 4; Length 114;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TLVSTP 26  
DB 65 TLVSTP 70

RESULT 8  
US-09-384-162-8

Sequence 8, Application US/09384162  
Patent No. 6376747  
GENERAL INFORMATION:  
APPLICANT: King, Ti  
APPLICANT: Malik, Kamal  
APPLICANT: Martin-Heller, Teresa  
APPLICANT: Miki, L., Brian  
TITLE OF INVENTION: NO. 6376747el Plant-Derived Map Kinase Kinase  
FILE REFERENCE: 08-884280US  
CURRENT APPLICATION NUMBER: US/09/384,162  
CURRENT FILING DATE: 1999-08-27  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 222  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-09-384-162-8

Query Match 9.4%; Score 6; DB 4; Length 222;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 DCKYIV 47  
DB 56 DCKYIV 61

RESULT 9  
US-08-460-309-17  
Sequence 17, Application US/08460309  
Patent No. 5837496  
GENERAL INFORMATION:  
APPLICANT: Engvall, Eva  
APPLICANT: Leivo, Ilmo  
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin  
TITLE OF INVENTION: Fragments and Uses Thereof  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,309  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/125,077  
FILING DATE: 22-SEP-1993  
APPLICATION NUMBER: US PCT/US 94/10730  
FILING DATE: 21-SEP-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/472,319  
FILING DATE: 30-JAN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/919,951  
FILING DATE: 27-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LA 9721  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-460-309-17

Query Match 9.4%; Score 6; DB 2; Length 241;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCETCT 11  
DB 103 NCETCT 108

RESULT 10  
US-08-125-077-17  
Sequence 17, Application US/08125077  
Patent No. 5872231  
Patent No. 5872231 5840863  
GENERAL INFORMATION:  
APPLICANT: Engvall, Eva  
APPLICANT: Leivo, Ilmo  
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin  
TITLE OF INVENTION: Fragments and Uses Thereof  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/125,077  
FILING DATE: 22-SEP-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/US 94/10730  
FILING DATE: 21-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/472,319  
FILING DATE: 30-JAN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/919,951  
FILING DATE: 27-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LA 9721  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 17:

Fri Mar 12 09:42:18 2004

us-09-977-406a-58.olg.rat

Page 5

SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-125-077-17

Query Match  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCECT 11  
DB 103 NCECT 108

RESULT 11  
US-09-543-681A-6305  
Sequence 6305, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
FILE REFERENCE: 2709,1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 6305  
LENGTH: 265  
TYPE: PRT  
ORGANISM: Proteus mirabilis  
US-09-543-681A-6305

Query Match  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 QRIFFX 40  
DB 125 QRIFFX 130

RESULT 12  
US-09-328-352-5693  
Sequence 5693, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 5693  
LENGTH: 363  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-5693

Query Match  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 RIFKE 41  
DB 7 RIFKE 12

RESULT 13  
US-08-888-429A-21

Sequence 21, Application US/08888429A  
Patent No. 6136596  
GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
APPLICANT: Whitmarsh, Alan  
APPLICANT: Tourlier, Cathy  
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-  
TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE KINASES  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/888,429A  
FILING DATE: 07-JUL-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/530,950  
FILING DATE: 19-SEP-1995  
APPLICATION NUMBER: 08/446,083  
FILING DATE: 19-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, Peter J.  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/053001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 299354  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 393 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-888-429A-21

Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 DCKYIV 47  
DB 155 DCKYIV 160

RESULT 14  
US-09-593-653-21  
Sequence 21, Application US/09593653  
Patent No. 6610523  
GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
APPLICANT: Whitmarsh, Alan  
APPLICANT: Tourlier, Cathy  
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-  
TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE KINASES  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:

Search completed: March 11, 2004, 18:14:42  
Job time : 21.6774 secs

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/593,653
;   FILING DATE: 13-Jun-2000
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/888,429A
;   FILING DATE: 07-JUL-1997
;   APPLICATION NUMBER: 08/530,950
;   FILING DATE: 19-SEP-1995
;   APPLICATION NUMBER: 08/446,083
;   FILING DATE: 19-MAY-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: Fasse, Peter J.
;   REGISTRATION NUMBER: 32,983
;   REFERENCE/DOCKET NUMBER: 07917/053001
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617/542-5070
;   TELEFAX: 617/542-8906
;   TELEX: 299354
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 393 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-593-653-21

Query March          9.4%; Score 6; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      42 DCKYIV 47
      |||||
Db      155 DCKYIV 160

RESULT 15
US-09-634-955B-19
; Sequence 19, Application US/09634955B
; Patent No. 6511834
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 32142, 21481, 25964, 21686, NOVEL HUMAN DEHYDROGENASE
; FILE REFERENCE: MNI-134
; CURRENT APPLICATION NUMBER: US/09/634,955B
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/192,002
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.
; SEQ ID NO 19
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3-beta hydroxysteroid dehydrogenase domain
US-09-634-955B-19

Query Match          9.4%; Score 6; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 ISCTL 22
      |||||
Db      84 ISCTL 89
```

Fri Mar 12 09:42:23 2004

us-09-977-406a-88.ra1

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2004, 17:50:06 ; Search time 15.9677 Seconds

(without alignments)  
145.491 Million cell updates/sec

Title: US-09-977-406A-88

Perfect score: 268  
Sequence: 1 SCVFIPNEGVPDSTRKCMD.....HPINSEWQDNCETCTCYET 45

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	268	100.0	94	1	US-07-899-535A-1 Sequence 1, Appl1
2	96	35.8	17	1	US-07-899-535A-3 Sequence 3, Appl1
3	79	29.5	176	1	US-08-726-525-2 Sequence 2, Appl1
4	79	29.5	176	1	US-08-487-942-2 Sequence 2, Appl1
5	79	29.5	176	2	US-08-726-536A-2 Sequence 2, Appl1
6	79	29.5	176	4	US-09-083-516-2 Sequence 2, Appl1
7	67	25.0	1276	3	US-08-937-236-3 Sequence 3, Appl1
8	67	25.0	1277	3	US-08-937-236-6 Sequence 3, Appl1
9	67	25.0	1291	3	US-08-569-214-3 Sequence 3, Appl1
10	67	25.0	1291	3	US-08-937-236-2 Sequence 2, Appl1
11	67	25.0	1292	3	US-08-569-214-5 Sequence 5, Appl1
12	67	25.0	1292	3	US-08-569-214-6 Sequence 6, Appl1
13	67	25.0	1292	3	US-08-937-236-5 Sequence 5, Appl1
14	67	25.0	1295	3	US-08-569-214-2 Sequence 2, Appl1
15	67	25.0	2476	2	US-08-276-967-2 Sequence 2, Appl1
16	66	24.6	2050	2	US-08-347-594A-2 Sequence 2, Appl1
17	66	24.6	2813	4	US-09-381-261A-1 Sequence 1, Appl1
18	63	23.5	1010	3	US-08-882-046-7 Sequence 7, Appl1
19	63	23.5	1036	4	US-09-068-740A-6 Sequence 6, Appl1
20	63	23.5	1187	4	US-09-068-740A-7 Sequence 7, Appl1
21	63	23.5	1208	4	US-09-199-865-1 Sequence 1, Appl1
22	63	23.5	1218	2	US-08-400-159-6 Sequence 6, Appl1
23	63	23.5	1218	3	US-08-611-729A-6 Sequence 2, Appl1
24	63	23.5	1218	3	US-08-882-046-2 Sequence 2, Appl1
25	63	23.5	1218	3	US-09-214-278-7 Sequence 11, Appl1
26	63	23.5	1218	4	US-09-068-740A-11 Sequence 7, Appl1
27	63	23.5	1218	4	US-09-855-722-7 Sequence 7, Appl1

28	62	23.1	2613	3	US-08-896-449A-2 Sequence 2, Appl1
29	62	23.1	2613	3	US-09-133-652-2 Sequence 2, Appl1
30	57.5	21.5	466	4	US-09-724-864-14 Sequence 4, Appl1
31	57	21.3	1172	1	US-08-313-288B-19 Sequence 19, Appl1
32	56	20.9	810	2	US-08-820-170A-34 Sequence 34, Appl1
33	56	20.9	810	3	US-09-055-699-34 Sequence 34, Appl1
34	56	20.9	810	3	US-09-273-565-34 Sequence 34, Appl1
35	56	20.9	810	4	US-09-565-538-34 Sequence 34, Appl1
36	56	20.9	810	4	US-09-661-468-34 Sequence 34, Appl1
37	56	20.9	810	4	US-09-976-165-34 Sequence 34, Appl1
38	54.5	20.3	2231	1	US-08-153-799-16 Sequence 16, Appl1
39	54.5	20.3	2324	1	US-08-283-857-1 Sequence 1, Appl1
40	54.5	20.3	2324	5	PCT-US95-09819-1 Sequence 5, Appl1
41	54.5	20.3	2327	6	5455158-1 Patent No. 5455158
42	54.5	20.3	2386	2	US-09-016-366A-12 Sequence 12, Appl1
43	54.5	20.3	2446	2	US-08-551-356-2 Sequence 2, Appl1
44	54.5	20.3	2446	5	PCT-US93-12687-2 Sequence 5, Appl1
45	54	20.1	738	3	US-08-478-208-32 Sequence 32, Appl1

#### ALIGNMENTS

RESULT 1  
US-07-899-535A-1  
Sequence 1, Application US/07899535A  
Patent No. 5428011  
GENERAL INFORMATION:  
APPLICANT: Sheth, Anil R.  
APPLICANT: Garde, Seema  
TITLE OF INVENTION: Pharmaceutical Preparations For  
TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate  
TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Mr. George Loud  
STREET: 2001 Jefferson Davis Highway, Suite 306  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/899,535A  
FILING DATE: 16-JUN-1992  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Loud, George A.  
REGISTRATION NUMBER: 25,814  
REFERENCE/DOCKET NUMBER: S&B-A835  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-415-0960  
TELEFAX: 703-415-0962  
TELEX: 24 8614  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 94 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
HYPOTHETICAL: NO  
US-07-899-535A-1

Query Match 100.0% Score 268; DB 1; Length 94;  
Best Local Similarity 100.0%; Pred. No. 2,3e-28;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPEGVGDSTRKMDLKGKHPINSEWQJDNCTCTCT 45  
 DB 1 SCYFIPEGVGDSTRKMDLKGKHPINSEWQJDNCTCTCT 45

RESULT 2  
 US-07-899-535A-3  
 Sequence 3, Application US/07899535A  
 Patent No. 5428011

GENERAL INFORMATION:  
 APPLICANT: Sheeh, Anil R.  
 APPLICANT: Garde, Seema  
 APPLICANT: Panchal, Chandra J.  
 TITLE OF INVENTION: Pharmaceutical Preparations For  
 TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate  
 TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Mr. George Loud  
 STREET: 2001 Jefferson Davis Highway, Suite 306  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: U.S.A.  
 ZIP: 22202

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/899,535A  
 FILING DATE: 16-JUN-1992  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Loud, George A. 25,814  
 REGISTRATION NUMBER: 25,814  
 REFERENCE/DOCKET NUMBER: SSB-A835  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-415-0960  
 TELEFAX: 703-415-0962  
 TELEX: 24 8614

INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 17 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 HYPOTHEICAL: NO  
 US-07-899-535A-3

Query Match 35.8%; Score 96; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPEGVGDSTRK 17  
 DB 1 SCYFIPEGVGDSTRK 17

RESULT 3  
 US-08-726-525-2  
 Sequence 2, Application US/08726525  
 Patent No. 5789181

GENERAL INFORMATION:  
 APPLICANT: Lin, Lih-Ling  
 APPLICANT: Graham, James  
 TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR  
 TITLE OF INVENTION: INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND  
 TITLE OF INVENTION: BINDING  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.  
 STREET: 87 Cambridgepark Drive

CITY: Cambridge  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02140

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/726,525  
 FILING DATE: 07-OCT-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/487,942  
 FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:  
 NAME: Brown, Scott A.  
 REGISTRATION NUMBER: 32,724  
 REFERENCE/DOCKET NUMBER: G15258  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 498-8224  
 TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 176 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-726-525-2

Query Match 29.5%; Score 79; DB 1; Length 176;  
 Best Local Similarity 41.4%; Pred. No. 0.0065;  
 Matches 12; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 14 STRKMDLKGKHPINSEWQJDNCTCTC 42  
 DB 108 STTECVADGESHANNITWKDQACTTGC 136

RESULT 4  
 US-08-487-942-2  
 Sequence 2, Application US/08487942  
 Patent No. 5817476

GENERAL INFORMATION:  
 APPLICANT: Lin, Lih-Ling  
 APPLICANT: Graham, James  
 TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR  
 TITLE OF INVENTION: INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND  
 TITLE OF INVENTION: BINDING  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.  
 STREET: 87 Cambridgepark Drive  
 CITY: Cambridge  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02140

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/487,942  
 FILING DATE:

CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brown, Scott A.  
 REGISTRATION NUMBER: 32,724  
 REFERENCE/DOCKET NUMBER: G15258  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 176 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-487-942-2

Query Match 29.5%; Score 79; DB 2; Length 176;  
 Best Local Similarity 41.4%; Pred. No. 0.0065;  
 Matches 12; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 14 STRKCMDLKGKHPINSEWQDNCETCTC 42  
 DB 108 STECVADGSGSHANNTKWKDACTICEC 136

RESULT 5  
 US-08-726-036A-2  
 Sequence 2, Application US/08726036A  
 Patent No. 5981482

GENERAL INFORMATION:  
 APPLICANT: Lih, Lih-Ling  
 TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR  
 TITLE OF INVENTION: INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.  
 STREET: 87 Cambridgepark Drive  
 CITY: Cambridge  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02140

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/726,036A  
 FILING DATE:

CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brown, Scott A.  
 REGISTRATION NUMBER: 32,724  
 REFERENCE/DOCKET NUMBER: G15258  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 498-8224  
 TELEFAX: (617) 876-5851  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 176 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-726-036A-2

Query Match 29.5%; Score 79; DB 2; Length 176;  
 Best Local Similarity 41.4%; Pred. No. 0.0065;  
 Matches 12; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 14 STRKCMDLKGKHPINSEWQDNCETCTC 42  
 DB 108 STECVADGSGSHANNTKWKDACTICEC 136

RESULT 6  
 US-09-083-516-2  
 Sequence 2, Application US/09083516  
 Patent No. 6300086

GENERAL INFORMATION:  
 APPLICANT: Lih, Lih-Ling  
 TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR  
 TITLE OF INVENTION: INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.  
 STREET: 87 Cambridgepark Drive  
 CITY: Cambridge  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02140

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/083,516  
 FILING DATE:

CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/487,942  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brown, Scott A.  
 REGISTRATION NUMBER: 32,724  
 REFERENCE/DOCKET NUMBER: G15258  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 498-8224  
 TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 176 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-083-516-2

Query Match 29.5%; Score 79; DB 4; Length 176;  
 Best Local Similarity 41.4%; Pred. No. 0.0065;  
 Matches 12; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 14 STRKCMDLKGKHPINSEWQDNCETCTC 42  
 DB 108 STECVADGSGSHANNTKWKDACTICEC 136

RESULT 7  
 US-08-937-236-3  
 Sequence 3, Application US/08937236  
 Patent No. 6187310  
 GENERAL INFORMATION:  
 APPLICANT: MANN, BARBARA J.  
 APPLICANT: PETRI, WILLIAM A.  
 TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN  
 TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORRISON & FOERSTER  
 STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500  
 CITY: WASHINGTON  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20006-1812  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/937,236  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/569,214  
FILING DATE: 16 SEPTEMBER 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: LIVNAT, SHMUEL  
REGISTRATION NUMBER: 33,949  
REFERENCE/DOCKET NUMBER: 291482000622  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1276 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-937-236-3

Query Match 25.0%; Score 67; DB 3; Length 1276;  
Best Local Similarity 31.7%; Pred. No. 2.6;  
Matches 13; Conservative 6; Mismatches 10; Indels 12; Gaps 1;

QY 17 KCMDLKGNKHPINSEWQTDN-----CETCTCYET 45  
DB 1084 KCVESKSGDKITHKWEIDTERSNANPKRPNCETATCNOT 1124

RESULT 8  
US-08-937-236-6  
Sequence 6, Application US/08937236  
Patent No. 6187310  
GENERAL INFORMATION:  
APPLICANT: MANN, BARBARA J.  
APPLICANT: PETRI, WILLIAM A.  
TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN  
TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE  
TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/937,236  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/569,214  
FILING DATE: 16 SEPTEMBER 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: LIVNAT, SHMUEL  
REGISTRATION NUMBER: 33,949  
REFERENCE/DOCKET NUMBER: 291482000622  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1277 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-937-236-6

Query Match 25.0%; Score 67; DB 3; Length 1277;  
Best Local Similarity 31.7%; Pred. No. 2.6;  
Matches 13; Conservative 6; Mismatches 10; Indels 12; Gaps 1;

QY 17 KCMDLKGNKHPINSEWQTDN-----CETCTCYET 45  
DB 1084 KCVESKSGDKITHKWEIDTERSNANPKRPNCETATCNOT 1124

RESULT 9  
US-08-569-214-3  
Sequence 3, Application US/08569214  
Patent No. 6165469  
GENERAL INFORMATION:  
APPLICANT: MANN, BARBARA J.  
APPLICANT: PETRI, WILLIAM A.  
TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN  
TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE  
TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,214  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/06890  
FILING DATE: 17-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 9148-0006.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1291 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-569-214-3

Query Match 25.0%; Score 67; DB 3; Length 1291;  
Best Local Similarity 31.7%; Pred. No. 2.6;  
Matches 13; Conservative 6; Mismatches 10; Indels 12; Gaps 1;

QY 17 KCMDLKGNKHPINSEWQTDN-----CETCTCYET 45  
DB 1099 KCVESKSGDKITHKWEIDTERSNANPKRPNCETATCNOT 1139

RESULT 10  
US-08-937-236-2



Page 5

MEDIUM TYPE: Floppy disk  
COMPUTER : IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #I.O., Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,214  
FILING DATE:

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/06890  
FILING DATE: 17-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: MORASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 9148-0006.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1292 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-569-214-5

Query Match                25.0%; Score 67; DB 3; Length 1292;  
Best Local Similarity     31.7%; Pred.No.2.6;  
Matches      13; Conservative          6; Mismatches      10; Indels      12; Gaps      1;

DQ                        17 KCMDLKNKHPINSEWQTDN-----CETCTCYET 45  
|||:::||:|||||:|  
  
DB                        1099 KCVESKGSDGKITPKKEIDTERSNANPRNCFCATTCNOT 1139  
|||:::||:|||||:|

RESULT 12  
US-08-569-214-6  
Sequence 6, Application US/08569214  
Patent No. 6165469

GENERAL INFORMATION:  
APPLICANT: MANU, BARBARA J.  
APPlicant: PETRI, WILLIAM A.  
TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN  
TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #I.O., Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,214  
FILING DATE:

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/06890  
FILING DATE: 17-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: MORASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 9148-0006.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1292 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-569-214-5

TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1292 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-569-214-6

Query Match 25.0%; Score 67; DB 3; Length 1292;  
Best Local Similarity 31.7%; Pred. No. 2.6;  
Matches 13; Conservative 6; Mismatches 10; Indels 12; Gaps 1;

QY 17 KCMDLKGNKHPINSEWOTDN-----CETCTCYET 45  
DB 1099 KCVESKSGDKITHKWEIDTFRSNANPKRNPCTATNCNT 1139

RESULT 13  
US-08-937-236-5  
Sequence 5, Application US/08937236  
Patent No. 6187310  
GENERAL INFORMATION:  
APPLICANT: MANN, BARBARA J.  
APPLICANT: PETRI, WILLIAM A.  
APPLICANT: DODSON, JAMES M.  
TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN  
TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE  
TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/937,236  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/569,214  
FILING DATE: 16 SEPTEMBER 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: LIVNAT, SHMUEL  
REGISTRATION NUMBER: 33,949  
REFERENCE/DOCKET NUMBER: 291482000622  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1292 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-937-236-5

Query Match 25.0%; Score 67; DB 3; Length 1292;  
Best Local Similarity 31.7%; Pred. No. 2.6;  
Matches 13; Conservative 6; Mismatches 10; Indels 12; Gaps 1;

QY 17 KCMDLKGNKHPINSEWOTDN-----CETCTCYET 45  
DB 1099 KCVESKSGDKITHKWEIDTFRSNANPKRNPCTATNCNT 1139

RESULT 14  
US-08-569-214-2  
Sequence 2, Application US/08569214  
Patent No. 6165469  
GENERAL INFORMATION:  
APPLICANT: MANN, BARBARA J.  
APPLICANT: PETRI, WILLIAM A.  
TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN  
TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE  
TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,214  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/06890  
FILING DATE: 17-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: WITSHICE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 9148-0006.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1295 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-214-2

Query Match 25.0%; Score 67; DB 3; Length 1295;  
Best Local Similarity 31.7%; Pred. No. 2.6;  
Matches 13; Conservative 6; Mismatches 10; Indels 12; Gaps 1;

QY 17 KCMDLKGNKHPINSEWOTDN-----CETCTCYET 45  
DB 1099 KCVESKSGDKITHKWEIDTFRSNANPKRNPCTATNCNT 1139

RESULT 15  
US-08-276-967-2  
Sequence 2, Application US/08276967  
Patent No. 5851817  
GENERAL INFORMATION:  
APPLICANT: HARDY, DANIEL M.  
APPLICANT: GABERS, DAVID B.  
TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of  
TITLE OF INVENTION: Sperm  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210-4433

Fri Mar 12 09:42:23 2004

us-09-977-406a-88.ra1

Page 7

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/276,967  
FILING DATE: Submitted Herewith  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: UTSD:418/KIT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-787-1400  
TELEFAX: 713-789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2476 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-276-967-2

Query Match 25.0%; Score 67; DB 2; Length 2476;  
Best Local Similarity 40.7%; Pred. NO. 5.7;  
Matches 11; Conservative 3; Mismatches 11; Indels 2; Gaps 1;  
QY 18 CVDLKGKHPINSEWQTDN--CEYCTC 42  
Db 1513 CTQRGSYHPVGSWYTDNCSRLCTC 1539

Search completed: March 11, 2004, 17:56:56  
Job time: 16.9677 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2004, 17:50:06 ; Search time 22.7097 Seconds  
(without alignments)  
145.491 Million cell updates/sec

Title: US-09-977-406A-58  
Perfect score: 368  
Sequence: 1 EMQDNCETCTCYETBISCC.....YIVVEKKDKPKTCVSEWII 64

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A-COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B-COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A-COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B-COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS-COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	368	100.0	94	1	US-07-899-535A-1
2	144	39.1	28	1	US-07-899-535A-4
3	64.5	17.5	94.0	2	US-08-938-365-4
4	64.5	17.5	94.1	1	US-08-343-760A-2
5	62.5	17.0	218	3	US-08-985-526-1
6	62.5	17.0	239	5	PCT-US93-01652-1
7	62.5	17.0	441	3	US-08-985-526-3
8	62.5	17.0	443	4	US-09-328-352-8124
9	62.5	17.0	1170	1	US-08-313-288B-20
10	62	16.8	120	6	5447911-1
11	62	16.8	306	4	US-09-489-039A-11260
12	61	16.6	119	1	US-08-468-347-20
13	61	16.6	119	1	US-08-226-264-24
14	61	16.6	119	2	US-08-467-389-20
15	61	16.6	119	2	US-08-779-379-20
16	61	16.6	119	2	US-08-469-219-20
17	61	16.6	119	2	US-09-228-152-19
18	61	16.6	136	2	US-08-560-098A-59
19	61	16.6	136	6	5189019-6
20	60	16.3	753	3	US-08-942-686-2
21	59.5	16.2	106	4	US-09-543-681A-4251
22	59.5	16.2	129	2	US-08-325-480-5
23	59.5	16.2	129	4	US-09-118-445-5
24	59	16.0	572	5	PCT-US91-08177-11
25	59	16.0	572	5	PCT-US91-08177-19
26	59	16.0	1172	1	US-08-313-288B-19
27	58.5	15.9	810	2	US-08-820-170A-34

28	58.5	15.9	810	3	US-09-055-699-34	Sequence 34, Appl
29	58.5	15.9	810	3	US-09-273-585-34	Sequence 34, Appl
30	58.5	15.9	810	4	US-09-565-538-34	Sequence 34, Appl
31	58.5	15.9	810	4	US-09-661-468-34	Sequence 34, Appl
32	58.5	15.9	810	4	US-09-976-165-34	Sequence 34, Appl
33	58.5	15.9	816	2	US-08-820-170A-37	Sequence 37, Appl
34	58.5	15.9	816	3	US-09-055-699-37	Sequence 37, Appl
35	58.5	15.9	816	3	US-09-273-565-37	Sequence 37, Appl
36	58.5	15.9	816	4	US-09-565-538-37	Sequence 37, Appl
37	58.5	15.9	816	4	US-09-661-468-37	Sequence 37, Appl
38	58.5	15.9	816	4	US-09-976-165-37	Sequence 37, Appl
39	58	15.8	94	4	US-09-621-976-5132	Sequence 5132, Ap
40	58	15.8	114	4	US-09-621-976-5130	Sequence 5130, Ap
41	58	15.8	164	2	US-08-911-319A-1	Sequence 1, Appl
42	58	15.8	164	3	US-09-352-619-1	Sequence 1, Appl
43	58	15.8	487	4	US-09-198-452A-907	Sequence 907, App
44	58	15.8	2409	6	5180808-2	Patent No. 5180808
45	57.5	15.6	140	4	US-09-489-039A-9535	Sequence 9535, Ap

## ALIGNMENTS

RESULT 1  
US-07-899-535A-1  
; Sequence 1, Application US/07899535A  
; Patent No. 5428011  
; GENERAL INFORMATION:  
; APPLICANT: Sheth, Anil R.  
; APPLICANT: Garde, Seema  
; APPLICANT: Panchal, Chandra J.  
; TITLE OF INVENTION: Pharmaceutical Preparations For  
; TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate  
; TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Mr. George Loud  
; STREET: 2001 Jefferson Davis Highway, Suite 306  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/07/899,535A  
; FILING DATE: 16-JUN-1992  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Loud, George A.  
; REGISTRATION NUMBER: 25,814  
; REFERENCE/DOCKET NUMBER: S&B-A835  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-415-0960  
; TELEFAX: 703-415-0962  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 94 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-07-899-535A-1

Query Match 100.0%; Score 368; DB 1; Length 94;  
Best Local Similarity 100.0%; Pred. No. 8.4e-35;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCTCTCYETEISCTLVSTPVGVDKNCQRIKFKEDCKYIVVEKDPKKTCSVS 60  
DB 31 EWQDNCTCTCYETEISCTLVSTPVGVDKNCQRIKFKEDCKYIVVEKDPKKTCSVS 90

QY 61 EWII 64  
DB 91 EWII 94

## RESULT 2

US-07-899-535A-4  
; Sequence 4, Application US/07899535A  
; Patent No. 5428011  
; GENERAL INFORMATION:  
; APPLICANT: Sheth, Anil R.  
; APPLICANT: Garde, Seema  
; APPLICANT: Panchal, Chandra J.  
; TITLE OF INVENTION: Pharmaceutical Preparations For  
; TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate  
; TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Mr. George Loud  
; STREET: 2001 Jefferson Davis Highway, Suite 306  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/899,535A  
; FILING DATE: 16-JUN-1992  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Loud, George A.  
; REGISTRATION NUMBER: 25,814  
; REFERENCE/DOCKET NUMBER: SEB-A835  
; TELEPHONE: 703-415-0960  
; TELEFAX: 703-415-0962  
; TELEX: 24 8614

; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
US-07-899-535A-4

Query Match 39.1%; Score 144; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 6.3e-10;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 IFKEDCKYIVVEKDPKKTCSVSEW 62  
DB 1 IFKEDCKYIVVEKDPKKTCSVSEW 26

## RESULT 3

US-08-938-365-4  
; Sequence 4, Application US/08938365  
; Patent No. 5989909  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Pan  
; TITLE OF INVENTION: HUCHORDIN AND USES THEREOF  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/938,365  
; FILING DATE: 26-SEP-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:

; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 09404/040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 940 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-938-365-4

Query Match 17.5%; Score 64.5; DB 2; Length 940;  
Best Local Similarity 25.9%; Pred. No. 31;  
Matches 15; Conservative 11; Mismatches 23; Indels 9; Gaps 3;

QY 2 WQTD---NCETCTCYETEISCTLVSTPVGVDKNC-QRIFKEDCKYIVVEKDPK 55  
DB 705 WAPDYDRKGVCSQKRTVICDPVCPPL-----NCSQPVHLPDQCCPVCEKRE 757

## RESULT 4

US-08-343-760A-2  
; Sequence 2, Application US/08343760A  
; Patent No. 5679783  
; GENERAL INFORMATION:  
; APPLICANT: De Robertis, Edward M  
; APPLICANT: Sasai, Yoshiki  
; TITLE OF INVENTION: Tissue Differentiation Affecting  
; TITLE OF INVENTION: Factor and Composition  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue  
; STREET: Four Embarcadero Center, Suite 1450  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111

; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: IBM PC compatible  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/343,760A  
; FILING DATE: 22-NOV-1994  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Siebert, J. Suzanne  
; REGISTRATION NUMBER: 28,758  
; REFERENCE/DOCKET NUMBER: 3100.1  
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (415) 363-5556
; TELEFAX: (415) 362-5418
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 941 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-343-760A-2

Query Match 17.5%; Score 64.5; DB 1; Length 941;
Best Local Similarity 25.9%; Pred. No. 31;
Matches 15; Conservative 11; Mismatches 23; Indels 9; Gaps 3;

Qy 2 WQTD---NCEFTCTCYETEISCTLVSTPGVDKDC-ORIFKEDCKYIVVEKKDKPK 55
Db 706 WAPDYDRKSCVSCQKRTVICDPVCPPL-----NCSQPVLHPDQCPVCEERKEMKE 758

RESULT 5
US-08-985-526-1
; Sequence 1, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorrow Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-985-526-1

Query Match 17.0%; Score 62.5; DB 3; Length 218;
Best Local Similarity 37.0%; Pred. No. 11;
Matches 10; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

Qy 1 EWQTDNCETCTCYETEISCTLVSTPV 27
Db 30 EWTVDSCTECHC-QNSVTICKVSCPI 55

RESULT 6
PCT-US93-01652-1
; Sequence 1, Application PC/TUS9301652
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; GENERAL INFORMATION:
; APPLICANT: Bouck, Noel P.
; APPLICANT: Polverini, Peter J.
; APPLICANT: Good, Deborah J.
; APPLICANT: Frazier, William A.
; TITLE OF INVENTION: Method and Composition for
; TITLE OF INVENTION: Inhibiting Angiogenesis
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 South Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01652
; FILING DATE: 19930222
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/841,656
; FILING DATE: 24-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/464,369
; FILING DATE: 12-JAN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Fentress, Susan B.
; REGISTRATION NUMBER: 31,327
; REFERENCE/DOCKET NUMBER: 92005-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)-456-8000
; TELEFAX: (312)-456-7776
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US93-01652-1

Query Match 17.0%; Score 62.5; DB 5; Length 239;
Best Local Similarity 37.0%; Pred. No. 12;
Matches 10; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

Qy 1 EWQTDNCETCTCYETEISCTLVSTPV 27
Db 19 EWTVDSCTECHC-QNSVTICKVSCPI 44

RESULT 7
US-08-985-526-3
; Sequence 3, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorow Jr., Robert G
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-985-526-3

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Query Match 17.0%; Score 62.5; DB 3; Length 441;
Best Local Similarity 37.0%; Pred. No. 23;
Matches 10; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

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QY 1 EQWTDNCCTCTCYETEISCTLVSTPV 27
DB 253 EWTVDSCTECHC-QNSVTICKVSCFI 278

```

```

RESULT 8
US-09-328-352-8124
; Sequence 8124, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 8124
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-8124

```

```

Query Match 17.0%; Score 62.5; DB 4; Length 443;
Best Local Similarity 27.7%; Pred. No. 23;
Matches 18; Conservative 9; Mismatches 27; Indels 11; Gaps 3;

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QY 3 QTDNC-EICTCYETEISCT--LVSTPVGYDKDNCQRIFFKEDCKYIVVEKDKPKTCSV 59
DB 66 EKDPSCSTQPCSTQNSCCTPDSISP-----ETVSDNEVDVATFISDYKIPRMDCSA 117

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```

QY 60 SEWII 64
DB 118 BEQMV 122

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RESULT 9
US-08-313-288B-20
; Sequence 20, Application US/08313288B
; Patent No. 5750502
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M. and AviHu Klar
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,288B
; FILING DATE: January 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1170 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-313-288B-20

```

```

Query Match 17.0%; Score 62.5; DB 1; Length 1170;
Best Local Similarity 37.0%; Pred. No. 66;
Matches 10; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

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QY 1 EQWTDNCCTCTCYETEISCTLVSTPV 27
DB 330 EWTVDSCTECHC-QNSVTICKVSCFI 355

```

```

RESULT 10
5447911-1
; Patent No. 5447911
; APPLICANT: CARDIN, ALAN D.; SUNKARA, SAI P.
; TITLE OF INVENTION: GHILANTEN ANTIMETASTATIC PRINCIPLE FROM
; THE SOUTH AMERICAN LEECH, HAEMENTERIA GHILIANII
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,096
; FILING DATE: 06-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 975,259
; FILING DATE: 19-DEC-1991
; APPLICATION NUMBER: 438,365
; FILING DATE: 14-DEC-1989
; APPLICATION NUMBER: 368,616
; FILING DATE: 20-JUN-1989
; SEQ ID NO: 1
; LENGTH: 120
; 5447911-1

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Query Match 16.8%; Score 62; DB 6; Length 120;
Best Local Similarity 32.7%; Pred. No. 6.3;
Matches 17; Conservative 6; Mismatches 21; Indels 8; Gaps 3;

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QY 7 CETCTC-YETEISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKDKPKKTC 57
DB 49 CEVCRCTRTPMKATCDISECPGM---MCSRLTNKDCCKIDI---NCRKTC 93

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RESULT 11
US-09-489-039A-11260

```



```

; Sequence 11260, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11260
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11260

```

```

Query Match      16.8%; Score 62; DB 4; Length 306;
Best Local Similarity 34.8%; Pred. No. 17;
Matches 23; Conservative 6; Mismatches 23; Indels 14; Gaps 5;

Qy 1 EWDTGNCCTCTCYET-----EIS---CCTLVSTPGVDKNCORIEK--KEDCKYIVVEK 50
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 208 QWLDNGSANTAYETWRFARELNLEPCTTAVSSP--QSNMGARFVTKMKED--YIAFMP 263
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 51 KDPKKT 56
    :|||:
Db 264 KPDVRT 269
    :|||:

```

```

RESULT 12
US-08-468-347-20
; Sequence 20, Application US/08468347
; Patent No. 5783421
; GENERAL INFORMATION:
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; TITLE OF INVENTION: INHIBITORY ACTIVITY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,347
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/225,442
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..119
US-08-468-347-20

Query Match      16.6%; Score 61; DB 1; Length 119;
Best Local Similarity 32.7%; Pred. No. 8.2;
Matches 17; Conservative 6; Mismatches 21; Indels 8; Gaps 3;

Qy 7 CETCTC-YETEISCTLVSTPGVDKNCORIFKEDCKYIVVEKDKPKTC 57
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 48 CEFCKRLPEPKATCDISECEGM--NCSRLTNKCDCKIDI----NCRKTC 92
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-08-226-264-24
; Sequence 24, Application US/08226264
; Patent No. 5801017
; GENERAL INFORMATION:
; APPLICANT: Werber, Moshe M.
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Levanon, Avigdor
; APPLICANT: Guy, Rachel
; APPLICANT: Goldlust, Azie
; APPLICANT: Rigbi, Meir
; APPLICANT: Panet, Amos
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: PRODUCTION OF RECOMBINANT FACTOR Xa
; TITLE OF INVENTION: INHIBITORS OF LEECH HIRUDO MEDICINALIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/226,264
; FILING DATE: 08-APR-94
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40017-A/JPW/GJG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-226-264-24

Query Match      16.6%; Score 61; DB 1; Length 119;
Best Local Similarity 32.7%; Pred. No. 8.2;
Matches 17; Conservative 6; Mismatches 21; Indels 8; Gaps 3;

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2004, 17:45:11; Search time 74.8387 Seconds  
(without alignments)  
241.627 Million cell updates/sec

Title: US-09-977-406A-58  
Perfect score: 368  
Sequence: 1 EQWTDNCETCTCTETEISCC.....YIVVEKDKPKKTCVSEWII 64

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_29Jan04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	368	100.0	64	5 AAO17965	Aao17965 Human pro
2	368	100.0	94	5 AAO17911	Aao17911 Human pro
3	368	100.0	94	7 ABR56227	AbR56227 Native Hu
4	368	100.0	102	5 AAO17912	Aao17912 Human pro
5	368	100.0	102	7 ABR56228	AbR56228 Recombina
6	368	100.0	114	3 AAG03726	Aag03726 Human sec
7	368	100.0	114	4 AAU28067	Aau28067 Novel hum
8	368	100.0	114	6 ABR54574	AbR54574 Prostati
9	368	100.0	114	7 ADB75447	AdB75447 Prostati
10	368	100.0	114	7 ADB14453	AdB14453 Human pro
11	368	100.0	132	3 AAB56449	Aab56449 Human pro
12	364	98.9	63	5 AAO17964	Aao17964 Human pro
13	360	97.8	62	5 AAO17963	Aao17963 Human pro
14	360	97.8	94	2 AAR47117	Aar47117 Complete
15	349	94.8	61	5 AAO17962	Aao17962 Human pro
16	344	93.5	60	5 AAO17961	Aao17961 Human pro
17	340	92.4	59	5 AAO17960	Aao17960 Human pro
18	336	91.3	58	5 AAO17959	Aao17959 Human pro
19	332	90.2	57	5 AAO17958	Aao17958 Human pro
20	323	87.8	56	5 AAO17957	Aao17957 Human pro
21	318	86.4	55	5 AAO17956	Aao17956 Human pro
22	313	85.1	54	5 AAO17955	Aao17955 Human pro
23	308	83.7	53	5 AAO17954	Aao17954 Human pro
24	301	81.8	52	5 AAO17953	Aao17953 Human pro
25	295	80.2	51	5 AAO17952	Aao17952 Human pro

26	290	78.8	50	5 AAO17951	Aao17951 Human pro
27	285	77.4	49	5 AAO17950	Aao17950 Human pro
28	280	76.1	48	5 AAO17949	Aao17949 Human pro
29	279	75.8	119	4 AAU28255	Aau28255 Novel hum
30	276	75.0	47	5 AAO17948	Aao17948 Human pro
31	272	73.9	46	5 AAO17947	Aao17947 Human pro
32	268	72.8	45	5 AAO17946	Aao17946 Human pro
33	261	70.9	44	5 AAO17945	Aao17945 Human pro
34	256	69.6	43	5 AAO17944	Aao17944 Human pro
35	247	67.1	42	5 AAO17943	Aao17943 Human pro
36	241	65.5	41	5 AAO17942	Aao17942 Human pro
37	236	64.1	40	5 AAO17941	Aao17941 Human pro
38	231	62.8	39	5 AAO17940	Aao17940 Human pro
39	226	61.4	38	5 AAO17939	Aao17939 Human pro
40	220	59.8	37	5 AAO17938	Aao17938 Human pro
41	216	58.7	36	5 AAO17937	Aao17937 Human pro
42	211	57.3	35	5 AAO17936	Aao17936 Human pro
43	206	56.0	34	5 AAO17935	Aao17935 Human pro
44	197	53.5	33	5 AAO17934	Aao17934 Human pro
45	191	51.9	32	5 AAO17933	Aao17933 Human pro

## ALIGNMENTS

RESULT 1  
AAO17965  
ID AAO17965 standard; protein; 64 AA.  
XX AC AAO17965;  
XX AC AAO17965;  
XX AC AAO17965;  
DT 30-AUG-2002 (first entry)  
XX  
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #54.  
XX  
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPT; beta-MSP;  
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
KW benign prostate hyperplasia; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO200233090-A2.  
XX  
PD 25-APR-2002.  
XX  
PF 15-OCT-2001; 2001WO-CA001463.  
XX  
PR 16-OCT-2000; 2000CA-02321256.  
XX  
PA 20-AUG-2001; 2001CA-02355334.  
XX  
XX (PROC-) PROCYON BIOPHARMA INC.  
XX  
PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
XX WPI; 2002-471401/50.  
XX  
PT New human prostate secretory protein of 94 amino acids, useful for  
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
PT gastrointestinal, breast, endometrial, and ovarian cancers.  
XX  
PS Claim 2; Page 93-94; 185pp; English.  
XX  
CC The present invention relates to analogues of the human prostate  
CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
CC inhibin peptide (PIP), human seminal plasma inhibin (HSPT) and beta-  
CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
CC growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal  
CC cancer, breast cancer, endometrial, ovarian or other cancers of  
CC epithelial secretion, or benign prostate hyperplasia and for treating  
CC patients with a disease characterized by elevated levels of FSH. The  
CC present sequence is an analogue of the invention

XX SQ Sequence 64 AA;  
 Query Match 100.0%; Score 368; DB 5; Length 64;  
 Best Local Similarity 100.0%; Pred. No. 6e-33; Mismatches 0; Indels 0; Gaps 0;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYETEISCTLVSTPVGVDKNCORIFPKEDCKYIVVEKDPKKTCSVS 60  
 DB 1 EWQDNCETCTCYETEISCTLVSTPVGVDKNCORIFPKEDCKYIVVEKDPKKTCSVS 60

QY 61 EWII 64  
 DB 61 EWII 64

RESULT 2  
 AAO17911  
 ID AAO17911 standard; protein; 94 AA.  
 XX AAO17911;  
 AC  
 DT 30-AUG-2002 (first entry)  
 DE Human prostate secretory protein of 94 amino acids PSP94.  
 XX  
 KW Cancer; human; PSP94; prostatic inhibin protein; FIP; HSP1; beta-MSP;  
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW benign prostate hyperplasia; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX WO200233090-A2.  
 PN 25-APR-2002.  
 PD 15-OCT-2001; 2001WO-CA001463.  
 PF 16-OCT-2000; 2000CA-02321256.  
 PR 20-AUG-2001; 2001CA-02355334.  
 XX (PROC-) PROCYON BIOPHARMA INC.  
 PA Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
 PI WPI; 2002-471401/50.  
 DR  
 XX New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.  
 XX  
 PS Disclosure; Page 73; 185pp; English.

XX The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-  
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is the human PSP94 protein

XX SQ Sequence 94 AA;  
 Query Match 100.0%; Score 368; DB 5; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-33;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYETEISCTLVSTPVGVDKNCORIFPKEDCKYIVVEKDPKKTCSVS 60

DB 31 EWQDNCETCTCYETEISCTLVSTPVGVDKNCORIFPKEDCKYIVVEKDPKKTCSVS 90  
 QY 61 EWII 64  
 DB 91 EWII 94

RESULT 3  
 ABR56227  
 ID ABR56227 standard; protein; 94 AA.  
 XX ABR56227;  
 AC  
 XX 20-NOV-2003 (first entry)  
 DT Native Human prostate secretory protein-94 (PSP-94).  
 DE  
 XX Human; cytostatic; prostate secretory protein-94; PSP-94;  
 KW hypercalcaemia of malignancy; carcinoma; prostate cancer; breast cancer;  
 KW parathyroid hormone related peptide; PTHrP; skeletal metastasis.  
 XX  
 OS Homo sapiens.  
 XX WO2003039576-A1.  
 PN 15-MAY-2003.  
 PD 08-NOV-2002; 2002WO-CA001737.  
 XX 08-NOV-2001; 2001CA-02361736.  
 PR (PROC-) PROCYON BIOPHARMA INC.  
 PA Rabbani SA, Shukeir N, Panchal CJ, Newman C;  
 PI WPI; 2003-441476/41.  
 DR  
 XX Use of prostate secretory protein-94 for treating hypercalcaemia of  
 PT malignancy and reducing skeletal metastasis arising from carcinomas,  
 PT prostate and breast cancers.  
 XX  
 PS Disclosure; Page 35; 61pp; English.

XX The present invention relates to the use of prostate secretory protein-94  
 CC (PSP-94; the present sequence) for treating a patient suffering from  
 CC hypercalcaemia of malignancy. PSP-94 is useful for treating a patient  
 CC suffering from hypercalcaemia of malignancy arising from carcinomas,  
 CC prostate and breast cancer. The PSP-94 is also useful for reducing  
 CC parathyroid hormone related peptide (PTHrP) levels in a patient in need  
 CC and reducing the development of skeletal metastasis. The PSP-94 is also  
 CC used for the manufacture of a pharmaceutical composition for the  
 CC treatment of hypercalcaemia of malignancy and/or skeletal metastasis

XX SQ Sequence 94 AA;  
 Query Match 100.0%; Score 368; DB 7; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-33;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYETEISCTLVSTPVGVDKNCORIFPKEDCKYIVVEKDPKKTCSVS 60  
 DB 31 EWQDNCETCTCYETEISCTLVSTPVGVDKNCORIFPKEDCKYIVVEKDPKKTCSVS 90

QY 61 EWII 64  
 DB 91 EWII 94

RESULT 4  
 AAO17912  
 ID AAO17912 standard; protein; 102 AA.  
 XX AAO17912;  
 AC

30-AUG-2002 (first entry)  
Human prostate secretory protein of 94 amino acids PSP94 analogue #1.  
Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;  
beta-microseminoprotein; human seminal plasma inhibitor; analogue;  
prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
benign prostate hyperplasia; cytostatic.  
Homo sapiens.  
WO200233090-A2.  
25-APR-2002.  
15-OCT-2001; 2001WO-CA001463.  
16-OCT-2000; 2000CA-02321256.  
20-AUG-2001; 2001CA-02355334.  
(PROC-) PROCYON BIOPHARMA INC.  
Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
WPI; 2002-471401/50.  
New human prostate secretory protein of 94 amino acids, useful for  
inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
PT gastrointestinal, breast, endometrial, and ovarian cancers.  
Claim 2; Page 73-74; 185pp; English.  
The present invention relates to analogues of the human prostate  
secretory protein of 94 amino acids (PSP94, also known as prostatic  
inhibin peptide (PIP), human seminal plasma inhibitor (HSPI) and beta-  
microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
cancer, breast cancer, endometrial, ovarian or other cancers of  
epithelial secretion, or benign prostate hyperplasia and for treating  
patients with a disease characterized by elevated levels of FSH. The  
present sequence is an analogue of the invention  
Sequence 102 AA;  
Query Match 100.0%; Score 368; DB 5; Length 102;  
Best Local Similarity 100.0%; Pred. No. 1e-32;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 EWQDNCETCTCYETETISCTLVSTPGVYKDNQCRIFKEDCKYIVVEKDPKKTCSVS 60  
DB 39 EWQDNCETCTCYETETISCTLVSTPGVYKDNQCRIFKEDCKYIVVEKDPKKTCSVS 98  
OY 61 EWII 64  
DB 99 EWII 102  
RESULT 5  
ABR56228  
ID ABR56228 standard; protein; 102 AA.  
AC ABR56228;  
XX 20-NOV-2003 (first entry)  
DE Recombinate prostate secretory protein-94 (PSP-94).  
XX Cytostatic; prostate secretory protein-94; PSP-94;  
KW hypercalcaemia of malignancy; carcinoma; prostate cancer; breast cancer;  
KW parathyroid hormone related peptide; PTHrP; skeletal metastasis.  
XX

Unidentified.  
WO2003039576-A1.  
15-MAY-2003.  
08-NOV-2002; 2002WO-CA001737.  
08-NOV-2001; 2001CA-02361736.  
(PROC-) PROCYON BIOPHARMA INC.  
Rabbani SA, Shukeir N, Panchal CJ, Newman C;  
WPI; 2003-441476/41.  
Use of prostate secretory protein-94 for treating hypercalcaemia of  
malignancy and reducing skeletal metastasis arising from carcinomas,  
prostate and breast cancers.  
Disclosure; Page 35-36; 61pp; English.  
The present invention relates to the use of prostate secretory protein-94  
(PSP-94; the present sequence) for treating a patient suffering from  
hypercalcaemia of malignancy. PSP-94 is useful for treating a patient  
suffering from hypercalcaemia of malignancy arising from carcinomas,  
prostate and breast cancer. The PSP-94 is also useful for reducing  
parathyroid hormone related peptide (PTHrP) levels in a patient in need  
and reducing the development of skeletal metastasis. The PSP-94 is also  
used for the manufacture of a pharmaceutical composition for the  
treatment of hypercalcaemia of malignancy and/or skeletal metastasis  
Sequence 102 AA;  
Query Match 100.0%; Score 368; DB 7; Length 102;  
Best Local Similarity 100.0%; Pred. No. 1e-32;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 EWQDNCETCTCYETETISCTLVSTPGVYKDNQCRIFKEDCKYIVVEKDPKKTCSVS 60  
DB 39 EWQDNCETCTCYETETISCTLVSTPGVYKDNQCRIFKEDCKYIVVEKDPKKTCSVS 98  
OY 61 EWII 64  
DB 99 EWII 102  
RESULT 6  
AAG03726  
ID AAG03726 standard; protein; 114 AA.  
AC AAG03726;  
XX 06-OCT-2000 (first entry)  
DE Human secreted protein, SEQ ID NO: 7807.  
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping.  
XX Homo sapiens.  
XX EP1033401-A2.  
XX 06-SEP-2000.  
XX 21-FEB-2000; 2000EP-00200610.  
XX 26-FEB-1999; 99US-0122487P.  
XX (GEST) GENSET.  
PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.  
DR N-PSDB; AAC03732.  
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
XX  
XX Claim 13; SEQ ID NO 7807; 71pp + Sequence Listing; English.  
XX  
XX The present sequence is a polypeptide encoded by one of a large number of  
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different  
CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
CC sequences derived from the 5' ends of mRNAs and even in those cases where  
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
CC are also used in diagnostic, forensic, gene therapy and chromosome  
CC mapping procedures. They are used to obtain upstream regulatory sequences  
CC and to design expression and secretion vectors  
XX  
XX Sequence 114 AA;  
XX  
XX Query Match 100.0%; Score 368; DB 3; Length 114;  
XX Best Local Similarity 100.0%; Pred. No. 1.1e-32;  
XX Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 EWQDNCETCTCYETETISCTLVSTPGVDKNCQRIFFKEDCKYIWEKDPKKTCSVS 60  
XX Db 51 EWQDNCETCTCYETETISCTLVSTPGVDKNCQRIFFKEDCKYIWEKDPKKTCSVS 110  
XX  
XX QY 61 EWII 64  
XX Db 111 EWII 114  
XX  
XX RESULT 7  
XX AAU28067  
XX ID AAU28067 standard; protein; 114 AA.  
XX AC AAU28067;  
XX  
XX DT 18-DEC-2001 (first entry)  
XX DE Novel human secretory protein, Seq ID No 236.  
XX  
XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;  
XX ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;  
XX transgenic animal; Alzheimer's disease; Parkinson's disease; burn;  
XX amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;  
XX ulcer; osteoporosis; bone degenerative disorder; periodontal disease;  
XX gut protection; lung; liver fibrosis; immune deficiency; infection;  
XX severe combined immunodeficiency; SCID; autoimmune disorder; allergy;  
XX multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;  
XX fertility; analgesic; pain; antigen.  
XX  
XX Homo sapiens.  
XX  
XX WO200166689-A2.  
XX  
XX 13-SEP-2001.  
XX  
XX 05-MAR-2001; 2001WO-US004942.  
XX  
XX 07-MAR-2000; 2000US-00519705.  
XX 19-MAY-2000; 2000US-00574454.  
XX 17-JUN-2000; 2000US-00596193.  
XX 14-JUL-2000; 2000US-00616847.  
XX 19-SEP-2000; 2000US-00665363.  
XX 20-OCT-2000; 2000US-00693267.  
XX

(HYSE-) HYSEQ INC.  
Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;  
Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;  
WPI; 2001-589934/66.  
N-PSDB; AAS44967.  
Novel polypeptides and nucleic acids obtained from cDNA libraries  
prepared from various human tissues, for diagnosis and treatment of  
cancer, neurological, inflammatory, and autoimmune disorders.  
Example 3; SEQ ID NO 236; 107pp; English.  
The invention relates to novel isolated human secreted polypeptides (I)  
and polynucleotides (II). (I) and (II) are useful for treating  
inflammatory conditions such as arthritis, nephritis, Crohn's disease,  
ischaemia-reperfusion injury, shock, sepsis, immune responses, and is  
involved in increasing haematopoiesis, stem cell survival, bone growth  
and remodeling. (I), (II) and modulators of (II) are useful for  
prophylaxis or treatment of one or more cancers. (II) is also useful for  
creating transgenic animals useful for studying the in vivo activities of  
the polypeptide as well as for studying modulators of the polypeptides.  
(I) induces the proliferation of neural cells and regeneration of nerve  
and brain tissue and is useful for the treatment of central and  
peripheral nervous system diseases and neuropathies, such as Alzheimer's,  
Parkinson's disease, Huntington's disease, and amyotrophic lateral  
sclerosis. In addition, (I) is involved in chemotactic or chemokinetic  
activity, regulation of haematopoiesis and is useful for treating myeloid  
or lymphoid cell disorders, platelet disorders such as thrombocytopenia  
and for regeneration of bone, cartilage, tendon, ligament and/or nerve  
tissue growth, and in tissue repair, healing of burns, incisions, ulcers,  
for treating osteoporosis, osteoarthritis, bone degenerative disorders,  
or periodontal disease. Furthermore, (I) is also useful for gut  
protection or regeneration and treatment of lung or liver fibrosis,  
reperfusion injury in various tissues, various immune deficiencies and  
disorders including severe combined immunodeficiency (SCID), bacterial or  
fungal infections, autoimmune disorders e.g. multiple sclerosis,  
rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic  
reactions and conditions, such as asthma or other respiratory problems.  
In addition, (I) affects biorhythms or circadian cycles of rhythms,  
fertility, metabolism, catabolism, anabolism, storage or elimination of  
dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides  
analgesic effects or other pain reducing effects, immunoglobulin like  
activity and can act as an antigen in a vaccine composition to raise an  
immune response. AAU28020-AAU28395 represent novel human secreted protein  
amino acid sequences of the invention  
Sequence 114 AA;  
Query Match 100.0%; Score 368; DB 4; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.1e-32;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EWQDNCETCTCYETETISCTLVSTPGVDKNCQRIFFKEDCKYIWEKDPKKTCSVS 60  
Db 51 EWQDNCETCTCYETETISCTLVSTPGVDKNCQRIFFKEDCKYIWEKDPKKTCSVS 110  
QY 61 EWII 64  
Db 111 EWII 114  
RESULT 8  
ABR54574  
ID ABR54574 standard; protein; 114 AA.  
XX ABR54574;  
XX ABR54574;  
XX 28-AUG-2003 (first entry)  
XX Prostatic secretory protein SEQ ID 1003.  
DE

XX KW Cytostatic; gene therapy; prostate-specific protein; PSP; human;  
XX KW immune response; prostate cancer.  
XX OS Homo sapiens.  
XX EN WO200289747-A2.  
XX PD 14-NOV-2002.  
XX PF 09-MAY-2002; 2002WO-US014753.  
XX PR 09-MAY-2001; 2001US-00852911.  
XX PR 29-JUN-2001; 2001US-00895814.  
XX PR 10-DEC-2001; 2001US-00012896.  
XX PA (CORI-) CORIXA CORP.  
XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;  
PI Kalos MD, Fanger GR, Retter MW, Stoik JA, Day CH, Vedvick TS;  
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;  
PI McNeill PD, Houghton RL, Vinals Y De BassolisC, Foy TW, Watanabe Y;  
PI Deng T;  
XX DR WPI; 2003-167130/16.  
XX PT New prostate-specific proteins and genes, useful in gene therapy,  
XX PT particularly for stimulating an immune response in a patient, or treating  
XX PT prostate cancer in a patient, as well as for diagnosing prostate cancer  
XX PT in a patient.  
XX PS Claim 2; Page 666; 691pp; English.  
XX CC The present invention relates to novel prostate-specific proteins (PSP)  
XX CC and their coding sequences. The PSPs and their coding sequences are  
XX CC useful for stimulating an immune response in a patient, or for treating  
XX CC prostate cancer in a patient and for determining, detecting or diagnosing  
XX CC the presence of a cancer in a patient. The present sequence was used to  
XX CC illustrate the invention  
XX SQ Sequence 114 AA;  
Query Match 100.0%; Score 368; DB 6; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.1e-32;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EWQTDNCCTCTCYETETISCTLVSTPVGVDKNCQRIFFKEDCKYIVVEKDPKKTCSVS 60  
Db 51 EWQTDNCCTCTCYETETISCTLVSTPVGVDKNCQRIFFKEDCKYIVVEKDPKKTCSVS 110  
QY 61 EWII 64  
Db 111 EWII 114  
RESULT 9  
ADB75447  
ID ADB75447 standard; protein; 114 AA.  
XX AC ADB75447;  
XX DT 04-DEC-2003 (first entry)  
XX DE Prostate cancer marker protein.  
XX KW Prostate; cancer; cytostatic; gene therapy; marker.  
XX OS Homo sapiens.  
XX PN WO2003009814-A2.  
XX PD 06-FEB-2003.  
XX PF

PF 25-JUL-2002; 2002WO-US023913.  
XX PR 25-JUL-2001; 2001US-0307982P.  
XX PR 22-AUG-2001; 2001US-0314358P.  
XX PR 25-SEP-2001; 2001US-0325020P.  
XX PR 12-DEC-2001; 2001US-0341746P.  
XX PR 05-MAR-2002; 2002US-0362158P.  
XX PA (MILL-) MILLENNIUM PHARM INC.  
XX PI Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;  
PI Hoersht S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;  
XX DR WPI; 2003-248033/24.  
XX PT New nucleic acid molecule, useful for diagnosing or treating prostate  
XX PT cancer.  
XX PS Disclosure; SEQ ID NO 271; 99pp; English.  
XX CC The invention relates to newly discovered cancer markers associated with  
XX CC the cancerous state of prostate cells. Also disclosed is a method of  
XX CC assessing whether a patient is afflicted with prostate cancer. The method  
XX CC of the invention involves assessing whether a patient is afflicted with  
XX CC prostate cancer by comparing the level of expression of a marker in a  
XX CC patient sample and the normal level of expression of the marker in a  
XX CC control non-prostate cancer sample, where a significant increase in the  
XX CC level of expression of the marker in the patient sample and the normal  
XX CC level indicates that the patient is afflicted with prostate cancer.  
XX CC Nucleic acids of the invention are useful for diagnosing or treating  
XX CC prostate cancer, and may be useful in gene therapy. Sequences given in  
XX CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence  
XX CC data for this patent did not form part of the printed specification, but  
XX CC was obtained in electronic format directly from WIPO at  
XX CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX SQ Sequence 114 AA;  
Query Match 100.0%; Score 368; DB 7; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.1e-32;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EWQTDNCCTCTCYETETISCTLVSTPVGVDKNCQRIFFKEDCKYIVVEKDPKKTCSVS 60  
Db 51 EWQTDNCCTCTCYETETISCTLVSTPVGVDKNCQRIFFKEDCKYIVVEKDPKKTCSVS 110  
QY 61 EWII 64  
Db 111 EWII 114  
RESULT 10  
ADB14453  
ID ADB14453 standard; protein; 114 AA.  
XX AC ADB14453;  
XX DT 18-DEC-2003 (first entry)  
XX DE Human prostatic secretory protein (PSP).  
XX KW Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;  
XX KW cell therapy; vaccine; T-cell epitope;  
XX KW class I major histocompatibility complex allele; MHC; prostate cancer;  
XX KW tumour; antigen presenting cell.  
XX OS Homo sapiens.  
XX PN US2003185830-A1.  
XX PD 02-OCT-2003.  
XX PF 12-NOV-2002; 2002US-00294025.

XX 25-FEB-1997; 97US-00806099.  
PR 01-AUG-1997; 97US-00304804.  
PR 09-FEB-1998; 98US-00020956.  
PR 25-FEB-1998; 98US-00030607.  
PR 14-JUL-1998; 98US-00115453.  
PR 23-SEP-1998; 98US-00159812.  
PR 15-JAN-1999; 99US-00232149.  
PR 09-APR-1999; 99US-00288946.  
PR 13-JUL-1999; 99US-00352616.  
PR 12-NOV-1999; 99US-00439313.  
PR 18-NOV-1999; 99US-00443686.  
PR 14-JAN-2000; 2000US-00483672.  
PR 27-MAR-2000; 2000US-00536857.  
PR 09-MAY-2000; 2000US-00568100.  
PR 12-MAY-2000; 2000US-00570737.  
PR 13-JUN-2000; 2000US-00593793.  
PR 27-JUN-2000; 2000US-00605783.  
PR 09-AUG-2000; 2000US-00636213.  
PR 29-AUG-2000; 2000US-00651236.  
PR 06-SEP-2000; 2000US-00657279.  
PR 02-OCT-2000; 2000US-00679426.  
PR 10-OCT-2000; 2000US-00685166.  
PR 09-NOV-2000; 2000US-00709729.  
PR 12-JAN-2001; 2001US-00758143.  
PR 09-FEB-2001; 2001US-00780669.  
PR 09-MAY-2001; 2001US-00852911.  
PR 29-JUN-2001; 2001US-00895814.  
PR 10-DEC-2001; 2001US-00012896.  
PR 09-MAY-2002; 2002US-00144678.  
XX (CORI-) CORIXA CORP.  
XX  
XX Xu J, Stolk JA, Kalos MD;  
XX WPI; 2003-756193/71.  
XX  
XX New isolated polypeptide for use in a vaccine for stimulating an immune  
PT response, or for treating or diagnosis cancer, preferably prostate  
PT cancer.  
XX  
XX Example 34; Page; 101pp; English.  
XX  
XX The invention relates to an isolated polypeptide comprising no more than  
CC 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The  
CC peptides comprise a fragment ADB13563 of that contain naturally processed  
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)  
CC alleles. ADB13563 is a polypeptide encoded by a human prostate specific  
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids  
CC encoding the proteins and peptides, expression vectors, a host cell  
CC transformed with the vector, an isolated antibody (or antigen binding  
CC fragment) that specifically binds to the protein or peptide, detecting  
CC the presence of a cancer in a patient (comprising contacting a patient  
CC sample with a binding agent that binds to the peptides or a polypeptide  
CC appearing as ADB13563, detecting the amount of polypeptide that binds to  
CC the agent and comparing the amount of polypeptide to a predetermined cut-  
CC off value to determine the presence of cancer), a fusion protein  
CC comprising the peptides or proteins, stimulating or expanding T cells  
CC specific for a tumor protein comprising contacting T cells with the  
CC peptides or the isolated T cell population, treating prostate cancer in a  
CC patient comprising administering a composition comprising the peptides,  
CC nucleic acids, antibodies or compounds, determining the presence of a  
CC cancer in a patient and treating prostate cancer in a patient comprising  
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated  
CC from a patient with the peptides or antigen presenting cells that express  
CC (the peptides so that the T cells proliferate, and administering the  
CC proliferated T cells to the patient. The peptides (or an oligonucleotide  
CC that hybridises to nucleic acid encoding them), is used to detect the  
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or  
CC antigen-presenting cells expressing the nucleic acid, are used to  
CC stimulate or expand T cells specific for a tumour protein. The peptides,  
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen  
CC presenting cells are used to stimulate an immune response or treat

CC prostate cancer in a patient. The present sequence is a prostate specific  
CC protein of the invention. Note: Except where otherwise indicated, the  
CC sequence data for this patent did not form part of the printed, the  
CC specification, but was obtained in electronic format directly from USPTO  
CC at seqdata.uspto.gov/sequence.html?DocID=20030185830.

XX Sequence 114 AA;

Query Match 100.0%; Score 368; DB 7; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.1e-32;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EQQTNCETCTCYETEISCTLVSTFVGVDKNCQRIFFKEDCKIIVVEKDPKTKCSVS 60  
Db 51 EQQTNCETCTCYETEISCTLVSTFVGVDKNCQRIFFKEDCKIIVVEKDPKTKCSVS 110  
QY 61 EWII 64  
Db 111 EWII 114

RESULT 11

AAAB56449

ID AAAB56449 standard; protein; 132 AA.

XX AC AAAB56449;

XX DT 13-MAR-2001 (first entry)

XX DE Human prostate cancer antigen protein sequence SEQ ID NO:1027.

XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
XX neuroprotective; cytostatic; cardiocactive; immunomodulatory; muscular;  
XX vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;  
XX antibacterial; gene therapy; neural; immune; reproductive; renal;  
XX gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
XX wound; infectious disease.

XX Homo sapiens.

XX WO2000055174-A1.

XX PD 21-SEP-2000.

XX PF 08-MAR-2000; 2000WO-US0005988.

XX PR 12-MAR-1999; 99US-0124270P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX FA (ROSE/) ROSEN C A.

XX PI Rosen CA, Ruben SM;

XX WPI: 2000-587513/55.

XX N-PSDB; AAF15652.

PT Prostate cancer associated gene sequences, referred to as prostate cancer  
PT antigens, useful for treatment, prevention, and diagnosis of disorders  
PT such as prostate cancer.  
PS Claim 11; Page 1457; 2338pp; English.

XX AAF1566 to AAF16505 encode the human prostate cancer associated  
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.  
CC The prostate cancer antigens can have neuroprotective, cytostatic,  
CC cardiocactive, immunomodulatory, muscular, vulnary, gastrointestinal,  
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,  
CC and can be used in gene therapy. The prostate cancer antigen  
CC polynucleotides may be used for detection of prostate cancer, chromosome  
CC identification, as chromosome markers, and for numerous other diagnostic  
CC or research purposes. The prostate cancer antigens may be used to treat  
CC disorders such as neural, immune, muscular, reproductive, and  
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative



CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to  
CC AAF57303 represent sequences used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 132 AA;  
Query Match 100.0%; Score 368; DB 3; Length 132;  
Best Local Similarity 100.0%; Pred. No. 1.3e-32;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EWQTDNCETCTCYETEISCTLVSTPVGVDKNCQRIFFKEDCKYIVVEKDPKKTCSVS 60  
Db 69 EWQTDNCETCTCYETEISCTLVSTPVGVDKNCQRIFFKEDCKYIVVEKDPKKTCSVS 128  
Qy 61 EWII 64  
Db 129 EWII 132  
RESULT 12  
AAOI17964  
ID AAOI17964 standard; protein; 63 AA.  
XX  
AC AAOI17964;  
XX  
DT 30-AUG-2002 (first entry)  
XX  
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #53.  
XX  
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;  
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
KW benign prostate hyperplasia; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO200233090-A2.  
XX  
PD 25-APR-2002.  
XX  
PF 15-OCT-2001; 2001WO-CA001463.  
XX  
PR 16-OCT-2000; 2000CA-02321256.  
XX  
PR 20-AUG-2001; 2001CA-02355334.  
XX  
PA (PROC-) PROCYON BIOPHARMA INC.  
XX  
PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
XX  
DR WPI; 2002-471401/50.  
XX  
XX New human prostate secretory protein of 94 amino acids, useful for  
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
PT gastrointestinal, breast, endometrial, and ovarian cancers.  
XX  
PS Claim 2; Page 93; 185pp; English.  
XX  
CC The present invention relates to analogues of the human prostate  
CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-  
CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting  
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
CC cancer, breast cancer, endometrial, ovarian or other cancers of  
CC epithelial secretion, or benign prostate hyperplasia and for treating  
CC patients with a disease characterized by elevated levels of FSH. The  
CC present sequence is an analogue of the invention  
XX  
SQ Sequence 63 AA;  
Query Match 98.9%; Score 364; DB 5; Length 63;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EWQTDNCETCTCYETEISCTLVSTPVGVDKNCQRIFFKEDCKYIVVEKDPKKTCSVS 60  
Db 1 EWQTDNCETCTCYETEISCTLVSTPVGVDKNCQRIFFKEDCKYIVVEKDPKKTCSVS 60  
Qy 61 EWI 63  
Db 61 EWI 63  
RESULT 13  
AAOI17963  
ID AAOI17963 standard; protein; 62 AA.  
XX  
AC AAOI17963;  
XX  
DT 30-AUG-2002 (first entry)  
XX  
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #52.  
XX  
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;  
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
KW benign prostate hyperplasia; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO200233090-A2.  
XX  
PD 25-APR-2002.  
XX  
PF 15-OCT-2001; 2001WO-CA001463.  
XX  
PR 16-OCT-2000; 2000CA-02321256.  
XX  
PR 20-AUG-2001; 2001CA-02355334.  
XX  
PA (PROC-) PROCYON BIOPHARMA INC.  
XX  
PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
XX  
DR WPI; 2002-471401/50.  
XX  
XX New human prostate secretory protein of 94 amino acids, useful for  
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
PT gastrointestinal, breast, endometrial, and ovarian cancers.  
XX  
PS Claim 2; Page 93; 185pp; English.  
XX  
CC The present invention relates to analogues of the human prostate  
CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-  
CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting  
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
CC cancer, breast cancer, endometrial, ovarian or other cancers of  
CC epithelial secretion, or benign prostate hyperplasia and for treating  
CC patients with a disease characterized by elevated levels of FSH. The  
CC present sequence is an analogue of the invention  
XX  
SQ Sequence 62 AA;  
Query Match 97.8%; Score 360; DB 5; Length 62;  
Best Local Similarity 100.0%; Pred. No. 4.4e-32;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EWQTDNCETCTCYETEISCTLVSTPVGVDKNCQRIFFKEDCKYIVVEKDPKKTCSVS 60  
Db 1 EWQTDNCETCTCYETEISCTLVSTPVGVDKNCQRIFFKEDCKYIVVEKDPKKTCSVS 60  
Qy 61 EW 62  
Db 61 EW 62

RESULT 14  
AA017962  
ID AAR47117 standard; peptide; 94 AA.  
XX  
AC AAR47117;  
XX  
XX 25-MAR-2003 (revised)  
DT 30-JUN-1994 (first entry)  
XX  
XX Complete sequence of human prostatic inhibin peptide.  
DE  
XX Prostatic inhibin peptide; cancer; adenocarcinoma; breast cancer;  
KW hyperplasia; PIP; follicle stimulating hormone; FSH; tumour; inhibition;  
KW prostate cancer; gastrointestinal tract.  
XX  
XX Homo sapiens.  
OS  
XX WO9325224-A1.  
PN  
XX 23-DEC-1993.  
PD  
XX 16-JUN-1993; 93WO-CA000252.  
PF  
XX 16-JUN-1992; 92US-00899535.  
PR  
XX (VETR-) VETROGEN CORP.  
PA  
XX Sheth AR, Garde S, Panchal CJ;  
PI  
XX WPI; 1994-007191/01.  
DR  
XX Prepn. contg. prostatic inhibin peptide or analogues - used for treating  
PT benign prostatic hyperplasia, adenocarcinoma or diseases with high FSH  
PT levels.  
PT  
XX Disclosure; Fig 1; 48pp; English.  
PS  
XX Peptides or analogues of prostatic inhibin peptide (PIP) are used in a  
XX pharmaceutical preparation for treating patients with benign prostatic  
CC hyperplasia or adenocarcinoma, particularly adenocarcinoma of the  
CC prostate or gastrointestinal tract or breast cancer. The preparation can  
CC also be used to treat patients with diseases characterised by elevated  
CC levels of follicle stimulating hormone (FSH). The PIP and its analogues  
CC inhibit tumour growth and decrease FSH levels without adversely affecting  
CC testosterone levels. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 94 AA;  
SQ  
Query Match 97.8%; Score 360; DB 2; Length 94;  
Best Local Similarity 100.0%; Pred. No. 6.9e-32;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EWQTDNCETCTCYETETISCTLVSTPVGVDKNCORIFPKEDCKYIVVEKDPKKTCSVS 60  
Db 31 EWQTDNCETCTCYETETISCTLVSTPVGVDKNCORIFPKEDCKYIVVEKDPKKTCSVS 90  
QY 61 EW 62  
Db 91 EW 92  
RESULT 15  
AA017962  
ID AAO17962 standard; protein; 61 AA.  
XX  
AC AAO17962;  
XX  
DT 30-AUG-2002 (first entry)  
XX  
XX Human prostate secretory protein of 94 amino acids PSP94 analogue #51.  
DE  
XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;  
KW

KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
XX benign prostate hyperplasia; cytostatic.  
OS  
XX Homo sapiens.  
XX  
PN WO200233090-A2.  
XX  
PD 25-APR-2002.  
XX  
XX 15-OCT-2001; 2001WO-CA001463.  
PF  
XX 16-OCT-2000; 2000CA-02321256.  
PR  
XX 20-AUG-2001; 2001CA-02355334.  
PR  
XX (PROC-) PROCYON BIOPHARMA INC.  
PA  
XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
PI  
XX WPI; 2002-471401/50.  
DR  
XX New human prostate secretory protein of 94 amino acids, useful for  
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
PT gastrointestinal, breast, endometrial, and ovarian cancers.  
XX  
XX Claim 2; Page 92; 185pp; English.  
XX  
XX The present invention relates to analogues of the human prostate  
CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-  
CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
CC cancer, breast cancer, endometrial, ovarian or other cancers of  
CC epithelial secretion, or benign prostate hyperplasia and for treating  
CC patients with a disease characterized by elevated levels of FSH. The  
CC present sequence is an analogue of the invention  
XX  
SQ Sequence 61 AA;  
Query Match 94.8%; Score 349; DB 5; Length 61;  
Best Local Similarity 100.0%; Pred. No. 6.9e-31;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EWQTDNCETCTCYETETISCTLVSTPVGVDKNCORIFPKEDCKYIVVEKDPKKTCSVS 60  
Db 1 EWQTDNCETCTCYETETISCTLVSTPVGVDKNCORIFPKEDCKYIVVEKDPKKTCSVS 60  
QY 61 E 61  
Db 61 E 61  
Search completed: March 11, 2004, 17:52:41  
Job time : 75.8387 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2004, 17:45:11 ; Search time 17.5403 Seconds  
 (without alignments)  
 241.627 Million cell updates/sec

Title: US-09-977-406A-5

Perfect score: 97  
 Sequence: 1 EWQDNCECTCYET 15

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A Geneseq\_29Jan04:\*  
 1: geneseqp1980s.\*  
 2: geneseqp1980s.\*  
 3: geneseqp2000s.\*  
 4: geneseqp2001s.\*  
 5: geneseqp2002s.\*  
 6: geneseqp2003as.\*  
 7: geneseqp2003bs.\*  
 8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	15	5 AAO17915	AAO17915 Human pro
2	97	100.0	15	7 ABR56231	ABR56231 Prostate
3	97	100.0	16	5 AAO17917	AAO17917 Human pro
4	97	100.0	16	5 AAO17966	AAO17966 Human pro
5	97	100.0	17	5 AAO17967	AAO17967 Human pro
6	97	100.0	17	5 AAO17918	AAO17918 Human pro
7	97	100.0	18	5 AAO17919	AAO17919 Human pro
8	97	100.0	18	5 AAO17968	AAO17968 Human pro
9	97	100.0	19	5 AAO17969	AAO17969 Human pro
10	97	100.0	19	5 AAO17920	AAO17920 Human pro
11	97	100.0	20	5 AAO17921	AAO17921 Human pro
12	97	100.0	20	5 AAO17970	AAO17970 Human pro
13	97	100.0	21	5 AAO17922	AAO17922 Human pro
14	97	100.0	21	5 AAO17971	AAO17971 Human pro
15	97	100.0	22	5 AAO17923	AAO17923 Human pro
16	97	100.0	22	5 AAO17972	AAO17972 Human pro
17	97	100.0	23	5 AAO17973	AAO17973 Human pro
18	97	100.0	23	5 AAO17924	AAO17924 Human pro
19	97	100.0	24	5 AAO17925	AAO17925 Human pro
20	97	100.0	24	5 AAO17974	AAO17974 Human pro
21	97	100.0	25	5 AAO17975	AAO17975 Human pro
22	97	100.0	25	5 AAO17926	AAO17926 Human pro
23	97	100.0	26	5 AAO17976	AAO17976 Human pro
24	97	100.0	26	5 AAO17927	AAO17927 Human pro
25	97	100.0	27	5 AAO17977	AAO17977 Human pro

26	97	100.0	27	5 AAO17928	AAO17928 Human pro
27	97	100.0	28	5 AAO17929	AAO17929 Human pro
28	97	100.0	28	5 AAO17978	AAO17978 Human pro
29	97	100.0	29	5 AAO17930	AAO17930 Human pro
30	97	100.0	29	5 AAO17979	AAO17979 Human pro
31	97	100.0	30	5 AAO17980	AAO17980 Human pro
32	97	100.0	30	5 AAO17997	AAO17997 Human pro
33	97	100.0	31	5 AAO17931	AAO17931 Human pro
34	97	100.0	31	5 AAO17981	AAO17981 Human pro
35	97	100.0	31	5 AAO17932	AAO17932 Human pro
36	97	100.0	32	5 AAO17933	AAO17933 Human pro
37	97	100.0	32	5 AAO17982	AAO17982 Human pro
38	97	100.0	33	5 AAO17934	AAO17934 Human pro
39	97	100.0	33	5 AAO17983	AAO17983 Human pro
40	97	100.0	34	5 AAO17935	AAO17935 Human pro
41	97	100.0	34	5 AAO17984	AAO17984 Human pro
42	97	100.0	35	5 AAO17936	AAO17936 Human pro
43	97	100.0	35	5 AAO17985	AAO17985 Human pro
44	97	100.0	36	5 AAO17937	AAO17937 Human pro
45	97	100.0	36	5 AAO17986	AAO17986 Human pro

## ALIGNMENTS

### RESULT 1

AAO17915  
 ID AAO17915 standard; peptide; 15 AA.

XX AC AAO17915;

XX DT 30-AUG-2002 (first entry)

XX DE Human prostate secretory protein of 94 amino acids PSP94 analogue #4.  
 XX KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW benign prostate hyperplasia; cytostatic.

XX OS Homo sapiens.

XX PN WO200233090-A2.

XX PD 25-APR-2002.

XX PF 15-OCT-2001; 2001WO-CA001463.

XX PR 16-OCT-2000; 2000CA-02321256.

XX XX 20-AUG-2001; 2001CA-02355334.

XX PA (PROC-) PROCYON BIOPHARMA INC.

XX PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;

XX DR WPI; 2002-471401/50.

XX PT New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.

XX PS Claim 1; Page 74; 185pp; English.

XX CC The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-  
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention

XX SQ Sequence 15 AA;  
 Query Match 100.0%; Score 97; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQTDNCETCTCYET 15  
 DB 1 EWQTDNCETCTCYET 15

RESULT 2  
 ABR56231  
 ID ABR56231 standard; peptide; 15 AA.  
 AC ABR56231;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Prostate secretory protein-94 (PSP-94) peptide fragment PK3145.  
 DE  
 KW Cytostatic; prostate secretory protein-94; PSP-94; human;  
 KW hypercalcaemia of malignancy; carcinoma; prostate cancer; breast cancer;  
 KW parathyroid hormone related peptide; PTHrP; skeletal metastasis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003039576-A1.  
 PD 15-MAY-2003.  
 XX  
 PF 08-NOV-2002; 2003WO-CA001737.  
 XX  
 PR 08-NOV-2001; 2001CA-02361736.  
 XX  
 PA (PROC-) PROCYON BIOPHARMA INC.  
 XX  
 PI Rabbani SA, Shukeir N, Panchal CJ, Newman C;  
 XX  
 DR WPI; 2003-441476/41.  
 XX  
 PT Use of prostate secretory protein-94 for treating hypercalcaemia of  
 PT malignancy and reducing skeletal metastasis arising from carcinomas,  
 PT prostate and breast cancers.  
 XX  
 PS Disclosure; Page 37; 61pp; English.  
 XX  
 CC The present invention relates to the use of prostate secretory protein-94  
 CC (PSP-94; ABR56227-ABR56228) for treating a patient suffering from  
 CC hypercalcaemia of malignancy. PSP-94 is useful for treating a patient  
 CC suffering from hypercalcaemia of malignancy arising from carcinomas,  
 CC prostate and breast cancer. The PSP-94 is also useful for reducing  
 CC parathyroid hormone related peptide (PTHrP) levels in a patient in need  
 CC and reducing the development of skeletal metastasis. The PSP-94 is also  
 CC used for the manufacture of a pharmaceutical composition for the  
 CC treatment of hypercalcaemia of malignancy and/or skeletal metastasis. The  
 CC present sequence is a peptide fragment of PSP-94, used to illustrate the  
 CC invention

XX SQ Sequence 15 AA;  
 Query Match 100.0%; Score 97; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQTDNCETCTCYET 15  
 DB 1 EWQTDNCETCTCYET 15

RESULT 3  
 AAO17917  
 ID AAO17917 standard; peptide; 16 AA.  
 AC AAO17917;  
 XX  
 DT 30-AUG-2002 (first entry)  
 XX  
 DE Human prostate secretory protein of 94 amino acids PSP94 analogue #6.  
 DE  
 KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW benign prostate hyperplasia; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200233090-A2.  
 PD 25-APR-2002.  
 XX  
 PF 15-OCT-2001; 2001WO-CA001463.  
 XX  
 PR 16-OCT-2000; 2000CA-02321256.  
 PR 20-AUG-2001; 2001CA-02355334.  
 XX  
 PA (PROC-) PROCYON BIOPHARMA INC.  
 XX  
 PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
 XX  
 DR WPI; 2002-471401/50.  
 XX  
 PT New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.  
 XX  
 PS Claim 2; Page 76; 185pp; English.  
 XX  
 CC The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-  
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention

QY 1 EWQTDNCETCTCYET 15  
 DB 1 EWQTDNCETCTCYET 15

RESULT 4  
 AAO17966  
 ID AAO17966 standard; peptide; 16 AA.  
 AC AAO17966;  
 XX  
 DT 30-AUG-2002 (first entry)  
 XX  
 DE Human prostate secretory protein of 94 amino acids PSP94 analogue #55.  
 DE  
 KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW benign prostate hyperplasia; cytostatic.

XX OS Homo sapiens.  
XX PN WO200233090-A2.  
XX PD 25-APR-2002.  
XX PF 15-OCT-2001; 2001WO-CA001463.  
XX PR 16-OCT-2000; 2000CA-02321256.  
XX PR 20-AUG-2001; 2001CA-02355334.  
XX PA (PROC-) PROCYON BIOPHARMA INC.  
XX PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
XX DR WPI; 2002-471401/50.  
XX PT New human prostate secretory protein of 94 amino acids, useful for  
XX PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
XX PT gastrointestinal, breast, endometrial, and ovarian cancers.  
XX PS Claim 2; Page 94; 185pp; English.  
XX CC The present invention relates to analogues of the human prostate  
XX CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
XX CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-  
XX CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting  
XX CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
XX CC cancer, breast cancer, endometrial, ovarian or other cancers of  
XX CC epithelial secretion, or benign prostate hyperplasia and for treating  
XX CC patients with a disease characterized by elevated levels of FSH. The  
XX CC present sequence is an analogue of the invention  
XX SQ Sequence 16 AA;  
XX  
XX Query Match 100.0%; Score 97; DB 5; Length 16;  
XX Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX Qy 1 EQWTDNCETCTCYET 15  
XX Db 2 EQWTDNCETCTCYET 16  
XX  
XX RESULT 5  
XX AAO17967  
XX ID AAO17967 standard; peptide; 17 AA.  
XX AC AAO17967;  
XX DT 30-AUG-2002 (first entry)  
XX DE Human prostate secretory protein of 94 amino acids PSP94 analogue #56.  
XX KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;  
XX KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
XX KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
XX KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
XX KW benign prostate hyperplasia; cytostatic.  
XX OS Homo sapiens.  
XX PN WO200233090-A2.  
XX PD 25-APR-2002.  
XX PF 15-OCT-2001; 2001WO-CA001463.  
XX PR 16-OCT-2000; 2000CA-02321256.  
XX PR 20-AUG-2001; 2001CA-02355334.  
XX PA (PROC-) PROCYON BIOPHARMA INC.

XX PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
XX DR WPI; 2002-471401/50.  
XX PT New human prostate secretory protein of 94 amino acids, useful for  
XX PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
XX PT gastrointestinal, breast, endometrial, and ovarian cancers.  
XX PS Claim 2; Page 94; 185pp; English.  
XX CC The present invention relates to analogues of the human prostate  
XX CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
XX CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-  
XX CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting  
XX CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
XX CC cancer, breast cancer, endometrial, ovarian or other cancers of  
XX CC epithelial secretion, or benign prostate hyperplasia and for treating  
XX CC patients with a disease characterized by elevated levels of FSH. The  
XX CC present sequence is an analogue of the invention  
XX SQ Sequence 17 AA;  
XX  
XX Query Match 100.0%; Score 97; DB 5; Length 17;  
XX Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX Qy 1 EQWTDNCETCTCYET 15  
XX Db 3 EQWTDNCETCTCYET 17  
XX  
XX RESULT 6  
XX AAO17918  
XX ID AAO17918 standard; peptide; 17 AA.  
XX AC AAO17918;  
XX DT 30-AUG-2002 (first entry)  
XX DE Human prostate secretory protein of 94 amino acids PSP94 analogue #7.  
XX KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;  
XX KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
XX KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
XX KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
XX KW benign prostate hyperplasia; cytostatic.  
XX OS Homo sapiens.  
XX PN WO200233090-A2.  
XX PD 25-APR-2002.  
XX PF 15-OCT-2001; 2001WO-CA001463.  
XX PR 16-OCT-2000; 2000CA-02321256.  
XX PR 20-AUG-2001; 2001CA-02355334.  
XX PA (PROC-) PROCYON BIOPHARMA INC.  
XX PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
XX DR WPI; 2002-471401/50.  
XX PT New human prostate secretory protein of 94 amino acids, useful for  
XX PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
XX PT gastrointestinal, breast, endometrial, and ovarian cancers.  
XX PS Claim 2; Page 76; 185pp; English.  
XX CC The present invention relates to analogues of the human prostate  
XX CC secretory protein of 94 amino acids (PSP94, also known as prostatic



XX DE Human prostate secretory protein of 94 amino acids PSP94 analogue #58.  
 XX KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;  
 XX KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW KW benign prostate hyperplasia; cytostatic.  
 XX OS Homo sapiens.  
 XX PN WO200233090-A2.  
 XX PD 25-APR-2002.  
 XX PF 15-OCT-2001; 2001WO-CA001463.  
 XX PR 16-OCT-2000; 2000CA-02321256.  
 XX PR 20-AUG-2001; 2001CA-02355334.  
 XX PA (PROC-) PROCYON BIOPHARMA INC.  
 XX PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
 XX DR WPI; 2002-471401/50.  
 XX PT New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.  
 XX PS Claim 2; Page 95; 185pp; English.  
 XX CC The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-  
 CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting  
 CC growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention  
 XX SQ Sequence 19 AA;  
 Query Match 100.0%; Score 97; DB 5; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EWQTDNCETCTCYET 15  
 Db 5 EWQTDNCETCTCYET 19  
 RESULT 10  
 AAO17920  
 ID AAO17920 standard; peptide; 19 AA.  
 XX AC AAO17920;  
 XX DT 30-AUG-2002 (first entry)  
 XX DE Human prostate secretory protein of 94 amino acids PSP94 analogue #9.  
 XX KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;  
 KW KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW KW benign prostate hyperplasia; cytostatic.  
 XX OS Homo sapiens.  
 XX PN WO200233090-A2.  
 XX PD 25-APR-2002.  
 XX PF 15-OCT-2001; 2001WO-CA001463.  
 XX PR 16-OCT-2000; 2000CA-02321256.  
 XX PR 20-AUG-2001; 2001CA-02355334.  
 XX PA (PROC-) PROCYON BIOPHARMA INC.  
 XX PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
 XX DR WPI; 2002-471401/50.  
 XX PT New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.  
 XX PS Claim 2; Page 95; 185pp; English.  
 XX CC The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-  
 CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting  
 CC growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention  
 XX SQ Sequence 19 AA;  
 Query Match 100.0%; Score 97; DB 5; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EWQTDNCETCTCYET 15  
 Db 5 EWQTDNCETCTCYET 19  
 RESULT 11  
 AAO17921  
 ID AAO17921 standard; peptide; 20 AA.  
 XX AC AAO17921;  
 XX DT 30-AUG-2002 (first entry)  
 XX DE Human prostate secretory protein of 94 amino acids PSP94 analogue #10.  
 XX KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;  
 KW KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW KW benign prostate hyperplasia; cytostatic.  
 XX OS Homo sapiens.  
 XX PN WO200233090-A2.  
 XX PD 25-APR-2002.  
 XX PF 15-OCT-2001; 2001WO-CA001463.  
 XX PR 16-OCT-2000; 2000CA-02321256.  
 XX PR 20-AUG-2001; 2001CA-02355334.  
 XX PA (PROC-) PROCYON BIOPHARMA INC.  
 XX PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
 XX DR WPI; 2002-471401/50.  
 XX SQ

PD 25-APR-2002.  
 XX 15-OCT-2001; 2001WO-CA001463.  
 XX 16-OCT-2000; 2000CA-02321256.  
 PR 20-AUG-2001; 2001CA-02355334.  
 XX (PROC-) PROCYON BIOPHARMA INC.  
 XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
 XX WPI; 2002-471401/50.  
 XX New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.  
 XX Claim 2; Page 77; 185pp; English.  
 XX The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-  
 CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting  
 CC growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention  
 XX SQ Sequence 19 AA;  
 Query Match 100.0%; Score 97; DB 5; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EWQTDNCETCTCYET 15  
 Db 1 EWQTDNCETCTCYET 15  
 RESULT 11  
 AAO17921  
 ID AAO17921 standard; peptide; 20 AA.  
 XX AC AAO17921;  
 XX DT 30-AUG-2002 (first entry)  
 XX DE Human prostate secretory protein of 94 amino acids PSP94 analogue #10.  
 XX KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;  
 KW KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW KW benign prostate hyperplasia; cytostatic.  
 XX OS Homo sapiens.  
 XX PN WO200233090-A2.  
 XX PD 25-APR-2002.  
 XX PF 15-OCT-2001; 2001WO-CA001463.  
 XX PR 16-OCT-2000; 2000CA-02321256.  
 PR 20-AUG-2001; 2001CA-02355334.  
 XX (PROC-) PROCYON BIOPHARMA INC.  
 XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
 XX WPI; 2002-471401/50.  
 XX SQ





RESULT 14	
AAO17971	
ID	AAO17971 standard; peptide; 21 AA.
XX	
AC	AAO17971;
XX	
DT	30-AUG-2002 (first entry)
XX	
DE	Human prostate secretory protein of 94 amino acids PSP94 analogue #60.
XX	
KW	Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW	beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW	prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW	stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW	benign prostate hyperplasia; cytostatic.
XX	
OS	Homo sapiens.
XX	
WO	WO200233090-A2.
XX	
PN	
XX	
XX	25-APR-2002.
PD	
XX	
XX	15-OCT-2001; 2001WO-CA001463.
XX	
PR	16-OCT-2000; 2000CA-02321256.
PR	20-AUG-2001; 2001CA-02355334.
XX	
XX	(PROC-) PROCTON BIOPHARMA INC.
PA	
XX	
PI	Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kachhim S;
PI	WPI; 2002-471401/50.
DR	
XX	
PT	New human prostate secretory protein of 94 amino acids, useful for
PT	inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT	gastrointestinal, breast, endometrial, and ovarian cancers.
XX	
XX	Claim 2; Page 95; 185pp; English.
XX	
CC	The present invention relates to analogues of the human prostate
CC	secretory protein of 94 amino acids (PSP94, also known as prostatic
CC	inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
CC	microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
CC	growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC	cancer, breast cancer, endometrial, ovarian or other cancers of
CC	epithelial secretion, or benign prostate hyperplasia and for treating
CC	patients with a disease characterized by elevated levels of FSH. The
CC	present sequence is an analogue of the invention
XX	
XX	Sequence 21 AA;
SQ	

```
Query Match      100.0%; Score 97; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. NO. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	EWQTDNCETCTCYET	15
Db	7	EWQTDNCETCTCYET	21

RESULT 15	
AAO17923	
ID	AAO17923 standard; peptide; 22 AA.
XX	
XX	
AC	AAO17923;
XX	
DT	30-AUG-2002 (first entry)
XX	
DE	Human prostate secretory protein of 94 amino acids P9P94 analogue #12.
XX	
KW	Cancer; human; P9P94; prostatic inhibin protein; PIP; HSPI; beta-MSP;
KW	Beta-microseminoprotein; human seminal plasma inhibin; analogue;

KW	prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW	stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KX	benign prostate hyperplasia; cytostatic.
XX	
OS	Homo sapiens.
XX	
FN	WO200233090-A2.
XX	
PD	25-APR-2002.
XX	
XX	15-OCT-2001; 2001WO-COA001463.
XX	
XX	16-OCT-2000; 2000CA-02321256.
PR	20-AUG-2001; 2001CA-02355334.
XX	
XX	(PROC-) PROCYON BIOPHARMA INC.
PA	
XX	
Pt	Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX	
DR	WPI; 2002-471401/50.
XX	
PT	New human prostate secretory protein of 94 amino acids, useful for
PT	inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT	gastrointestinal, breast, endometrial, and ovarian cancers.
XX	
PS	Claim 2; Page 78; 185pp; English.
XX	
CC	The present invention relates to analogues of the human prostate
CC	secretory protein of 94 amino acids (PSP94, also known as prostatic
CC	inhibit peptide (PIP), human seminal plasma inhibin (HSPI), and beta-
CC	microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
CC	growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC	cancer, breast cancer, endometrial, ovarian or other cancers of
CC	epithelial secretion, or benign prostate hyperplasia and for treating
CC	patients with a disease characterized by elevated levels of FSH. The
CC	present sequence is an analogue of the invention
XX	
SQ	Sequence 22 AA;
Query Match	100.0%; Score 97; DB 5; Length 22;
Best Local Similarity	100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative	0; Mismatches 0; Indels 0; Gaps

Sequence 22 AA;

```
Query Match          100.0%; Score 97; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	EWQTDNCETCTCYET	15
DB	EWQTDNCETCTCYET	15

Search completed: March 11, 2004, 17:52:40  
Job time : 17.5403 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2004, 17:45:11 ; Search time 52.621 Seconds  
(without alignments)  
241.627 Million cell updates/sec

Title: US-09-977-406A-88

Perfect score: 268

Sequence: 1 SCVFIPNEGVPGRSTRKMD.....HPINSEWQTDNCSTCTCYET 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	268	100.0	45	AAO17995	Aao17995 Human pro
2	268	100.0	94	AAO17911	Aar47117 Complete
3	268	100.0	94	AAO17911	Aao17911 Human pro
4	268	100.0	94	ABR56227	AbR56227 Native Hu
5	268	100.0	102	AAO17912	Aao17912 Human pro
6	268	100.0	102	ABR56228	AbR56228 Recombina
7	268	100.0	114	AAO33726	Aag03726 Human sec
8	268	100.0	114	AAU28067	Aau28067 Novel hum
9	268	100.0	114	ABR54574	AbR54574 Prostati
10	268	100.0	114	ADB75447	AdB75447 Prostati
11	268	100.0	114	ADB14453	AdB14453 Human pro
12	268	100.0	132	AAO17988	Aao17988 Human pro
13	264	98.5	43	AAO17994	Aao17994 Human pro
14	255	95.1	43	AAO17993	Aao17993 Human pro
15	248	92.5	42	AAO17992	Aao17992 Human pro
16	242	90.3	41	AAO17991	Aao17991 Human pro
17	238	88.8	40	AAO17990	Aao17990 Human pro
18	231	86.2	39	AAO17989	Aao17989 Human pro
19	225	84.0	38	AAO17988	Aao17988 Human pro
20	221.5	82.6	119	AAU28255	Aau28255 Novel hum
21	220	82.1	37	AAO17987	Aao17987 Human pro
22	214	79.9	36	AAO17986	Aao17986 Human pro
23	210	78.4	35	AAO17985	Aao17985 Human pro
24	203	75.7	34	AAO17984	Aao17984 Human pro
25	197	73.5	33	AAO17983	Aao17983 Human pro

26	191	71.3	32	5	AAO17982	Aao17982 Human pro
27	187	69.8	31	5	AAO17981	Aao17981 Human pro
28	182	67.9	30	5	AAO17980	Aao17980 Human pro
29	177	66.0	29	5	AAO17979	Aao17979 Human pro
30	172	64.2	28	5	AAO17978	Aao17978 Human pro
31	163	60.8	27	5	AAO17977	Aao17977 Human pro
32	158	59.0	26	5	AAO17976	Aao17976 Human pro
33	152	56.7	25	5	AAO17975	Aao17975 Human pro
34	148	55.2	24	5	AAO17974	Aao17974 Human pro
35	143	53.4	23	5	AAO17973	Aao17973 Human pro
36	137	51.1	22	5	AAO17972	Aao17972 Human pro
37	131	48.9	21	5	AAO17971	Aao17971 Human pro
38	126	47.0	20	5	AAO17970	Aao17970 Human pro
39	118	44.0	19	5	AAO17969	Aao17969 Human pro
40	111	41.4	18	5	AAO17968	Aao17968 Human pro
41	107	39.9	17	5	AAO17967	Aao17967 Human pro
42	101	37.7	16	5	AAO17966	Aao17966 Human pro
43	98	36.6	30	5	AAO17997	Aao17997 Human PSP
44	98	36.6	45	5	AAO17998	Aao17998 Human PSP
45	98	36.6	60	5	AAO17999	Aao17999 Human PSP

ALIGNMENTS

RESULT 1  
AAO17995  
ID AAO17995 standard; protein; 45 AA.

XX AAO17995;

XX AC AAO17995;

XX DT 30-AUG-2002 (first entry)

XX DE Human prostate secretory protein of 94 amino acids PSP94 analogue #84.  
XX KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
KW benign prostate hyperplasia; cytostatic.

XX OS Homo sapiens.

XX WO200233090-A2.

XX PD 25-APR-2002.

XX PF 15-OCT-2001; 2001WO-CA001463.

XX PR 16-OCT-2000; 2000CA-02321256.

XX XX 20-AUG-2001; 2001CA-02355334.

XX PA (PROC-) PROCTON BIOPHARMA INC.

XX PI Garde S, Panchal CV, Baijal-Gupta M, Fraser J, Kadhim S;

XX WPI; 2002-471401/50.

XX PT New human prostate secretory protein of 94 amino acids, useful for  
inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
gastrointestinal, breast, endometrial, and ovarian cancers.

XX PS Claim 2; Page 104; 185pp; English.

XX CC The present invention relates to analogues of the human prostate  
secretory protein of 94 amino acids (PSP94, also known as prostatic  
inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-  
microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
cancer, breast cancer, endometrial, ovarian or other cancers of  
epithelial secretion, or benign prostate hyperplasia and for treating  
patients with a disease characterized by elevated levels of FSH. The  
present sequence is an analogue of the invention

```

XX Sequence 45 AA;
SQ
  Query Match      100.0%; Score 268; DB 5; Length 45;
  Best Local Similarity 100.0%; Pred. No. 1.2e-26;
  Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKCDLKGKHPINSEWQTDNCETCTCYET 45
    |||||
DB 1 SCYFIPNEGVPDSTRKCDLKGKHPINSEWQTDNCETCTCYET 45

RESULT 2
AAR47117
ID AAR47117 standard; peptide; 94 AA.
XX
AC AAR47117;
XX
DT 25-MAR-2003 (revised)
DT 30-JUN-1994 (first entry)
XX
DE Complete sequence of human prostatic inhibin peptide.
XX
KW Prostatic inhibin peptide; cancer; adenocarcinoma; breast cancer;
KW hyperplasia; PIP; follicle stimulating hormone; FSH; tumour; inhibition;
KW prostate cancer; gastrointestinal tract.
XX
OS Homo sapiens.
XX
PN WO9325224-A1.
XX
PD 23-DEC-1993.
XX
PF 16-JUN-1993; 93WO-CA000252.
XX
PR 16-JUN-1992; 92US-00899535.
XX
PA (VETR-) VETROGEN CORP.
XX
PI Sheth AR, Garde S, Panchal CJ;
XX
DR WPI; 1994-007191/01.
XX
PT Prepn. contg. prostatic inhibin peptide or analogues - used for treating
PT benign prostatic hyperplasia, adenocarcinoma or diseases with high FSH
PT levels.
XX
PS Disclosure; Fig 1; 48pp; English.
XX
CC Peptides or analogues of prostatic inhibin peptide (PIP) are used in a
CC pharmaceutical preparation for treating patients with benign prostatic
CC hyperplasia or adenocarcinoma, particularly adenocarcinoma of the
CC prostate or gastrointestinal tract or breast cancer. The preparation can
CC also be used to treat patients with diseases characterised by elevated
CC levels of follicle stimulating hormone (FSH). The PIP and its analogues
CC inhibit tumour growth and decrease FSH levels without adversely affecting
CC testosterone levels. (Updated on 25-MAR-2003 to correct FN field.)
XX
SQ Sequence 94 AA;

  Query Match      100.0%; Score 268; DB 2; Length 94;
  Best Local Similarity 100.0%; Pred. No. 2.7e-26;
  Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKCDLKGKHPINSEWQTDNCETCTCYET 45
    |||||
DB 1 SCYFIPNEGVPDSTRKCDLKGKHPINSEWQTDNCETCTCYET 45

RESULT 3
AAR47117
ID AAR47117 standard; protein; 94 AA.
XX
  Query Match      100.0%; Score 268; DB 5; Length 94;
  Best Local Similarity 100.0%; Pred. No. 2.7e-26;
  Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKCDLKGKHPINSEWQTDNCETCTCYET 45
    |||||
DB 1 SCYFIPNEGVPDSTRKCDLKGKHPINSEWQTDNCETCTCYET 45

RESULT 4
ABR56227
ID ABR56227 standard; protein; 94 AA.
XX
AC ABR56227;
XX
DT 20-NOV-2003 (first entry)
XX
DE Native Human prostate secretory protein-94 (PSP-94).
XX
KW Human; cytostatic; prostate secretory protein-94; PSP-94;
KW hypercalcaemia of malignancy; carcinoma; prostate cancer; breast cancer;
KW parathyroid hormone related peptide; PTHrP; skeletal metastasis.
XX
OS Homo sapiens.
XX
PN WO2003039576-A1.

```

XX 15-MAY-2003.  
XX 08-NOV-2002; 2002WO-CA001737.  
XX 08-NOV-2001; 2001CA-02361736.  
XX (PROC-) PROCYON BIOPHARMA INC.  
XX Rabbani SA, Shukeir N, Panchal CJ, Newman C;  
XX WPI; 2003-441476/41.  
XX Use of prostate secretory protein-94 for treating hypercalcaemia of  
PT malignancy and reducing skeletal metastasis arising from carcinomas,  
PT prostate and breast cancers.  
XX Disclosure; Page 35; 61pp; English.  
XX The present invention relates to the use of prostate secretory protein-94  
CC (PSP-94; the present sequence) for treating a patient suffering from  
CC hypercalcaemia of malignancy. PSP-94 is useful for treating a patient  
CC suffering from hypercalcaemia of malignancy arising from carcinomas,  
CC prostate and breast cancer. The PSP-94 is also useful for reducing  
CC parathyroid hormone related peptide (PTHrP) levels in a patient in need  
CC and reducing the development of skeletal metastasis. The PSP-94 is also  
CC used for the manufacture of a pharmaceutical composition for the  
CC treatment of hypercalcaemia of malignancy and/or skeletal metastasis  
XX Sequence 94 AA;  
XX Query Match 100.0%; Score 268; DB 7; Length 94;  
XX Best Local Similarity 100.0%; Pred. No. 2.7e-26;  
XX Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SCYFIPNEGVPDSTRKQMDLKGKHPINSEWQTDNCETCTCYET 45  
Db 1 SCYFIPNEGVPDSTRKQMDLKGKHPINSEWQTDNCETCTCYET 45  
RESULT 5  
AA017912  
ID AA017912 standard; protein; 102 AA.  
XX AA017912;  
XX 30-AUG-2002 (first entry)  
XX Human prostate secretory protein of 94 amino acids PSP94 analogue #1.  
XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
XX beta-microseminoprotein; human seminal plasma inhibin; analogue;  
XX prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
XX stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
XX benign prostate hyperplasia; cytostatic.  
XX Homo sapiens.  
XX OS  
XX WO200233090-A2.  
XX 25-APR-2002.  
XX 15-OCT-2001; 2001WO-CA001463.  
XX 16-OCT-2000; 2000CA-02321256.  
XX 20-AUG-2001; 2001CA-02355334.  
XX (PROC-) PROCYON BIOPHARMA INC.  
XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
XX WPI; 2002-471401/50.  
XX

PT New human prostate secretory protein of 94 amino acids, useful for  
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
PT gastrointestinal, breast, endometrial, and ovarian cancers.  
XX Claim 2; Page 73-74; 185pp; English.  
XX The present invention relates to analogues of the human prostate  
CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-  
CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
CC cancer, breast cancer, endometrial, ovarian or other cancers of  
CC epithelial secretion, or benign prostate hyperplasia and for treating  
CC patients with a disease characterized by elevated levels of FSH. The  
CC present sequence is an analogue of the invention  
XX Sequence 102 AA;  
XX Query Match 100.0%; Score 268; DB 5; Length 102;  
XX Best Local Similarity 100.0%; Pred. No. 3e-26;  
XX Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SCYFIPNEGVPDSTRKQMDLKGKHPINSEWQTDNCETCTCYET 45  
Db 9 SCYFIPNEGVPDSTRKQMDLKGKHPINSEWQTDNCETCTCYET 53  
RESULT 6  
ABR56228  
ID ABR56228 standard; protein; 102 AA.  
XX ABR56228;  
XX 20-NOV-2003 (first entry)  
XX Recombinate prostate secretory protein-94 (PSP-94).  
XX Cytostatic; prostate secretory protein-94; PSP-94;  
XX hypercalcaemia of malignancy; carcinoma; prostate cancer; breast cancer;  
XX parathyroid hormone related peptide; PTHrP; skeletal metastasis.  
XX Unidentified.  
XX WO2003039576-A1.  
XX 15-MAY-2003.  
XX 08-NOV-2002; 2002WO-CA001737.  
XX 08-NOV-2001; 2001CA-02361736.  
XX (PROC-) PROCYON BIOPHARMA INC.  
XX Rabbani SA, Shukeir N, Panchal CJ, Newman C;  
XX WPI; 2003-441476/41.  
XX Use of prostate secretory protein-94 for treating hypercalcaemia of  
PT malignancy and reducing skeletal metastasis arising from carcinomas,  
PT prostate and breast cancers.  
XX Disclosure; Page 35-36; 61pp; English.  
XX The present invention relates to the use of prostate secretory protein-94  
CC (PSP-94; the present sequence) for treating a patient suffering from  
CC hypercalcaemia of malignancy. PSP-94 is useful for treating a patient  
CC suffering from hypercalcaemia of malignancy arising from carcinomas,  
CC prostate and breast cancer. The PSP-94 is also useful for reducing  
CC parathyroid hormone related peptide (PTHrP) levels in a patient in need  
CC and reducing the development of skeletal metastasis. The PSP-94 is also  
CC used for the manufacture of a pharmaceutical composition for the  
CC treatment of hypercalcaemia of malignancy and/or skeletal metastasis  
XX

SQ Sequence 102 AA;  
 Query Match 100.0%; Score 268; DB 7; Length 102;  
 Best Local Similarity 100.0%; Pred. No. 3e-26;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKCKMDLKGKHPINSEWQTDNCCTCYET 45  
 |||||  
 DB 9 SCYFIPNEGVPDSTRKCKMDLKGKHPINSEWQTDNCCTCYET 53  
 |||||

RESULT 7  
 AAG03726  
 ID AAG03726 standard; protein; 114 AA.  
 AC AAG03726;  
 XX  
 XX 06-OCT-2000 (first entry)  
 XX  
 XX Human secreted protein, SEQ ID NO: 7807.  
 XX  
 XX Human; 5' EST: expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping.  
 KW  
 XX Homo sapiens.  
 OS  
 XX EP1033401-A2.  
 PN  
 XX 06-SEP-2000.  
 PD  
 XX 21-FEB-2000; 2000EP-00200610.  
 PF  
 XX 26-FEB-1999; 99US-0122487P.  
 PR  
 XX (GIST) GENSET.  
 PA  
 XX Dumas Milne Edwards J, Duclert A, Giordano J;  
 PI WPI; 2000-500381/45.  
 DR N-PSDB; AAC03732.  
 DR  
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 PT  
 XX Claim 13; SEQ ID NO 7807; 71pp + Sequence Listing; English.  
 PS  
 XX The present sequence is a polypeptide encoded by one of a large number of  
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different  
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
 CC sequences derived from the 5' ends of mRNAs and even in those cases where  
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
 CC are also used in diagnostic, forensic, gene therapy and chromosome  
 CC mapping procedures. They are used to obtain upstream regulatory sequences  
 CC and to design expression and secretion vectors  
 CC  
 XX Sequence 114 AA;  
 Query Match 100.0%; Score 268; DB 3; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-26;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKCKMDLKGKHPINSEWQTDNCCTCYET 45  
 |||||  
 DB 21 SCYFIPNEGVPDSTRKCKMDLKGKHPINSEWQTDNCCTCYET 65  
 |||||

RESULT 8

AAU28067  
 ID AAU28067 standard; protein; 114 AA.  
 XX  
 AC AAU28067;  
 XX  
 XX 18-DEC-2001 (first entry)  
 DT  
 XX Novel human secretory protein, Seq ID No 236.  
 DE  
 XX  
 XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;  
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;  
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;  
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;  
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;  
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;  
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;  
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;  
 KW fertility; analgesic; pain; antigen.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200166689-A2.  
 PN  
 XX 13-SEP-2001.  
 PD  
 XX 05-MAR-2001; 2001WO-US004942.  
 PF  
 XX 07-MAR-2000; 2000US-00519705.  
 PR  
 XX 19-MAY-2000; 2000US-00574454.  
 PR  
 XX 17-JUN-2000; 2000US-00596193.  
 PR  
 XX 14-JUL-2000; 2000US-00618847.  
 PR  
 XX 19-SEP-2000; 2000US-00665363.  
 PR  
 XX 20-OCT-2000; 2000US-00693267.  
 XX  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;  
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;  
 DR WPI; 2001-589934/66.  
 DR N-PSDB; AAS44967.  
 DR  
 XX Novel polypeptides and nucleic acids obtained from cDNA libraries  
 PT prepared from various human tissues, for diagnosis and treatment of  
 PT cancer, neurological, inflammatory, and autoimmune disorders.  
 PT  
 XX Example 3; SEQ ID NO 236; 107pp; English.  
 PS  
 XX The invention relates to novel isolated human secreted polypeptides (I)  
 CC and polynucleotides (II). (I) and (II) are useful for treating  
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,  
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is  
 CC involved in increasing haematopoiesis, stem cell survival, bone growth  
 CC and remodeling. (I), (II) and modulators of (II) are useful for  
 CC creating transgenic animals useful for studying the in vivo activities of  
 CC the polypeptide as well as for studying modulators of the polypeptides.  
 CC (I) induces the proliferation of neural cells and regeneration of nerve  
 CC and brain tissue and is useful for the treatment of central and  
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,  
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral  
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic  
 CC activity, regulation of haematopoiesis and is useful for treating myeloid  
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia  
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve  
 CC tissue growth, and in tissue repair, healing of burns, incisions, ulcers,  
 CC for treating osteoporosis, osteoarthritis, bone degenerative disorders,  
 CC or periodontal disease. Furthermore, (I) is also useful for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues, various immune deficiencies and  
 CC disorders including severe combined immunodeficiency (SCID), bacterial or  
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,  
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic

CC reactions and conditions, such as asthma or other respiratory problems.  
CC in addition, (i) affects biorhythms or circadian cycles of rhythms,  
CC fertility, metabolism, catabolism, anabolism, storage or elimination of  
CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides  
CC analgesic effects or other pain reducing effects immunoglobulin like  
CC activity and can act as an antigen in a vaccine composition to raise an  
CC immune response. AAU28020-AAU28395 represent novel human secreted protein  
CC amino acid sequences of the invention  
XX  
SQ Sequence 114 AA;

Query Match 100.0%; Score 268; DB 4; Length 114;  
Best Local Similarity 100.0%; Pred. No. 3.4e-26;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET 45  
DB 21 SCYFIPNEGVPDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET 65

RESULT 9  
ABR54574  
ID ABR54574 standard; protein; 114 AA.

AC ABR54574;  
XX  
XX 28-AUG-2003 (first entry)  
XX  
XX Prostatic secretory protein SEQ ID 1003.

DE Cytostatic; gene therapy; prostate-specific protein; PSP; human;  
XX immune response; prostate cancer.

XX Homo sapiens.

XX WO200289747-A2.

XX 14-NOV-2002.

XX 09-MAY-2002; 2002WO-US014753.

XX 09-MAY-2001; 2001US-00852911.

XX 29-JUN-2001; 2001US-00895814.

XX 10-DEC-2001; 2001US-00012896.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;  
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick TS;  
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;  
PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TW, Watanabe Y;  
PI Deng T;

XX WPI; 2003-167130/16.

XX New prostate-specific proteins and genes, useful in gene therapy,  
PT particularly for stimulating an immune response in a patient, or treating  
PT prostate cancer in a patient, as well as for diagnosing prostate cancer  
PT in a patient.

XX Claim 2; Page 666; 691pp; English.

XX The present invention relates to novel prostate-specific proteins (PSP)  
CC and their coding sequences. The PSPs and their coding sequences are  
CC useful for stimulating an immune response in a patient, or for treating  
CC prostate cancer in a patient and for determining, detecting or diagnosing  
CC the presence of a cancer in a patient. The present sequence was used to  
CC illustrate the invention

XX Sequence 114 AA;

Query Match 100.0%; Score 268; DB 6; Length 114;  
Best Local Similarity 100.0%; Pred. No. 3.4e-26;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SCYFIPNEGVPDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET 45  
DB 21 SCYFIPNEGVPDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET 65

RESULT 10  
ADB75447  
ID ADB75447 standard; protein; 114 AA.

XX ADB75447;

XX 04-DEC-2003 (first entry)

XX Prostate cancer marker protein.

XX Prostate; cancer; cytostatic; gene therapy; marker.

XX Homo sapiens.

XX WO2003009814-A2.

XX 06-FEB-2003.

XX 25-JUL-2002; 2002WO-US023913.

XX 25-JUL-2001; 2001US-0307982P.

XX 22-AUG-2001; 2001US-0314356P.

XX 25-SEP-2001; 2001US-0325020P.

XX 12-DEC-2001; 2001US-0341746P.

XX 05-MAR-2002; 2002US-0362158P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;

PI Hoersht S, Kamatkar S, Womsey AM, Glatt K, Zhao X, Anderson D;

XX WPI; 2003-248033/24.

XX New nucleic acid molecule, useful for diagnosing or treating prostate

XX cancer.

XX Disclosure; SEQ ID NO 271; 99pp; English.

XX The invention relates to newly discovered cancer markers associated with  
CC the cancerous state of prostate cells. Also disclosed is a method of  
CC assessing whether a patient is afflicted with prostate cancer. The method  
CC of the invention involves assessing whether a patient is afflicted with  
CC prostate cancer by comparing the level of expression of a marker in a  
CC patient sample and the normal level of expression of the marker in a  
CC control non-prostate cancer sample, where a significant increase in the  
CC level of expression of the marker in the patient sample and the normal  
CC level indicates that the patient is afflicted with prostate cancer.  
CC Nucleic acids of the invention are useful for diagnosing or treating  
CC prostate cancer, and may be useful in gene therapy. Sequences given in  
CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 114 AA;

Query Match 100.0%; Score 268; DB 7; Length 114;  
Best Local Similarity 100.0%; Pred. No. 3.4e-26;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET 45  
DB 21 SCYFIPNEGVPDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET 65

RESULT 11

ADBI4453  
 ID ADBI4453 standard; protein; 114 AA.  
 AC ADBI4453;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Human prostatic secretory protein (PSP).  
 XX  
 KW Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;  
 KW cell therapy; vaccine; T-cell epitope;  
 KW class I major histocompatibility complex allele; MHC; prostate cancer;  
 KW tumour; antigen presenting cell.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003185830-A1.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PF 12-NOV-2002; 2002US-00294025.  
 XX  
 PR 25-FEB-1997; 97US-00806099.  
 PR 01-AUG-1997; 97US-00904804.  
 PR 09-FEB-1998; 98US-00020956.  
 PR 25-FEB-1998; 98US-00030607.  
 PR 14-JUL-1998; 98US-00115453.  
 PR 23-SEP-1998; 98US-00159812.  
 PR 15-JAN-1999; 98US-00232149.  
 PR 09-APR-1999; 98US-00288946.  
 PR 13-JUL-1999; 99US-00352648.  
 PR 12-NOV-1999; 99US-00439313.  
 PR 18-NOV-1999; 99US-00443686.  
 PR 14-JAN-2000; 2000US-00483672.  
 PR 27-MAR-2000; 2000US-00536857.  
 PR 09-MAY-2000; 2000US-00568100.  
 PR 12-MAY-2000; 2000US-00570737.  
 PR 13-JUN-2000; 2000US-00593793.  
 PR 27-JUN-2000; 2000US-00605783.  
 PR 09-AUG-2000; 2000US-00636215.  
 PR 29-AUG-2000; 2000US-00651236.  
 PR 06-SEP-2000; 2000US-00657279.  
 PR 02-OCT-2000; 2000US-00679426.  
 PR 10-OCT-2000; 2000US-00685166.  
 PR 09-NOV-2000; 2000US-00709729.  
 PR 12-JAN-2001; 2001US-00759143.  
 PR 09-FEB-2001; 2001US-00780669.  
 PR 09-MAY-2001; 2001US-00852911.  
 PR 29-JUN-2001; 2001US-00895814.  
 PR 10-DEC-2001; 2001US-00012896.  
 PR 09-MAY-2002; 2002US-00144678.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 XX Xu J, Stolk JA, Kalos MD;  
 XX WPI; 2003-756193/71.  
 XX  
 PT New isolated polypeptide for use in a vaccine for stimulating an immune  
 PT response, or for treating or diagnosis cancer, preferably prostate  
 PT cancer.  
 XX  
 XX Example 34; Page; 101pp; English.  
 PS  
 XX The invention relates to an isolated polypeptide comprising no more than  
 CC 11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The  
 CC peptides comprise a fragment ADBI3563 of that contain naturally processed  
 CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)  
 CC alleles. ADBI3563 is a polypeptide encoded by a human prostate specific  
 CC cDNA, one of 648 disclosed as new. Also included are nucleic acids  
 CC encoding the proteins and peptides, expression vectors, a host cell  
 CC transformed with the vector, an isolated antibody (or antigen binding  
 CC fragment) that specifically binds to the protein or peptide, detecting

the presence of a cancer in a patient (comprising contacting a patient sample with a binding agent that binds to the peptides or a polypeptide appearing as ADBI3558, detecting the amount of polypeptide that binds to the agent and comparing the amount of polypeptide to a predetermined cutoff value to determine the presence of cancer), a fusion protein comprising the peptides or proteins, stimulating or expanding T cells specific for a tumour protein comprising contacting T cells with the peptides or the isolated T cell population, treating prostate cancer in a patient comprising administering a composition comprising the peptides, nucleic acids, antibodies or compounds, determining the presence of a cancer in a patient and treating prostate cancer in a patient comprising incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated from a patient with the peptides or antigen presenting cells that express (the peptides so that the T cells proliferate, and administering the that hybridises to nucleic acid encoding them), is used to detect the presence of cancer in a patient. The peptides, nucleic acids encoding, or antigen-presenting cells expressing the nucleic acid, are used to stimulate or expand T cells specific for a tumour protein. The peptides, nucleic acids, antibodies, fusion proteins, T cell populations or antigen presenting cells are used to stimulate an immune response or treat prostate cancer in a patient. The present sequence is a prostate specific protein of the invention. Note: Except where otherwise indicated, the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030185830.

Query Match 100.0%; Score 268; DB 7; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 3,4e-26;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCYFIPEGVPGDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET 45  
 DB 21 SCYFIPEGVPGDSTRKCMDLKGNKHPINSEWQTDNCETCTCYET 65

RESULT 12  
 AAB56449  
 ID AAB56449 standard; protein; 132 AA.  
 XX  
 AC AAB56449;  
 XX  
 DT 13-MAR-2001 (first entry)  
 XX  
 DE Human prostate cancer antigen protein sequence SEQ ID NO:1027.  
 XX  
 KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;  
 KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;  
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
 KW wound; infectious disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055174-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US005989.  
 XX  
 PR 12-MAR-1999; 99US-0124270P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (ROSE/) ROSEN C A.  
 XX  
 PI Rosen CA, Ruben SM;  
 DR WPI; 2000-587513/55.  
 DR N-PSDB; AAF15652.  
 XX



PT Prostate cancer associated gene sequences, referred to as prostate cancer  
 PT antigens, useful for treatment, prevention, and diagnosis of disorders  
 PT such as prostate cancer.

XX Claim 11; Page 1457; 2338pp; English.

XX AAF1566 to AAF16505 encode the human prostate cancer associated  
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.  
 CC The prostate cancer antigens can have neuroprotective, cytostatic,  
 CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,  
 CC nephrotropic, antiinfective, synaecological and antibacterial activities,  
 CC and can be used in gene therapy. The prostate cancer antigen  
 CC polynucleotides may be used for detection of prostate cancer, chromosome  
 CC identification, as chromosome markers, and for numerous other diagnostic  
 CC or research purposes. The prostate cancer antigens may be used to treat  
 CC disorders such as neural, immune, muscular, reproductive,  
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to  
 CC AAB57303 represent sequences used in the exemplification of the present  
 CC invention

XX Sequence 132 AA;

Query Match 100.0%; Score 268; DB 3; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 4e-26;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWQTDNCCTCTCYET 45  
 |||||  
 Db 39 SCYFIPNEGVPDSTRKMDLKGKHPINSEWQTDNCCTCTCYET 83  
 |||||

RESULT 13

AAO17994  
 ID AAO17994 standard; protein; 44 AA.

XX AAO17994;

XX 30-AUG-2002 (first entry)

XX Human prostate secretory protein of 94 amino acids PSP94 analogue #83.  
 XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;  
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW benign prostate hyperplasia; cytostatic.

XX Homo sapiens.

XX WO200233090-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-CA001463.

XX 16-OCT-2000; 2000CA-02321256.

XX 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC.

XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;

XX WPI; 2002-471401/50.

XX New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.

XX Claim 2; Page 103; 185pp; English.

XX The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic

CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-  
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention

XX Sequence 44 AA;

Query Match 98.5%; Score 264; DB 5; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-26;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CYFIPNEGVPDSTRKMDLKGKHPINSEWQTDNCCTCTCYET 45  
 |||||  
 Db 1 CYFIPNEGVPDSTRKMDLKGKHPINSEWQTDNCCTCTCYET 44  
 |||||

RESULT 14

AAO17993  
 ID AAO17993 standard; protein; 43 AA.

XX AAO17993;

XX 30-AUG-2002 (first entry)

XX Human prostate secretory protein of 94 amino acids PSP94 analogue #82.  
 XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;  
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW benign prostate hyperplasia; cytostatic.

XX Homo sapiens.

XX WO200233090-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-CA001463.

XX 16-OCT-2000; 2000CA-02321256.

XX 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC.

XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;

XX WPI; 2002-471401/50.

XX New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.

XX Claim 2; Page 103; 185pp; English.

XX The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-  
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention

XX Sequence 43 AA;

Query Match 95.1%; Score 255; DB 5; Length 43;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-25;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YEIPNEGVPGDSTRKMDLKGKHKHPINSEWQTDNCETCTCYET 45  
 DB 1 YEIPNEGVPGDSTRKMDLKGKHKHPINSEWQTDNCETCTCYET 43

## RESULT 15

AAO17992  
 ID AAO17992 standard; protein; 42 AA.  
 XX  
 AC AAO17992;  
 XX  
 DT 30-AUG-2002 (first entry)  
 XX  
 DE Human prostate secretory protein of 94 amino acids PSP94 analogue #81.  
 XX  
 KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW benign prostate hyperplasia; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200233090-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 15-OCT-2001; 2001WO-CA001463.  
 XX  
 PR 16-OCT-2000; 2000CA-02321256.  
 PR 20-AUG-2001; 2001CA-02355334.  
 XX  
 PA (PROC-) PROCYON BIOPHARMA INC.  
 XX  
 PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
 XX  
 DR WPI; 2002-471401/50.  
 XX  
 XX New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.  
 XX  
 PS Claim 2; Page 103; 185pp; English.  
 XX  
 CC The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-  
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention  
 XX  
 SQ Sequence 42 AA;

Query Match 92.5%; Score 248; DB 5; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-24;  
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FIPNEGVPGDSTRKMDLKGKHKHPINSEWQTDNCETCTCYET 45  
 DB 1 FIPNEGVPGDSTRKMDLKGKHKHPINSEWQTDNCETCTCYET 42

Search completed: March 11, 2004, 17:52:41  
 Job time : 52.621 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2004, 17:56:07 ; Search time 17.4194 Seconds  
(without alignments)  
243.305 Million cell updates/sec

Title: US-09-977-406A-5

Perfect score: 15

Sequence: 1 EWQDNCETCTCYET 15

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	15	100.0	15	5 AAO17915	Aao17915 Human pro
2	15	100.0	15	7 ABR56231	Abr56231 Prostate
3	15	100.0	16	5 AAO17917	Aao17917 Human pro
4	15	100.0	16	5 AAO17966	Aao17966 Human pro
5	15	100.0	17	5 AAO17967	Aao17967 Human pro
6	15	100.0	17	5 AAO17918	Aao17918 Human pro
7	15	100.0	18	5 AAO17919	Aao17919 Human pro
8	15	100.0	18	5 AAO17968	Aao17968 Human pro
9	15	100.0	19	5 AAO17969	Aao17969 Human pro
10	15	100.0	19	5 AAO17920	Aao17920 Human pro
11	15	100.0	20	5 AAO17921	Aao17921 Human pro
12	15	100.0	20	5 AAO17970	Aao17970 Human pro
13	15	100.0	21	5 AAO17922	Aao17922 Human pro
14	15	100.0	21	5 AAO17971	Aao17971 Human pro
15	15	100.0	22	5 AAO17923	Aao17923 Human pro
16	15	100.0	22	5 AAO17972	Aao17972 Human pro
17	15	100.0	23	5 AAO17973	Aao17973 Human pro
18	15	100.0	23	5 AAO17924	Aao17924 Human pro
19	15	100.0	24	5 AAO17925	Aao17925 Human pro
20	15	100.0	24	5 AAO17974	Aao17974 Human pro
21	15	100.0	25	5 AAO17975	Aao17975 Human pro
22	15	100.0	25	5 AAO17926	Aao17926 Human pro
23	15	100.0	26	5 AAO17976	Aao17976 Human pro
24	15	100.0	26	5 AAO17927	Aao17927 Human pro
25	15	100.0	27	5 AAO17977	Aao17977 Human pro

26	15	100.0	27	5 AAO17928	Aao17928 Human pro
27	15	100.0	28	5 AAO17929	Aao17929 Human pro
28	15	100.0	28	5 AAO17978	Aao17978 Human pro
29	15	100.0	29	5 AAO17930	Aao17930 Human pro
30	15	100.0	30	5 AAO17979	Aao17979 Human pro
31	15	100.0	30	5 AAO17980	Aao17980 Human pro
32	15	100.0	30	5 AAO17997	Aao17997 Human pro
33	15	100.0	30	5 AAO17931	Aao17931 Human pro
34	15	100.0	31	5 AAO17981	Aao17981 Human pro
35	15	100.0	31	5 AAO17932	Aao17932 Human pro
36	15	100.0	32	5 AAO17933	Aao17933 Human pro
37	15	100.0	32	5 AAO17982	Aao17982 Human pro
38	15	100.0	33	5 AAO17934	Aao17934 Human pro
39	15	100.0	33	5 AAO17983	Aao17983 Human pro
40	15	100.0	34	5 AAO17935	Aao17935 Human pro
41	15	100.0	34	5 AAO17984	Aao17984 Human pro
42	15	100.0	35	5 AAO17936	Aao17936 Human pro
43	15	100.0	35	5 AAO17985	Aao17985 Human pro
44	15	100.0	36	5 AAO17937	Aao17937 Human pro
45	15	100.0	36	5 AAO17986	Aao17986 Human pro

ALIGNMENTS

RESULT 1

AAO17915

ID AAO17915 standard; peptide; 15 AA.

XX AAO17915;

XX 30-AUG-2002 (first entry)

XX Human prostate secretory protein of 94 amino acids PSP94 analogue #4.  
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPT; beta-MSP;  
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
KW benign prostate hyperplasia; cytostatic.  
XX Homo sapiens.  
XX OS  
XX WO200233090-A2.  
XX 25-APR-2002.  
XX 15-OCT-2001; 2001WO-CA001463.  
XX 16-OCT-2000; 2000CA-02321256.  
XX 20-AUG-2001; 2001CA-02355334.  
XX (PROC-) PROCYON BIOPHARMA INC.  
XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
XX WPI; 2002-471401/50.  
XX New human prostate secretory protein of 94 amino acids, useful for  
XX inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
XX gastrointestinal, breast, endometrial, and ovarian cancers.  
XX Claim 1; Page 74; 185pp; English.  
XX The present invention relates to analogues of the human prostate  
XX secretory protein of 94 amino acids (PSP94, also known as prostatic  
XX inhibin peptide (PIP), human seminal plasma inhibin (HSPT) and beta-  
XX microseminoprotein (bets-MSP)). The analogues are useful for inhibiting  
XX growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal  
XX cancer, breast cancer, endometrial, ovarian or other cancers of  
XX epithelial secretion, or benign prostate hyperplasia and for treating  
XX patients with a disease characterized by elevated levels of FSH. The  
XX present sequence is an analogue of the invention

XX SQ Sequence 15 AA;  
 Query Match 100.0%; Score 15; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-10;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EWQTDNCETCTCYET 15  
 DB 1 EWQTDNCETCTCYET 15  
 RESULT 2  
 ABR56231  
 ID ABR56231 standard; peptide; 15 AA.  
 XX AC  
 XX AC ABR56231;  
 XX DT 20-NOV-2003 (first entry)  
 XX DE Prostate secretory protein-94 (PSP-94) peptide fragment PK3145.  
 XX KW Cytostatic; prostate secretory protein-94; PSP-94; human;  
 KW hypercalcaemia of malignancy; carcinoma; prostate cancer; breast cancer;  
 KW parathyroid hormone related peptide; PTHrP; skeletal metastasis.  
 XX OS Homo sapiens.  
 XX PN WO2003039576-A1.  
 XX PD 15-MAY-2003.  
 XX PF 08-NOV-2002; 2002WO-CA001737.  
 XX PR 08-NOV-2001; 2001CA-02361736.  
 XX PA (PROC-) PROCYON BIOPHARMA INC.  
 XX PI Rabbani SA, Shukeir N, Panchal CJ, Newman C;  
 XX WPI; 2003-441476/41.  
 XX Use of prostate secretory protein-94 for treating hypercalcaemia of  
 PT malignancy and reducing skeletal metastasis arising from carcinomas,  
 PT prostate and breast cancers.  
 XX PS Disclosure; Page 37; 61pp; English.  
 XX CC The present invention relates to the use of prostate secretory protein-94  
 CC (PSP-94; ABR56227-ABR56228) for treating a patient suffering from  
 CC hypercalcaemia of malignancy. PSP-94 is useful for treating a patient  
 CC suffering from hypercalcaemia of malignancy arising from carcinomas,  
 CC prostate and breast cancer. The PSP-94 is also useful for reducing  
 CC parathyroid hormone related peptide (PTHrP) levels in a patient in need  
 CC and reducing the development of skeletal metastasis. The PSP-94 is also  
 CC used for the manufacture of a pharmaceutical composition for the  
 CC treatment of hypercalcaemia of malignancy and/or skeletal metastasis. The  
 CC present sequence is a peptide fragment of PSP-94, used to illustrate the  
 CC invention  
 XX SQ Sequence 15 AA;  
 Query Match 100.0%; Score 15; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-10;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EWQTDNCETCTCYET 15  
 DB 1 EWQTDNCETCTCYET 15  
 RESULT 3  
 AAO17917  
 ID AAO17917 standard; peptide; 16 AA.  
 XX AC AAO17917;  
 XX DT 30-AUG-2002 (first entry)  
 XX DE Human prostate secretory protein of 94 amino acids PSP94 analogue #6.  
 XX KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW benign prostate hyperplasia; cytostatic.  
 XX OS Homo sapiens.  
 XX PN WO200233090-A2.  
 XX PD 25-APR-2002.  
 XX PF 15-OCT-2001; 2001WO-CA001463.  
 XX PR 16-OCT-2000; 2000CA-02321256.  
 XX PR 20-AUG-2001; 2001CA-02355334.  
 XX PA (PROC-) PROCYON BIOPHARMA INC.  
 XX PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
 XX WPI; 2002-471401/50.  
 XX New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.  
 XX PS Claim 2; Page 76; 185pp; English.  
 XX CC The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-  
 CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting  
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention  
 XX SQ Sequence 16 AA;  
 Query Match 100.0%; Score 15; DB 5; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EWQTDNCETCTCYET 15  
 DB 1 EWQTDNCETCTCYET 15  
 RESULT 4  
 AAO17966  
 ID AAO17966 standard; peptide; 16 AA.  
 XX AC AAO17966;  
 XX DT 30-AUG-2002 (first entry)  
 XX DE Human prostate secretory protein of 94 amino acids PSP94 analogue #55.  
 XX KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW benign prostate hyperplasia; cytostatic.

```

Query Match      100.0%; Score 15; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EWQTDNCETCTCYET 15
         |||||
Db       2 EWQTDNCETCTCYET 16

RESULT 5
AA017967
ID  AA017967 standard; peptide; 17 AA.

```

OS  
XX  
XX  
XX  
XX  
XX  
XX  
Homo sapiens.  
WO200233090-A2.  
XX  
PD  
PD  
25-APR-2002.  
XX  
XX  
15-OCT-2001; 2001WO-COA001463.  
XX  
PPR  
16-OCT-2000; 2000CA-02321256.  
PPR  
20-AUG-2001; 2001CA-02355334.  
XX  
XX  
(PROC-) PROCYON BIOPHARMA INC.

XX	AAO17918;	
XX	AC	
XX	XX	
XX	DT	
XX	30-AUG-2002 (first entry)	
XX	XX	
DE	Human prostate secretory protein of 94 amino acids PS94 analogue #7.	
XX	DE	
XX	XX	
XX	Cancer; human; PS94; prostatic inhibin protein; PRP; HSP1; beta-MSP;	
KW	Beta-microseminoprotein; human seminal plasma inhibin; analogue;	
KW	Prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;	
KW	Stomach cancer; breast cancer; endometrial cancer; ovarian cancer;	
XX	benign prostate hyperplasia; cytostatic.	
XX	XX	

XX	Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX	WPI; 2002-471401/50.
XX	
XX	New human prostate secretory protein of 94 amino acids, useful for
XX	inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
XX	gastrointestinal, breast, endometrial, and ovarian cancers.
XX	
XX	Claim 2; Page 76; 185pp; English.
XX	
XX	The present invention relates to analogues of the human prostate
XX	secretory protein of 94 amino acids (PSP94), also known as prostatic
XX	

CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-  
 CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting  
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention  
 XX  
 SQ Sequence 17 AA;  
 Query Match 100.0%; Score 15; DB 5; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-10;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EWQTDNCETCTCYET 15  
 DB 1 EWQTDNCETCTCYET 15  
 RESULT 7  
 ID AAO17919 standard; peptide; 18 AA.  
 AC AAO17919;  
 XX  
 DT 30-AUG-2002 (first entry)  
 XX  
 DE Human prostate secretory protein of 94 amino acids PSP94 analogue #8.  
 XX  
 KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW benign prostate hyperplasia; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200233090-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 15-OCT-2001; 2001WO-CA001463.  
 XX  
 PR 16-OCT-2000; 2000CA-02321256.  
 PR 20-AUG-2001; 2001CA-02355334.  
 XX  
 PA (PROC-) PROCYON BIOPHARMA INC.  
 XX  
 PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
 PI WPI; 2002-471401/50.  
 XX  
 DR New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.  
 XX  
 PS Claim 2; Page 77; 185pp; English.  
 XX  
 CC The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-  
 CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting  
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention  
 XX  
 SQ Sequence 18 AA;  
 Query Match 100.0%; Score 15; DB 5; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2e-10;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EWQTDNCETCTCYET 15  
 DB 1 EWQTDNCETCTCYET 15  
 RESULT 9  
 ID AAO17969 standard; peptide; 19 AA.  
 AC AAO17969;  
 XX  
 DT 30-AUG-2002 (first entry)  
 XX  
 DE Human prostate secretory protein of 94 amino acids PSP94 analogue #57.  
 XX  
 KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW benign prostate hyperplasia; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200233090-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 15-OCT-2001; 2001WO-CA001463.  
 XX  
 PR 16-OCT-2000; 2000CA-02321256.  
 PR 20-AUG-2001; 2001CA-02355334.  
 XX  
 PA (PROC-) PROCYON BIOPHARMA INC.  
 XX  
 PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
 PI WPI; 2002-471401/50.  
 XX  
 DR New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.  
 XX  
 PS Claim 2; Page 94; 185pp; English.  
 XX  
 CC The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-  
 CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting  
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention  
 XX  
 SQ Sequence 18 AA;  
 Query Match 100.0%; Score 15; DB 5; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2e-10;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EWQTDNCETCTCYET 15  
 DB 4 EWQTDNCETCTCYET 18  
 RESULT 9  
 ID AAO17969 standard; peptide; 19 AA.  
 AC AAO17969;  
 XX  
 DT 30-AUG-2002 (first entry)  
 XX

QY 1 EWQTDNCETCTCYET 15  
 DB 1 EWQTDNCETCTCYET 15  
 RESULT 8  
 ID AAO17968 standard; peptide; 18 AA.  
 AC AAO17968;  
 XX  
 DT 30-AUG-2002 (first entry)  
 XX  
 DE Human prostate secretory protein of 94 amino acids PSP94 analogue #57.  
 XX  
 KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW benign prostate hyperplasia; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200233090-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 15-OCT-2001; 2001WO-CA001463.  
 XX  
 PR 16-OCT-2000; 2000CA-02321256.  
 PR 20-AUG-2001; 2001CA-02355334.  
 XX  
 PA (PROC-) PROCYON BIOPHARMA INC.  
 XX  
 PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;  
 PI WPI; 2002-471401/50.  
 XX  
 DR New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.  
 XX  
 PS Claim 2; Page 94; 185pp; English.  
 XX  
 CC The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-  
 CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting  
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention  
 XX  
 SQ Sequence 18 AA;  
 Query Match 100.0%; Score 15; DB 5; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2e-10;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EWQTDNCETCTCYET 15  
 DB 4 EWQTDNCETCTCYET 18  
 RESULT 9  
 ID AAO17969 standard; peptide; 19 AA.  
 AC AAO17969;  
 XX  
 DT 30-AUG-2002 (first entry)  
 XX

XX	Human prostate secretory protein of 94 amino acids PSP94 analogue #58.
DE	Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;
XX	beta-microseminoprotein; human seminal plasma inhibitor; analogue;
KW	prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW	stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW	benign prostate hyperplasia; cytostatic.
XX	
XX	Homo sapiens.
OS	
XX	WO200233090-A2.
XX	
PN	25-APR-2002.
XX	
PD	15-OCT-2001; 2001WO-CA001463.
XX	
FF	16-OCT-2000; 2000CA-02321256.
XX	
PR	20-AUG-2001; 2001CA-02355334.
PR	(PROC-) PROCYON BIOPHARMA INC.
XX	
PA	Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX	WPI; 2002-471401/50.
PI	
XX	New human prostate secretory protein of 94 amino acids, useful for
XX	inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT	gastrointestinal, breast, endometrial, and ovarian cancers.
PT	
XX	Claim 2; Page 95; 185pp; English.
XX	
PS	The present invention relates to analogues of the human prostate
XX	secretory protein of 94 amino acids (PSP94, also known as prostatic
XX	inhibin peptide (PIP), human seminal plasma inhibitor (HSPI) and beta-
CC	microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
CC	growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC	cancer, breast cancer, endometrial, ovarian or other cancers of
CC	epithelial secretion, or benign prostate hyperplasia and for treating
CC	patients with a disease characterized by elevated levels of FSH. The
CC	present sequence is an analogue of the invention
XX	
XX	Sequence 19 AA;
XX	
SQ	
	Query Match 100.0%; Score 15; DB 5; Length 19;
	Best Local Similarity 100.0%; Pred. No. 2,1e-10;
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 EWQTDNCETCTCYET 15
DB	5 EWQTDNCETCTCYET 19
RESULT 10	
AA017920	
ID	AA017920 standard; peptide; 19 AA.
AC	
XX	AA017920;
XX	
DT	30-AUG-2002 (first entry)
XX	
DE	Human prostate secretory protein of 94 amino acids PSP94 analogue #9.
XX	
KW	Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;
KW	beta-microseminoprotein; human seminal plasma inhibitor; analogue;
KW	prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW	stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW	benign prostate hyperplasia; cytostatic.
XX	
OS	Homo sapiens.
XX	
PN	WO200233090-A2.
XX	

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25-OCT-2001; 2001WO-CA001463.
16-OCT-2000; 2000CA-02321256.
20-AUG-2001; 2001CA-02355334.
(PROC-) PROCYON BIOPHARMA INC.
Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
WPI; 2002-471401/50.
New human prostate secretory protein of 94 amino acids, useful for
inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
gastrointestinal, breast, endometrial, and ovarian cancers.
Claim 2; Page 77; 185pp; English.
The present invention relates to analogues of the human prostate
secretory protein of 94 amino acids (PSP94, also known as prostatic
inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-
microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
cancer, breast cancer, endometrial, ovarian or other cancers of
epithelial secretion, or benign prostate hyperplasia and for treating
patients with a disease characterized by elevated levels of FSH. The
present sequence is an analogue of the invention
Sequence 19 AA;
Query Match 100.0%; Score 15; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EWQTDNCETCTCYET 15
| | | | | | | | | | | | | | |
Db 1 EWQTDNCETCTCYET 15

RESULT 11
AA017921
ID AA017921 standard; peptide; 20 AA.
AC AA017921;
XX
XX
30-AUG-2002 (first entry)
XX
XX
Human prostate secretory protein of 94 amino acids PSP94 analogue #10.
XX
XX
Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;
XX
XX
beta-microseminoprotein; human seminal plasma inhibin; analogue;
XX
XX
prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
XX
XX
stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
XX
XX
benign prostate hyperplasia; cytostatic.
XX
XX
Homo sapiens.
XX
XX
WO200233090-A2.
XX
XX
25-APR-2002.
XX
XX
15-OCT-2001; 2001WO-CA001463.
XX
XX
16-OCT-2000; 2000CA-02321256.
XX
XX
20-AUG-2001; 2001CA-02355334.
XX
XX
(PROC-) PROCYON BIOPHARMA INC.
XX
XX
Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX
XX
WPI; 2002-471401/50.
XX
XX

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KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW benign prostate hyperplasia; cytostatic.
XX
XX Homo sapiens.
XX WO200233090-A2.
PN
XX 25-APR-2002.
PD
XX
XX 15-OCT-2001; 2001WO-CA001463.
XX
XX 16-OCT-2000; 2000CA-02321256.
PR
XX 20-AUG-2001; 2001CA-02355334.
XX
XX (PROC-) PROCYON BIOPHARMA INC.
PA
XX
XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
XX
XX New human prostate secretory protein of 94 amino acids, useful for
XX inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
XX gastrointestinal, breast, endometrial, and ovarian cancers.
XX
XX Claim 2; Page 78; 185pp; English.
XX
XX The present invention relates to analogues of the human prostate
XX secretory protein of 94 amino acids (PSP94, also known as prostatic
XX inhibit peptide (PIP), human seminal plasma inhibin (HSPI) and beta-
XX microseminoprotein (bets-MSP)). The analogues are useful for inhibiting
XX growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
XX cancer, breast cancer, endometrial, ovarian or other cancers of
XX epithelial secretion, or benign prostate hyperplasia and for treating
XX patients with a disease characterized by elevated levels of FSH. The
XX present sequence is an analogue of the invention
XX
XX Sequence 22 AA;
XX
XX Query Match 100.0%; Score 15; DB 5; Length 22;
XX Best Local Similarity 100.0%; Pred.No.2.4e-10;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 EWQTNDNCETCTCYET 15
DB 1 EWQTNDNCETCTCYET 15

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Search completed: March 11, 2004, 18:10:32  
Job time : 17.4194 secs

RESULT 14	
AAO17971	
ID AAO17971 standard; peptide; 21 AA.	
XX AC	
XX AC	A AO17971;
XX DT	30-AUG-2002 (first entry)
XX DE	
XX DE	Human prostate secretory protein of 94 amino acids PSP94 analogue #60.
XX KW	Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
XX KW	beta-microseminoprotein; human seminal plasma inhibin; analogue;
XX KW	prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
XX KW	stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
XX KW	benign prostate hyperplasia; cytostatic.
XX OS	
XX OS	Homo sapiens.
XX PN	WO200233090-A2.
XX XX	25-APR-2002.
XX XX	15-OCT-2001; 2001WO-CA001463.
XX XX	16-OCT-2000; 2000CA-02321256.
PR PR	20-AUG-2001; 2001CA-02355334.
XX XX	(PROC-) PROCTON BIOPHARMA INC.
XX XX	
PPI PI	Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX XX	WPI; 2002-471401/50.
DR DR	
XX XX	New human prostate secretory protein of 94 amino acids, useful for
PPT PT	inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PPT PT	gastrointestinal, breast, endometrial, and ovarian cancers.
XX PS	
PPS PP	Claim 2; Page 95; 185pp; English.
XX CC	
CC CC	The present invention relates to analogues of the human prostate
CC CC	secretory protein of 94 amino acids (PSP94, also known as prostatic
CC CC	inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
CC CC	microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
CC CC	growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal
CC CC	cancer, breast cancer, endometrial, ovarian or other cancers of
CC CC	epithelial secretion, or benign prostate hyperplasia and for treating
CC CC	patients with a disease characterized by elevated levels of FSH. The
CC CC	present sequence is an analogue of the invention
XX SQ	
SQ SQ	Sequence 21 AA;

```

Query Match          100.0%; Score 15; DB 5; Length 21;
Best Local Similarity 100.0%; Pred.No. 2.3e-10;
Matches 15; Conservative 0; Mismatches -0; Indels 0; Gaps 0;

QY      1 EQWTDNCETCTCYET 15
         |||||
DB       7 EQWTDNCETCTCYET 21

RESULT 15
AAO17923
ID AAO17923 standard; peptide; 22 AA.
XX
AC AAO17923;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #12.
XX
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibitor; analogue;

```

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2004, 17:56:07 ; Search time 74.3226 Seconds  
(without alignments)  
243.305 Million cell updates/sec

Title: US-09-977-406a-58

Perfect score: 1 EMQTDNCETCTCTETETISCC.....YIVVEKDKPKTKCSVSEWII 64

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: Geneseqp1980s:\*\n2: Geneseqp1980s:\*\n3: Geneseqp2000s:\*\n4: Geneseqp2001s:\*\n5: Geneseqp2002s:\*\n6: Geneseqp2003as:\*\n7: Geneseqp2003bs:\*\n8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	100.0	64	AAO17965	AAO17965 Human pro
2	64	100.0	94	AAO17911	AAO17911 Human pro
3	64	100.0	94	ABR56227	ABR56227 Native Hu
4	64	100.0	102	AAO17912	AAO17912 Human pro
5	64	100.0	102	ABR56228	ABR56228 Recombina
6	64	100.0	114	AAO17926	AAO17926 Human sec
7	64	100.0	114	AAU28067	AAU28067 Novel hum
8	64	100.0	114	ABR54574	ABR54574 Prostatac
9	64	100.0	114	ADB75447	ADB75447 Prostatac
10	64	100.0	114	ADB14453	ADB14453 Human pro
11	64	100.0	132	AAO17964	AAO17964 Human pro
12	63	98.4	63	AAO17963	AAO17963 Human pro
13	62	96.9	62	AAO17962	AAO17962 Human pro
14	62	96.9	94	AAO17961	AAO17961 Human pro
15	61	95.3	61	AAO17960	AAO17960 Human pro
16	60	93.8	60	AAO17959	AAO17959 Human pro
17	59	92.2	59	AAO17958	AAO17958 Human pro
18	58	90.6	58	AAO17957	AAO17957 Human pro
19	57	89.1	57	AAO17956	AAO17956 Human pro
20	56	87.5	56	AAO17955	AAO17955 Human pro
21	55	85.9	55	AAO17954	AAO17954 Human pro
22	54	84.4	54	AAO17953	AAO17953 Human pro
23	53	82.8	53	AAO17952	AAO17952 Human pro
24	52	81.2	52	AAO17951	AAO17951 Human pro
25	51	79.7	51	AAO17950	AAO17950 Human pro

26	50	78.1	50	5	AAO17951	AAO17951 Human pro
27	49	76.6	49	5	AAO17950	AAO17950 Human pro
28	48	75.0	48	5	AAO17949	AAO17949 Human pro
29	47	73.4	47	5	AAO17948	AAO17948 Human pro
30	46	71.9	46	5	AAO17947	AAO17947 Human pro
31	45	70.3	45	5	AAO17946	AAO17946 Human pro
32	44	68.8	44	5	AAO17945	AAO17945 Human pro
33	43	67.2	43	5	AAO17944	AAO17944 Human pro
34	42	65.6	42	5	AAO17943	AAO17943 Human pro
35	41	64.1	41	5	AAO17942	AAO17942 Human pro
36	40	62.5	40	5	AAO17941	AAO17941 Human pro
37	39	60.9	39	5	AAO17940	AAO17940 Human pro
38	38	59.4	38	5	AAO17939	AAO17939 Human pro
39	37	57.8	37	5	AAO17938	AAO17938 Human pro
40	36	56.2	36	5	AAO17937	AAO17937 Human pro
41	35	54.7	35	5	AAO17936	AAO17936 Human pro
42	34	53.1	34	5	AAO17935	AAO17935 Human pro
43	33	51.6	33	5	AAO17934	AAO17934 Human pro
44	32	50.0	32	5	AAO17933	AAO17933 Human pro
45	31	48.4	31	5	AAO17932	AAO17932 Human pro

## ALIGNMENTS

RESULT 1

ID AAO17965 standard; protein; 64 AA.

AC AAO17965;

DT 30-AUG-2002 (first entry)

DE Human prostate secretory protein of 94 amino acids PSP94 analogue #54.

XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;

XX beta-microseminoprotein; human seminal plasma inhibin; analogue;

XX prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;

XX stomach cancer; breast cancer; endometrial cancer; ovarian cancer;

XX benign prostate hyperplasia; cytostatic.

XX Homo sapiens.

XX WO20023090-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-CA001463.

XX 16-OCT-2000; 2000CA-02321256.

XX 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC.

XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

XX WPI; 2002-471401/50.

XX Claim 2; Page 93-94; 185pp; English.

XX The present invention relates to analogues of the human prostate

XX secretory protein of 94 amino acids (PSP94, also known as prostatic

XX inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-

XX microseminoprotein (beta-MSP). The analogues are useful for inhibiting

XX growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal

XX cancer, breast cancer, endometrial, ovarian or other cancers of

XX epithelial secretion, or benign prostate hyperplasia and for treating

XX patients with a disease characterized by elevated levels of FSH. The

XX present sequence is an analogue of the invention

XX SQ Sequence 64 AA;  
 Query Match  
 Best Local Similarity 100.0%; Score 64; DB 5; Length 64;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGVDKDNCRIFKEDCKYIVVEKDPKKTCSVS 60  
 DB 1 EMQDNCETCTCYETETISCTLVSTPVGVDKDNCRIFKEDCKYIVVEKDPKKTCSVS 60  
 QY 61 EWII 64  
 DB 61 EWII 64

RESULT 2  
 ID AAO17911 standard; protein; 94 AA.  
 AC AAO17911;  
 XX 30-AUG-2002 (first entry)  
 DE Human prostate secretory protein of 94 amino acids PSP94.  
 XX  
 KM Cancer; human; PSP94; prostatic inhibin protein; PIP, HSP1; beta-MSP;  
 KM beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KM prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KM stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KM benign prostate hyperplasia; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO20023090-A2.  
 PD 25-APR-2002.  
 XX  
 PF 15-OCT-2001; 2001WO-CA001463.  
 XX  
 FR 16-OCT-2000; 2000CA-02321256.  
 FR 20-AUG-2001; 2001CA-02355334.  
 XX  
 PA (PROC-) PROCYON BIOPHARMA INC.  
 XX  
 PI Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;  
 DR WPI; 2002-471401/50.  
 XX  
 PT New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.  
 XX  
 PS Disclosure; Page 73; 185pp; English.  
 XX  
 CC The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-  
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is the human PSP94 protein  
 XX  
 SQ Sequence 94 AA;  
 Query Match  
 Best Local Similarity 100.0%; Score 64; DB 5; Length 94;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGVDKDNCRIFKEDCKYIVVEKDPKKTCSVS 60  
 DB 1 EMQDNCETCTCYETETISCTLVSTPVGVDKDNCRIFKEDCKYIVVEKDPKKTCSVS 60  
 QY 61 EWII 64  
 DB 61 EWII 64

DB 31 EMQDNCETCTCYETETISCTLVSTPVGVDKDNCRIFKEDCKYIVVEKDPKKTCSVS 90  
 QY 61 EWII 64  
 DB 91 EWII 94

RESULT 3  
 ID ABR56227 standard; protein; 94 AA.  
 AC ABR56227;  
 XX 20-NOV-2003 (first entry)  
 DE Native Human prostate secretory protein-94 (PSP-94).  
 XX  
 KM Human; cytostatic; prostate secretory protein-94; PSP-94;  
 KM hypercalcaemia of malignancy; carcinoma; prostate cancer; breast cancer;  
 KM parathyroid hormone related peptide; PTHrP; skeletal metastasis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003039576-A1.  
 PD 15-MAY-2003.  
 XX  
 PF 08-NOV-2002; 2002WO-CA001737.  
 XX  
 PR 08-NOV-2001; 2001CA-02361736.  
 XX  
 PA (PROC-) PROCYON BIOPHARMA INC.  
 XX  
 PI Rabbani SA, Shukeir N, Panchal CJ, Newman C;  
 DR WPI; 2003-441476/41.  
 XX  
 PT Use of prostate secretory protein-94 for treating hypercalcaemia of  
 PT malignancy and reducing skeletal metastasis arising from carcinomas,  
 PT prostate and breast cancers.  
 XX  
 PS Disclosure; Page 35; 61pp; English.  
 XX  
 CC The present invention relates to the use of prostate secretory protein-94  
 CC (PSP-94; the present sequence) for treating a patient suffering from  
 CC hypercalcaemia of malignancy. PSP-94 is useful for treating a patient  
 CC suffering from hypercalcaemia of malignancy arising from carcinomas,  
 CC prostate and breast cancer. The PSP-94 is also useful for reducing  
 CC parathyroid hormone related peptide (PTHrP) levels in a patient in need  
 CC and reducing the development of skeletal metastasis. The PSP-94 is also  
 CC used for the manufacture of a pharmaceutical composition for the  
 CC treatment of hypercalcaemia of malignancy and/or skeletal metastasis  
 XX  
 SQ Sequence 94 AA;  
 Query Match  
 Best Local Similarity 100.0%; Score 64; DB 7; Length 94;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGVDKDNCRIFKEDCKYIVVEKDPKKTCSVS 60  
 DB 31 EMQDNCETCTCYETETISCTLVSTPVGVDKDNCRIFKEDCKYIVVEKDPKKTCSVS 90  
 QY 61 EWII 64  
 DB 91 EWII 94

RESULT 4  
 ID AAO17912 standard; protein; 102 AA.  
 AC AAO17912;

XX 30-AUG-2002 (first entry)  
 DT Human prostate secretory protein of 94 amino acids PSP94 analogue #1.  
 XX  
 DE Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
 XX beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KM prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KM stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KM benign prostate hyperplasia; cytosolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200233090-A2.  
 PD  
 XX 25-APR-2002.  
 XX  
 PF 15-OCT-2001; 2001WO-CA001463.  
 XX  
 PR 16-OCT-2000; 2000CA-02321256.  
 XX  
 PR 20-AUG-2001; 2001CA-02355534.  
 XX  
 PA (PROC-) PROCYON BIOPHARMA INC.  
 XX  
 PI Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;  
 XX  
 DR WPI; 2002-471401/50.  
 XX  
 PT New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.  
 XX  
 PS Claim 2; Page 73-74; 185pp; English.  
 XX  
 SQ The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-  
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention  
 XX  
 SQ Sequence 102 AA;  
 CC  
 XX  
 Query Match 100.0%; Score 64; DB 5; Length 102;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-61; Indels 0; Gaps 0;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCGRIFKEDCKYIVVEKKDPKKTCSVS 60  
 DB 39 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCGRIFKEDCKYIVVEKKDPKKTCSVS 98  
 QY 61 EWII 64  
 DB 99 EWII 102  
 DB  
 XX  
 RESULT 5  
 ABR56228  
 ID ABR56228 standard; protein; 102 AA.  
 XX  
 AC ABR56228;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Recombinate prostate secretory protein-94 (PSP-94).  
 XX  
 KM Cytostatic; prostate secretory protein-94; PSP-94;  
 KM hypercalcaemia of malignancy; carcinoma; prostate cancer; breast cancer;  
 KM parathyroid hormone related peptide; PTHrP; skeletal metastasis.  
 XX

OS Unidentified.  
 XX  
 XX WO2003039576-A1.  
 XX  
 XX 15-MAY-2003.  
 PD  
 XX 08-NOV-2002; 2002WO-CA001737.  
 XX  
 XX 08-NOV-2001; 2001CA-02361736.  
 PR  
 XX (PROC-) PROCYON BIOPHARMA INC.  
 XX  
 PA Rabbani SA, Shukair N, Panchal CJ, Newman C;  
 XX  
 PI WPI; 2003-441476/41.  
 XX  
 DR Use of prostate secretory protein-94 for treating hypercalcaemia of  
 PT malignancy and reducing skeletal metastasis arising from carcinomas,  
 PT prostate and breast cancers.  
 XX  
 PS Disclosure; Page 35-36; 61pp; English.  
 XX  
 SQ The present invention relates to the use of prostate secretory protein-94  
 CC (PSP-94; the present sequence) for treating a patient suffering from  
 CC hypercalcaemia of malignancy. PSP-94 is useful for treating a patient  
 CC suffering from hypercalcaemia of malignancy arising from carcinomas,  
 CC prostate and breast cancer. The PSP-94 is also useful for reducing  
 CC parathyroid hormone related peptide (PTHrP) levels in a patient in need  
 CC and reducing the development of skeletal metastasis. The PSP-94 is also  
 CC used for the manufacture of a pharmaceutical composition for the  
 CC treatment of hypercalcaemia of malignancy and/or skeletal metastasis  
 XX  
 SQ Sequence 102 AA;  
 CC  
 XX  
 Query Match 100.0%; Score 64; DB 7; Length 102;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-61; Indels 0; Gaps 0;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCGRIFKEDCKYIVVEKKDPKKTCSVS 60  
 DB 39 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCGRIFKEDCKYIVVEKKDPKKTCSVS 98  
 QY 61 EWII 64  
 DB 99 EWII 102  
 DB  
 XX  
 RESULT 6  
 AAG03726  
 ID AAG03726 standard; protein; 114 AA.  
 XX  
 AC AAG03726;  
 XX  
 DT 06-OCT-2000 (first entry)  
 XX  
 DE Human secreted protein, SEQ ID NO: 7807.  
 XX  
 KM Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KM gene therapy; chromosome mapping.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1033401-A2.  
 XX  
 PD 06-SEP-2000.  
 PD  
 XX 21-FEB-2000; 2000EP-00200610.  
 XX  
 XX 26-FEB-1999; 99US-0122487P.  
 PR  
 XX (GEST) GENSET.  
 XX  
 PA Dumas Mline Edwards J, Duclert A, Giordano J;  
 XX  
 PI

XX	WP1; 2000-500381/45.
DR	N-PDSB; AAC03732.
XX	
XX	New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT	obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT	diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX	
PS	Claim 13; SEQ ID NO 7807; 71bp + Sequence Listing; English.
XX	
CC	The present sequence is a polypeptide encoded by one of a large number of
CC	5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC	prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC	tissues. EST sequences usually correspond mainly to the 3' untranslated
CC	region (UTR) of the mRNA because they are often obtained from oligo-dT
CC	primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC	sequences derived from the 5' ends of mRNAs and even in those cases where
CC	longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC	included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC	therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC	are also used in diagnostic, forensic, gene therapy and chromosome
CC	mapping procedures. They are used to obtain upstream regulatory sequences
CC	to design expression and secretion vectors
SQ	
SQ	Sequence 114 AA:
	Query Match 100.0%; Score 64; DB 3; Length 114;
	Best Local Similarity 100.0%; Pred.No. 7,1e-61;
	Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 EMQTDNCCTCTCETNESCCTLTSTPVGXDNDNQRIFFKEDCKYIVKKDKPKTCVS 60
DB	51 EMDTDCETCTCYEHSICCTLWSPVGVXDNDNQRIFFKEDCKYIVKKDKPKTCVS 110
OY	61 EWII 64 
DB	111 EWII 114
RESULT 7	
ID	AU28067
ID	AU28067 standard; protein; 114 AA.
AC	AU28067;
XX	
DT	18-DEC-2001 (first entry)
XX	
DE	Novel human secretory protein, Seq ID No 236.
XX	
KW	Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amphotropic lateral sclerosis; platelet disorder; thrombocytopenia; KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen.
KM	
OS	Homo sapiens.
XX	
PN	MO2001.66689-A2.
PD	13-SEP-2001.
XX	
FE	05-MAR-2001; 2001MO-US004942.
XX	
PR	07-MAR-2000; 2000US-00519705.
PR	19-MAY-2000; 2000US-00574454.
PR	17-JUN-2000; 2000US-00596193.
PR	14-JUL-2000; 2000US-00616847.
PR	19-SEP-2000; 2000US-00665365.
PR	20-OCT-2000; 2000US-00695267.

PA	XX	(HYSE-) HYSBQ INC.
XX	XX	
PI	XX	Tang YT, Liu C, Asundi V, Xu C, Wehman T, Ren F, Ma Y, Zhou P;
XX	XX	Zhao QA, Yang Y, Dimaac RT, Zhang J, Chen R, Xue AJ, Wang J;
DR	XX	WPI; 2001-589934/56.
DR	XX	N-PSDB; AAS44967.
XX	XX	
PS	XX	Example 3; SEQ ID NO 236; 107pp; English.
XX	XX	
CC	XX	The invention relates to novel isolated human secreted polypeptides (I)
CC	XX	and polynucleotides (II). (I) and (II) are useful for treating
CC	XX	inflammatory conditions such as arthritis, nephritis, Crohn's disease,
CC	XX	ischemia-reperfusion injury, shock, sepsis, immune responses, and is
CC	XX	involved in increasing haematopoiesis, stem cell survival, bone growth
CC	XX	and remodeling. (I), (II) and modulators of (II) are useful for
CC	XX	prophylaxis or treatment of one or more cancers. (II) is also useful for
CC	XX	creating transgenic animals useful for studying the in vivo activities of
CC	XX	the polypeptide as well as for studying modulators of the polypeptides.
CC	XX	(I) induces the proliferation of neural cells and regeneration of nerve
CC	XX	and brain tissue and is useful for the treatment of central and
CC	XX	peripheral nervous system diseases and neuropathies, such as Alzheimer's,
CC	XX	Parkinson's disease, Huntington's disease, and amyotrophic lateral
CC	XX	sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
CC	XX	activity, regulation of haematopoiesis and is useful for treating myeloid
CC	XX	or lymphoid cell disorders, platelet disorders such as thrombocytopenia
CC	XX	and for regeneration of bone, cartilage, tendon, ligament and/or nerve
CC	XX	tissue growth, and in tissue repair, healing of burns, incisions, ulcers,
CC	XX	for treating osteoporosis, osteoarthritis, bone degenerative disorders,
CC	XX	or periodontal disease. Furthermore, (I) is also useful for gut
CC	XX	protection or regeneration and treatment of lung or liver fibrosis,
CC	XX	reperfusion injury in various tissues, various immune deficiencies and
CC	XX	disorders including severe combined immunodeficiency (SCID), bacterial or
CC	XX	fungus infections, autoimmune disorders e.g. multiple sclerosis,
CC	XX	rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
CC	XX	reactions and conditions, such as asthma or other respiratory problems.
CC	XX	In addition, (I) affects biorythms or circadian cycles of rhythms,
CC	XX	fertility, metabolism, catabolism, anabolism, storage or elimination of
CC	XX	dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
CC	XX	analgesic effects or other pain reducing effects, immunoglobulin like
CC	XX	activity and can act as an antigen in a vaccine composition to raise an
CC	XX	immune response. AAU8020-ANU8395 represent novel human secreted protein
CC	XX	amino acid sequences of the invention
XX	XX	
SQ	XX	Sequence 114 AA;
		Query Match 100.0%; Score 64; DB 4; Length 114;
		Best Local Similarity 100.0%; Prev. NO. 7.1e-61;
		Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	XX	1 EMOTDNCCTCTCYEIEISCTCTVSPVYDNDQCRIFKKEDCYIIVEKKDKKCSVS 60
DB	XX	51 EMTDNCCTCTCTEIEISCTCTVSPVYDNDQCRIFKKEDCYIIVEKKDKKCSVS 110
QY	XX	61 EWIT 64
DB	XX	111 EWIT 114
XX	XX	
DT	XX	28-AUG-2003 (first entry)
DE	XX	Prostatic secretory protein SEQ ID 1003.
		RESULT 8
		ABR54574
		ID ABR54574 standard; protein; 114 AA.
		ABR54574;

XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;  
 KW Immune response; prostate cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200289747-A2.  
 XX  
 PD 14-NOV-2002.  
 XX  
 PF 09-MAY-2002; 2002WO-US014753.  
 XX  
 PR 09-MAY-2001; 2001US-00852811.  
 PR 29-JUN-2001; 2001US-00893814.  
 PR 10-DEC-2001; 2001US-00012896.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA,  
 PI Kalos MD, Ranger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;  
 PI Carter D, Li SX, Wang A, Seelky YAM, Hepier WT, Hural U;  
 PI McNeill PD, Houghton RL, Vinals Y De Baseolsc, Foy TM, Watanabe Y;  
 PI Deng T;  
 XX  
 DR WPI; 2003-167130/16.  
 XX  
 PT New prostate-specific proteins and genes, useful in gene therapy,  
 PT particularly for stimulating an immune response in a patient, or treating  
 PT prostate cancer in a patient, as well as for diagnosing prostate cancer  
 PT in a patient.  
 XX  
 PS Claim 2; Page 666; 691pp; English.  
 XX  
 CC The present invention relates to novel prostate-specific proteins (PSP)  
 CC and their coding sequences. The PSPs and their coding sequences are  
 CC useful for stimulating an immune response in a patient, or for treating  
 CC prostate cancer in a patient and for determining, detecting or diagnosing  
 CC the presence of a cancer in a patient. The present sequence was used to  
 CC illustrate the invention  
 CC  
 XX  
 SQ Sequence 114 AA;  
 XX

Query Match 100.0%; Score 64; DB 6; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-61;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQTDNCETCTCYETETISCTCTVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60  
 DB 51 EMQTDNCETCTCYETETISCTCTVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 110  
 XX  
 QY 61 EWII 64  
 DB 111 EWII 114  
 XX

RESULT 9  
 ADB75447  
 ID ADB75447 standard; protein; 114 AA.  
 XX  
 AC ADB75447;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Prostate cancer marker protein.  
 XX  
 KW Prostate; cancer; cytostatic; gene therapy; marker.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003009814-A2.  
 XX  
 PD 06-FEB-2003.  
 XX

PF 25-JUL-2002; 2002WO-US023913.  
 XX  
 XX 25-JUL-2001; 2001US-0307982P.  
 PR 22-AUG-2001; 2001US-0314356P.  
 PR 25-SEP-2001; 2001US-0325020P.  
 PR 12-DEC-2001; 2001US-0341746P.  
 PR 05-MAR-2002; 2002US-0362158P.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbatcheva B;  
 PI Hoernh S, Kamatkar S, Monsey AM, Glatt K, Zhao X, Anderson D;  
 XX  
 DR WPI; 2003-248033/24.  
 XX  
 PT New nucleic acid molecule, useful for diagnosing or treating prostate  
 PT cancer.  
 XX  
 PS Disclosure; SEQ ID NO 271; 99pp; English.  
 XX  
 CC The invention relates to newly discovered cancer markers associated with  
 CC the cancerous state of prostate cells. Also disclosed is a method of  
 CC assessing whether a patient is afflicted with prostate cancer. The method  
 CC of the invention involves assessing whether a patient is afflicted with  
 CC prostate cancer by comparing the level of expression of a marker in a  
 CC patient sample and the normal level of expression of the marker in a  
 CC control non-prostate cancer sample, where a significant increase in the  
 CC level of expression of the marker in the patient sample and the normal  
 CC level indicates that the patient is afflicted with prostate cancer.  
 CC Nucleic acids of the invention are useful for diagnosing or treating  
 CC prostate cancer, and may be useful in gene therapy. Sequences given in  
 CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 114 AA;  
 XX

Query Match 100.0%; Score 64; DB 7; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-61;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQTDNCETCTCYETETISCTCTVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60  
 DB 51 EMQTDNCETCTCYETETISCTCTVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 110  
 XX  
 QY 61 EWII 64  
 DB 111 EWII 114  
 XX

RESULT 10  
 ADB14453  
 ID ADB14453 standard; protein; 114 AA.  
 XX  
 AC ADB14453;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Human prostatic secretory protein (PSP).  
 XX  
 KW Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;  
 KW cell therapy; vaccine; T-cell epitope;  
 KW class I major histocompatibility complex allele; MHC; prostate cancer;  
 KW tumour; antigen presenting cell.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003185830-A1.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PF 12-NOV-2002; 2002US-00294025.  
 XX





CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to  
 CC AAB57303 represent sequences used in the exemplification of the present  
 CC invention  
 CC  
 SO Sequence 132 AA:

Query Match 100.0%; Score 64; DB 3; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-61;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCTCTEISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKTCVS 60  
 DB 69 EMQDNCETCTCTCTEISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKTCVS 128

QY 61 EMI 64  
 DB 129 EMI 132

RESULT 12  
 AAO17964  
 ID AAO17964 standard; protein; 63 AA.

AC AAO17964;  
 DT 30-AUG-2002 (first entry)

DE Human prostate secretory protein of 94 amino acids PSP94 analogue #53.

XX  
 XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW benign prostate hyperplasia; cytostatic.

XX Homo sapiens.

OS  
 XX WO200233090-A2.

PN 25-APR-2002.

PF 15-OCT-2001; 2001WO-CA001463.

PR 16-OCT-2000; 2000CA-02321256.

PR 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC.

PI Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

XX WPI; 2002-471401/50.

PT New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.

PS Claim 2; Page 93; 185pp; English.

CC The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-  
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
 CC growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention

XX Sequence 63 AA;

Query Match 98.4%; Score 63; DB 5; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-60;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCTCTEISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKTCVS 60  
 DB 1 EMQDNCETCTCTCTEISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKTCVS 60

QY 61 EMI 63  
 DB 61 EMI 63

RESULT 13  
 AAO17963  
 ID AAO17963 standard; protein; 62 AA.

AC AAO17963;  
 DT 30-AUG-2002 (first entry)

DE Human prostate secretory protein of 94 amino acids PSP94 analogue #52.

XX  
 XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW benign prostate hyperplasia; cytostatic.

XX Homo sapiens.

OS  
 XX WO200233090-A2.

PN 25-APR-2002.

PF 15-OCT-2001; 2001WO-CA001463.

PR 16-OCT-2000; 2000CA-02321256.

PR 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC.

PI Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

XX WPI; 2002-471401/50.

PT New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.

PS Claim 2; Page 93; 185pp; English.

CC The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-  
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
 CC growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention

XX Sequence 62 AA;

Query Match 96.9%; Score 62; DB 5; Length 62;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-59;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCTCTEISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKTCVS 60  
 DB 1 EMQDNCETCTCTCTEISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKTCVS 60

QY 61 EMI 62  
 DB 61 EMI 62

RESULT 14  
 AAR47117 standard; peptide; 94 AA.  
 ID AAR47117  
 XX  
 AC AAR47117;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 30-JUN-1994 (first entry)  
 XX  
 DE Complete sequence of human prostatic inhibin peptide.  
 XX  
 KW Prostatic inhibin peptide; cancer; adenocarcinoma; breast cancer;  
 KW hyperplasia; PIP; follicle stimulating hormone; FSH; tumour; inhibition;  
 KW prostate cancer; gastrointestinal tract.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO332524-A1.  
 XX  
 PD 23-DEC-1993.  
 XX  
 PF 16-JUN-1993; 93WO-CA000252.  
 XX  
 PR 16-JUN-1992; 92US-00899535.  
 XX  
 PA (VETRO-) VETROGEN CORP.  
 XX  
 PI Sheth AR, Garde S, Panchal CJ;  
 XX  
 DR WPI; 1994-007191/01.  
 XX  
 PT Pregn. contrg. prostatic inhibin peptide or analogues - used for treating  
 PT benign prostatic hyperplasia, adenocarcinoma or diseases with high FSH  
 PT levels.  
 XX  
 PS Disclosure; Fig 1; 48pp; English.  
 XX  
 CC Peptides or analogues of prostatic inhibin peptide (PIP) are used in a  
 CC pharmaceutical preparation for treating patients with benign prostatic  
 CC hyperplasia or adenocarcinoma, particularly adenocarcinoma of the  
 CC prostate or gastrointestinal tract or breast cancer. The preparation can  
 CC also be used to treat patients with diseases characterised by elevated  
 CC levels of follicle stimulating hormone (FSH). The PIP and its analogues  
 CC inhibit tumour growth and decrease FSH levels without adversely affecting  
 CC testosterone levels. (Updated on 25-MAR-2003 to correct FN-field.)  
 CC  
 XX  
 SQ Sequence 94 AA;  
 XX  
 Query Match 96.3%; Score 62; DB 2; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-59;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EWQTDNCECTCTCYETEISCTLVSTPVGYDKDNCQRIFKEDCKRYIVVEKKDPKKTCSVS 60  
 DB 31 EWQTDNCECTCTCYETEISCTLVSTPVGYDKDNCQRIFKEDCKRYIVVEKKDPKKTCSVS 90  
 QY 61 EW 62  
 DB 91 EW 92  
 XX  
 RESULT 15  
 AAO17962 standard; protein; 61 AA.  
 ID AAO17962  
 XX  
 AC AAO17962;  
 XX  
 DT 30-AUG-2002 (first entry)  
 DT 30-AUG-2002 (first entry)  
 XX  
 DE Human prostate secretory protein of 94 amino acids PSP94 analogue #51.  
 XX  
 KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;

beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW benign prostate hyperplasia; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200233090-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 15-OCT-2001; 2001WO-CA001463.  
 XX  
 PR 16-OCT-2000; 2000CA-02321256.  
 PR 20-AUG-2001; 2001CA-02355334.  
 XX  
 PA (PROC-) PROCYON BIOPHARMA INC.  
 XX  
 PI Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;  
 XX  
 DR WPI; 2002-471401/50.  
 XX  
 PT New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.  
 XX  
 PS Claim 2; Page 92; 185pp; English.  
 XX  
 CC The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-  
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention  
 CC  
 XX  
 SQ Sequence 61 AA;  
 XX  
 Query Match 95.3%; Score 61; DB 5; Length 61;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-58;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EWQTDNCECTCTCYETEISCTLVSTPVGYDKDNCQRIFKEDCKRYIVVEKKDPKKTCSVS 60  
 DB 1 EWQTDNCECTCTCYETEISCTLVSTPVGYDKDNCQRIFKEDCKRYIVVEKKDPKKTCSVS 60  
 QY 61 E 61  
 DB 61 E 61  
 XX  
 Search completed: March 11, 2004, 18:10:33  
 Job time : 75.326 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2004, 17:56:07 ; Search time 52.2581 Seconds  
(without alignments)  
243.305 Million cell updates/sec

Title: US-09-977-406A-88  
Perfect score: 45  
Sequence: 1 SCVFINEVPGDSTRKCMD.....HPINSEWTDNCECTCYET 45

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_290and4.\*

1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	45	AAO17995	AAO17995 Human pro
2	45	100.0	94	AAO17917	AAO17917 Complete
3	45	100.0	94	AAO17911	AAO17911 Human pro
4	45	100.0	94	ABR56227	ABR56227 Native hu
5	45	100.0	102	AAO17912	AAO17912 Human pro
6	45	100.0	102	ABR56228	ABR56228 Recombina
7	45	100.0	114	AAU28057	AAU28057 Novel hum
8	45	100.0	114	ABR54574	ABR54574 Prostati
9	45	100.0	114	ABR54574	ABR54574 Prostati
10	45	100.0	114	ABR54574	ABR54574 Prostati
11	45	100.0	114	ABR54574	ABR54574 Prostati
12	45	100.0	114	ABR54574	ABR54574 Prostati
13	45	100.0	114	ABR54574	ABR54574 Prostati
14	45	100.0	114	ABR54574	ABR54574 Prostati
15	45	100.0	114	ABR54574	ABR54574 Prostati
16	45	100.0	114	ABR54574	ABR54574 Prostati
17	45	100.0	114	ABR54574	ABR54574 Prostati
18	45	100.0	114	ABR54574	ABR54574 Prostati
19	45	100.0	114	ABR54574	ABR54574 Prostati
20	45	100.0	114	ABR54574	ABR54574 Prostati
21	45	100.0	114	ABR54574	ABR54574 Prostati
22	45	100.0	114	ABR54574	ABR54574 Prostati
23	45	100.0	114	ABR54574	ABR54574 Prostati
24	45	100.0	114	ABR54574	ABR54574 Prostati
25	45	100.0	114	ABR54574	ABR54574 Prostati

26	31	68.9	31	5	AAO17981	AAO17981 Human pro
27	30	66.7	30	5	AAO17980	AAO17980 Human pro
28	29	64.4	29	5	AAO17979	AAO17979 Human pro
29	29	64.4	119	4	AAU28255	AAU28255 Novel hum
30	28	62.2	28	5	AAO17978	AAO17978 Human pro
31	27	60.0	27	5	AAO17977	AAO17977 Human pro
32	26	57.8	26	5	AAO17976	AAO17976 Human pro
33	25	55.6	25	5	AAO17975	AAO17975 Human pro
34	24	53.3	24	5	AAO17974	AAO17974 Human pro
35	23	51.1	23	5	AAO17973	AAO17973 Human pro
36	22	48.9	22	5	AAO17972	AAO17972 Human pro
37	21	46.7	21	5	AAO17971	AAO17971 Human pro
38	20	44.4	20	5	AAO17970	AAO17970 Human pro
39	19	42.2	19	5	AAO17969	AAO17969 Human pro
40	18	40.0	18	5	AAO17968	AAO17968 Human pro
41	17	37.8	17	2	AAO17967	AAO17967 Human pro
42	16	35.6	16	5	AAO17966	AAO17966 Human pro
43	15	33.3	15	5	AAO17914	AAO17914 Human pro
44	15	33.3	15	5	AAO17915	AAO17915 Human pro

## ALIGNMENTS

RESULT 1  
ID AAO17995 standard; protein; 45 AA.  
AC  
XX AAO17995;  
DT 30-AUG-2002 (first entry)  
XX  
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #84.  
XX  
XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
XX beta-microseminoprotein; human seminal plasma inhibin; analogue;  
XX prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
XX stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
XX benign prostate hyperplasia; cytostatic.  
OS Homo sapiens.  
XX  
XX MO200233090-A2.  
XX  
XX 25-APR-2002.  
XX  
XX 15-OCT-2001; 2001WO-CA001463.  
XX  
XX 16-OCT-2000; 2000CA-02321256.  
XX 20-AUG-2001; 2001CA-02355334.  
XX  
XX (PROC-) PROCTON BIOPHARMA INC.  
XX  
XX Garde S, Panchal CJ, Baijal-Gupta M, Frazer J, Kadhim S;  
XX WPI; 2002-471401/50.  
XX  
XX New human prostate secretory protein of 94 amino acids; useful for  
XX inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
XX gastrointestinal, breast, endometrial, and ovarian cancers.  
XX  
XX Claim 2; Page 104; 185pp; English.  
XX  
XX The present invention relates to analogues of the human prostate  
XX secretory protein of 94 amino acids (PSP94, also known as prostatic  
XX inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-  
XX microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
XX growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
XX cancer, breast cancer, endometrial, ovarian or other cancers of  
XX epithelial secretion, or benign prostate hyperplasia and for treating  
XX patients with a disease characterized by elevated levels of FSH. The  
XX present sequence is an analogue of the invention

XX Sequence 45 AA;  
SQ

Query Match 100.0%; Score 45; DB 5; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.6e-39;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRCKMDLKGKHPINSEWQTDNCTCTCYET 45  
DB 1 SCYFIPNEGVPDSTRCKMDLKGKHPINSEWQTDNCTCTCYET 45

# RESULT 2

AA047117 standard; peptide; 94 AA.

AA047117;

25-MAR-2003 (revised)

30-JUN-1994 (first entry)

Complete sequence of human prostatic inhibin peptide.

Prostatic inhibin peptide; cancer; adenocarcinoma; breast cancer;  
hyperplasia; PIP; follicle stimulating hormone; FSH; tumour; inhibition;  
prostate cancer; gastrointestinal tract.

Homo sapiens.

WO9325224-A1.

23-DEC-1993.

16-JUN-1993; 93WO-CA000252.

16-JUN-1992; 92US-00899535.

(VETR-) VETROGEN CORP.

Sheth AR, Garde S, Panchal CJ;

WPI; 1994-007191/01.

Prepn. contg. prostatic inhibin peptide or analogues - used for treating  
benign prostatic hyperplasia, adenocarcinoma or diseases with high FSH  
levels.

Disclosure; Fig 1; 48pp; English.

Peptides or analogues of prostatic inhibin peptide (PIP) are used in a  
pharmaceutical preparation for treating patients with benign prostatic  
hyperplasia or adenocarcinoma, particularly adenocarcinoma of the  
prostate or gastrointestinal tract or breast cancer. The preparation can  
also be used to treat patients with diseases characterised by elevated  
levels of follicle stimulating hormone (FSH). The PIP and its analogues  
inhibit tumour growth and decrease FSH levels without adversely affecting  
testosterone levels. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 94 AA;

Query Match 100.0%; Score 45; DB 2; Length 94;  
Best Local Similarity 100.0%; Pred. No. 4.7e-39;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRCKMDLKGKHPINSEWQTDNCTCTCYET 45  
DB 1 SCYFIPNEGVPDSTRCKMDLKGKHPINSEWQTDNCTCTCYET 45

# RESULT 3

AA017911 standard; protein; 94 AA.

AA017911

AA017911;

30-AUG-2002 (first entry)

Human prostate secretory protein of 94 amino acids PSp94.

Cancer; human; PSp94; prostatic inhibin protein; PIP; HSP; beta-MSP;  
beta-microseminoprotein; human seminal plasma inhibin; analogue;  
prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
benign prostate hyperplasia; cytosstatic.

Homo sapiens.

WO200233090-A2.

25-APR-2002.

15-OCT-2001; 2001WO-CA001463.

16-OCT-2000; 2000CA-02321256.

20-AUG-2001; 2001CA-02355334.

(PROC-) PROCYON BIOPHARMA INC.

Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

WPI; 2002-471401/50.

New human prostate secretory protein of 94 amino acids, useful for  
inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
gastrointestinal, breast, endometrial, and ovarian cancers.

Disclosure; Page 73; 185pp; English.

The present invention relates to analogues of the human prostate  
secretory protein of 94 amino acids (PSp94, also known as prostatic  
inhibin peptide (PIP), human seminal plasma inhibin (HSP) and beta-  
microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal  
cancer, breast cancer, endometrial, ovarian or other cancers of  
epithelial secretion, or benign prostate hyperplasia and for treating  
patients with a disease characterized by elevated levels of FSH. The  
present sequence is the human PSp94 protein

Sequence 94 AA;

Query Match 100.0%; Score 45; DB 5; Length 94;  
Best Local Similarity 100.0%; Pred. No. 4.7e-39;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRCKMDLKGKHPINSEWQTDNCTCTCYET 45  
DB 1 SCYFIPNEGVPDSTRCKMDLKGKHPINSEWQTDNCTCTCYET 45

# RESULT 4

ABR56227 standard; protein; 94 AA.

ABR56227;

20-NOV-2003 (first entry)

Native Human prostate secretory protein-94 (PSP-94).

Human; cytosstatic; prostate secretory protein-94; PSp-94;  
hypercalcaemia of malignancy; carcinoma; prostate cancer; breast cancer;  
parathyroid hormone related peptide; PTHrP; skeletal metastasis.

Homo sapiens.

WO2003039576-A1.

XX 15-MAY-2003.  
 XX 08-NOV-2002; 2002WO-CA001737.  
 PF 08-NOV-2001; 2001CA-02361736.  
 XX (PROC-) PROCYON BIOPHARMA INC.  
 XX Rabbani SA, Shukleir N, Panchal CJ, Newman C;  
 XX WPI, 2003-441476/41.  
 DR Use of prostate secretory protein-94 for treating hypercalcaemia of  
 PT malignancy and reducing skeletal metastasis arising from carcinomas,  
 PT prostate and breast cancers.  
 XX Disclosure; Page 35; 61pp; English.  
 PS The present invention relates to the use of prostate secretory protein-94  
 CC (PSP-94; the present sequence) for treating a patient suffering from  
 CC hypercalcaemia of malignancy. PSP-94 is useful for treating a patient  
 CC suffering from hypercalcaemia of malignancy arising from carcinomas,  
 CC prostate and breast cancer. The PSP-94 is also useful for reducing  
 CC parathyroid hormone related peptide (PTHrP) levels in a patient in need  
 CC and reducing the development of skeletal metastasis. The PSP-94 is also  
 CC used for the manufacture of a pharmaceutical composition for the  
 CC treatment of hypercalcaemia of malignancy and/or skeletal metastasis  
 CC  
 XX Sequence 94 AA:  
 SQ  
 Query Match 100.0%; Score 45; DB 7; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-39;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCYFIPNEGVPDSTRKMDLKGNKHPINSEWQTDNCECTCYET 45  
 1 SCYFIPNEGVPDSTRKMDLKGNKHPINSEWQTDNCECTCYET 45  
 Db  
 RESULT 5  
 AA017912  
 ID AA017912 standard; protein; 102 AA.  
 AC AA017912;  
 XX 30-AUG-2002 (first entry)  
 DT Human prostate secretory protein of 94 amino acids PSP94 analogue #1.  
 XX  
 DE Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
 XX beta-macroglobulin; human seminal plasma inhibin; analogue;  
 KM prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KM stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KM benign prostate hyperplasia; cytosstatic.  
 XX  
 OS Homo sapiens.  
 XX WO200233090-A2.  
 FN 25-APR-2002.  
 PD 15-OCT-2001; 2001WO-CA001463.  
 PF 16-OCT-2000; 2000CA-02321256.  
 PR 20-AUG-2001; 2001CA-02355334.  
 XX (PROC-) PROCYON BIOPHARMA INC.  
 XX Rabbani SA, Shukleir N, Panchal CJ, Newman C;  
 XX WPI, 2003-441476/41.  
 DR Use of prostate secretory protein-94 for treating hypercalcaemia of  
 PT malignancy and reducing skeletal metastasis arising from carcinomas,  
 PT prostate and breast cancers.  
 XX Disclosure; Page 35; 61pp; English.  
 PS The present invention relates to the use of prostate secretory protein-94  
 CC (PSP-94; the present sequence) for treating a patient suffering from  
 CC hypercalcaemia of malignancy. PSP-94 is useful for treating a patient  
 CC suffering from hypercalcaemia of malignancy arising from carcinomas,  
 CC prostate and breast cancer. The PSP-94 is also useful for reducing  
 CC parathyroid hormone related peptide (PTHrP) levels in a patient in need  
 CC and reducing the development of skeletal metastasis. The PSP-94 is also  
 CC used for the manufacture of a pharmaceutical composition for the  
 CC treatment of hypercalcaemia of malignancy and/or skeletal metastasis  
 CC

PT New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.  
 XX  
 PS Claim 2; Page 73-74; 185pp; English.  
 XX The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-  
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
 CC growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention  
 CC  
 XX Sequence 102 AA;  
 SQ  
 Query Match 100.0%; Score 45; DB 5; Length 102;  
 Best Local Similarity 100.0%; Pred. No. 5e-39;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SCYFIPNEGVPDSTRKMDLKGNKHPINSEWQTDNCECTCYET 45  
 9 SCYFIPNEGVPDSTRKMDLKGNKHPINSEWQTDNCECTCYET 53  
 Db  
 RESULT 6  
 ABR56228  
 ID ABR56228 standard; protein; 102 AA.  
 AC ABR56228;  
 XX 20-NOV-2003 (first entry)  
 DT Recombinate prostate secretory protein-94 (PSP-94).  
 XX  
 DE Cytostatic; prostate secretory protein-94; PSP-94;  
 XX hypercalcaemia of malignancy; carcinoma; prostate cancer; breast cancer;  
 KM parathyroid hormone related peptide; PTHrP; skeletal metastasis.  
 XX  
 OS Unidentified.  
 XX WO2003039576-A1.  
 FN 15-MAY-2003.  
 PD 08-NOV-2002; 2002WO-CA001737.  
 PF 08-NOV-2001; 2001CA-02361736.  
 XX (PROC-) PROCYON BIOPHARMA INC.  
 XX Rabbani SA, Shukleir N, Panchal CJ, Newman C;  
 XX WPI, 2003-441476/41.  
 DR Use of prostate secretory protein-94 for treating hypercalcaemia of  
 PT malignancy and reducing skeletal metastasis arising from carcinomas,  
 PT prostate and breast cancers.  
 XX Disclosure; Page 35-36; 61pp; English.  
 PS The present invention relates to the use of prostate secretory protein-94  
 CC (PSP-94; the present sequence) for treating a patient suffering from  
 CC hypercalcaemia of malignancy. PSP-94 is useful for treating a patient  
 CC suffering from hypercalcaemia of malignancy arising from carcinomas,  
 CC prostate and breast cancer. The PSP-94 is also useful for reducing  
 CC parathyroid hormone related peptide (PTHrP) levels in a patient in need  
 CC and reducing the development of skeletal metastasis. The PSP-94 is also  
 CC used for the manufacture of a pharmaceutical composition for the  
 CC treatment of hypercalcaemia of malignancy and/or skeletal metastasis  
 CC

SQ Sequence 102 AA;

Query Match 100.0%; Score 45; DB 7; Length 102;  
 Best Local Similarity 100.0%; Pred. No. 5e-39;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRCKMDLKGNKHPINSEWQTDNCECTCYET 45  
 DB 9 SCYFIPNEGVPDSTRCKMDLKGNKHPINSEWQTDNCECTCYET 53

RESULT 7

AA03726  
 ID AAG03726 standard; protein; 114 AA.

AC AAG03726;

DT 06-OCT-2000 (first entry)

DE Human secreted protein, SEQ ID NO: 7807.

KM Human, 5' EST, expressed sequence tag; secreted protein; cDNA isolation;  
 gene therapy; chromosome mapping.

OS Homo sapiens.

FN E21033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-00200610.

PR 26-FEB-1999; 99US-0122487P.

PA (GEST) GENSET.

PI Dunas Milne Edwards J, Duclert A, Giordano J;

DR WPI: 2000-500381/45.

DR N-PSDB; AAC03732.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
 diagnostic, forensic, gene therapy and chromosome mapping procedures.

PS Claim 13; SEQ ID NO 7807; 71pp + Sequence Listing; English.

CC The present sequence is a polypeptide encoded by one of a large number of  
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different  
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
 CC sequences derived from the 5' ends of mRNAs and even in those cases where  
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
 CC are also used in diagnostic, forensic, gene therapy and chromosome  
 CC mapping procedures. They are used to obtain upstream regulatory sequences  
 CC and to design expression and secretion vectors

SQ Sequence 114 AA;

Query Match 100.0%; Score 45; DB 3; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-39;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRCKMDLKGNKHPINSEWQTDNCECTCYET 45  
 DB 21 SCYFIPNEGVPDSTRCKMDLKGNKHPINSEWQTDNCECTCYET 65

RESULT 8

AAU28067  
 ID AAU28067 standard; protein; 114 AA.

AC AAU28067;

DT 18-DEC-2001 (first entry)

DE Novel human secretory protein, Seq ID No 236.

KM Human, secreted protein; arthritis; Crohn's disease; sepsis; shock;  
 KM ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;  
 KM transgenic animal; Alzheimer's disease; Parkinson's disease; burn;  
 KM amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;  
 KM ulcer; osteoporosis; bone degenerative disorder; periodontal disease;  
 KM gut protection; lung; liver fibrosis; immune deficiency; infection;  
 KM severe combined immunodeficiency; SCID; autoimmune disorder; allergy;  
 KM multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;  
 KM fertility; analgesic; pain; antigen.

OS Homo sapiens.

FN WO200166689-A2.

PD 13-SEP-2001.

PF 05-MAR-2001; 2001WO-US004942.

PR 07-MAR-2000; 2000US-00519705.

PR 19-MAY-2000; 2000US-00574454.

PR 17-JUN-2000; 2000US-00586193.

PR 14-JUL-2000; 2000US-00616847.

PR 19-SEP-2000; 2000US-00665363.

PR 20-OCT-2000; 2000US-00693267.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;

PI Zhao Q, Yang Y, Dmanac RT, Zhang J, Chen R, Xue AJ, Wang J;  
 DR N-PSDB; AAS44967.

PS Example 3; SEQ ID NO 236; 107pp; English.

CC The invention relates to novel isolated human secreted polypeptides (I)  
 CC and polynucleotides (II). (I) and (II) are useful for treating  
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,  
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is  
 CC involved in increasing haematopoiesis, stem cell survival, bone growth  
 CC and remodeling. (I), (II) and modulators of (II) are useful for  
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for  
 CC creating transgenic animals useful for studying the in vivo activities of  
 CC the polypeptide as well as for studying modulators of the polypeptides.  
 CC (I) induces the proliferation of neural cells and regeneration of nerve  
 CC and brain tissue and is useful for the treatment of central and  
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,  
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral  
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic  
 CC activity, regulation of haematopoiesis and is useful for promoting myeloid  
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia  
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve  
 CC tissue growth, and in tissue repair, healing of burns, incisions, ulcers,  
 CC for treating osteoporosis, osteoarthritis, bone degenerative disorders,  
 CC or periodontal disease. Furthermore, (I) is also useful for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues, various immune deficiencies and  
 CC disorders including severe combined immunodeficiency (SCID), bacterial or  
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis, or  
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic

CC reactions and conditions, such as asthma or other respiratory problems.  
 CC In addition, (1) affects biorythms or circadian cycles of rhythms,  
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of  
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides  
 CC analgesic effects or other pain reducing effects, immunoglobulin like  
 CC activity and can act as antigen in a vaccine composition to raise an  
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein  
 CC amino acid sequences of the invention

XX Sequence 114 AA;

Query Match 100.0%; Score 45; DB 4; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-39;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCECTCYET 45  
 DB 21 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCECTCYET 65

# RESULT 9

ABR54574  
 ID ABR54574 standard; protein; 114 AA.

AC ABR54574;

DT 28-AUG-2003 (first entry)

DE Prostatic secretory protein SEQ ID 1003.

KM Cytostatic; gene therapy; prostate-specific protein; PSP; human;  
 KM immune response; prostate cancer.

OS Homo sapiens.

PN WO200289747-A2.

PD 14-NOV-2002.

PF 09-MAY-2002; 2002WO-US014753.

PR 09-MAY-2001; 2001US-00852811.

PR 29-JUN-2001; 2001US-00895814.

PR 10-DEC-2001; 2001US-00012896.

XX (CORI-) CORIXA CORP.

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;  
 PI Kalos MD, Fanger GR, Retter MW, Stolk UA, Day CH, Vedvick TS;  
 PI Carter D, Li SX, Wang A, Skelky YAW, Hepler WT, Hurst U;  
 PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;  
 PI Deng T;

XX WPI; 2003-167130/16.

DR WPI; 2003-167130/16.

XX New prostate-specific proteins and genes, useful in gene therapy,  
 PT particularly for stimulating an immune response in a patient, or treating  
 PT prostate cancer in a patient, as well as for diagnosing prostate cancer  
 PT in a patient.

XX Claim 2; Page 666; 691pp; English.

PS The present invention relates to novel prostate-specific proteins (PSP)

CC and their coding sequences. The PSPs and their coding sequences are

CC useful for stimulating an immune response in a patient, or for treating

CC prostate cancer in a patient and for determining, detecting or diagnosing

CC the presence of a cancer in a patient. The present sequence was used to

XX illustrate the invention

XX Sequence 114 AA;  
 Query Match 100.0%; Score 45; DB 6; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-39;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCECTCYET 45  
 DB 21 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCECTCYET 65

# RESULT 10

ADB75447  
 ID ADB75447 standard; protein; 114 AA.

AC ADB75447;

DT 04-DEC-2003 (first entry)

DE Prostate cancer marker protein.

KM Prostate; cancer; cytosstatic; gene therapy; marker.

OS Homo sapiens.

PN WO2003009814-A2.

PD 06-FEB-2003.

PF 25-JUL-2002; 2002WO-US023913.

PR 25-JUL-2001; 2001US-0307982P.

PR 22-AUG-2001; 2001US-0314356P.

PR 25-SEP-2001; 2001US-0325020P.

PR 12-DEC-2001; 2001US-0341746P.

PR 05-MAR-2002; 2002US-0362158P.

XX (MILL-) MILLENNIUM PHARM INC.

PI Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;  
 PI Hoersht S, Kamatkar S, Womsey AM, Glatk K, Zhao X, Anderson D;

XX WPI; 2003-248033/24.

PT New nucleic acid molecule, useful for diagnosing or treating prostate  
 PT cancer.

XX Disclosure; SEQ ID NO 271; 99pp; English.

XX The invention relates to newly discovered cancer markers associated with  
 CC the cancerous state of prostate cells. Also disclosed is a method of  
 CC assessing whether a patient is afflicted with prostate cancer. The method  
 CC of the invention involves assessing whether a patient is afflicted with  
 CC prostate cancer by comparing the level of expression of the marker in a  
 CC patient sample and the normal level of expression of the marker in a  
 CC control non-prostate cancer sample, where a significant increase in the  
 CC level of expression of the marker in the patient sample and the normal  
 CC level indicates that the patient is afflicted with prostate cancer.

CC Nucleic acids of the invention are useful for diagnosing or treating  
 CC prostate cancer, and may be useful in gene therapy. Sequences given in  
 CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 114 AA;

Query Match 100.0%; Score 45; DB 7; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-39;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCECTCYET 45  
 DB 21 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCECTCYET 65

# RESULT 11

ABD14453  
ID ABD14453 standard; protein; 114 AA.  
XX  
AC ABD14453;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Human prostatic secretory protein (PSP).  
XX  
KW Human; prostate specific cDNA; cytosolic; immunostimulant; gene therapy;  
KW cell therapy; vaccine; T-cell epitope;  
KW class I major histocompatibility complex allele; MHC; prostate cancer;  
KW tumour; antigen presenting cell.  
XX  
OS Homo sapiens.  
XX  
PN US2003185830-A1.  
XX  
PD 02-OCT-2003.  
XX  
PF 12-NOV-2002; 2002US-00294025.  
XX  
PR 25-FEB-1997; 97US-00806099.  
PR 01-AUG-1997; 97US-00804804.  
PR 09-FEB-1998; 98US-00020956.  
PR 25-FEB-1998; 98US-00030607.  
PR 14-JUL-1998; 98US-00115453.  
PR 23-SEP-1998; 98US-00159812.  
PR 15-JAN-1999; 99US-00232149.  
PR 09-APR-1999; 99US-00288946.  
PR 13-JUL-1999; 99US-00352616.  
PR 12-NOV-1999; 99US-00435313.  
PR 18-NOV-1999; 99US-00443686.  
PR 14-JAN-2000; 2000US-00483672.  
PR 27-MAR-2000; 2000US-00536857.  
PR 09-MAY-2000; 2000US-00568100.  
PR 12-MAY-2000; 2000US-00570737.  
PR 13-JUN-2000; 2000US-00593793.  
PR 27-JUN-2000; 2000US-00605783.  
PR 09-AUG-2000; 2000US-00636215.  
PR 29-AUG-2000; 2000US-00651236.  
PR 06-SEP-2000; 2000US-00657279.  
PR 02-OCT-2000; 2000US-00679426.  
PR 10-OCT-2000; 2000US-00685166.  
PR 09-NOV-2000; 2000US-00709729.  
PR 12-JAN-2001; 2001US-00759143.  
PR 09-FEB-2001; 2001US-00780669.  
PR 09-MAY-2001; 2001US-00852911.  
PR 29-JUN-2001; 2001US-00895814.  
PR 10-DEC-2001; 2001US-00012896.  
PR 09-MAY-2002; 2002US-00144678.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Xu J, Stolk JA, Kalos MD;  
XX  
DR WPI; 2003-756193/71.  
XX  
PT New isolated polypeptide for use in a vaccine for stimulating an immune  
PT response, or for treating or diagnosis cancer, preferably prostate  
PT cancer.  
XX  
PS Example 34; Page; 101pp; English.  
XX  
CC The invention relates to an isolated polypeptide comprising no more than  
CC 11-542 amino acids of ABD13563 comprising a sequence ABD14487. The  
CC peptides comprise a fragment ABD13563 of that contain naturally processed  
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)  
CC alleles. ABD13563 is a polypeptide encoded by a human prostate specific  
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids  
CC encoding the proteins and peptides, expression vectors, a host cell  
CC transformed with the vector, an isolated antibody (or antigen binding  
CC fragment) that specifically binds to the protein or peptide, detecting

CC the presence of a cancer in a patient (comprising contacting a patient  
CC sample with a binding agent that binds to the peptides or a polypeptide  
CC appearing as ABD1358, detecting the amount of polypeptide that binds to  
CC the agent and comparing the amount of polypeptide to a predetermined cut-  
CC off value to determine the presence of cancer), a fusion protein  
CC comprising the peptides or proteins, stimulating or expanding T cells  
CC specific for a tumour protein comprising contacting T cells with the  
CC peptides or the isolated T cell population, treating prostate cancer in a  
CC patient comprising administering a composition comprising the peptides,  
CC nucleic acids, antibodies or compounds, determining the presence of a  
CC cancer in a patient and treating prostate cancer in a patient comprising  
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated  
CC from a patient with the peptides or antigen presenting cells that express  
CC the peptides so that the T cells proliferate, and administering the  
CC proliferated T cells to the patient. The peptides (or an oligonucleotide  
CC that hybridises to nucleic acid encoding them), is used to detect the  
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or  
CC antigen-presenting cells expressing the nucleic acid, are used to  
CC stimulate or expand T cells specific for a tumour protein. The peptides,  
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen  
CC presenting cells are used to stimulate an immune response or treat  
CC prostate cancer in a patient. The present sequence is a prostate specific  
CC protein of the invention. Note: Except where otherwise indicated, the  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from USPTO  
CC at [seqdata.uspto.gov/sequence.html?DocID=20030185830](http://seqdata.uspto.gov/sequence.html?DocID=20030185830).  
XX  
SQ Sequence 114 AA;  
XX  
Query Match 100.0%; Score 45; DB 7; Length 114;  
XX  
Best Local Similarity 100.0%; Pred. No. 5.5e-39;  
XX  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 SCYFIPIGVPDSTRKCMDLKGNKHPINSEWQDNCCTCTCYER 45  
XX  
DB 21 SCYFIPIGVPDSTRKCMDLKGNKHPINSEWQDNCCTCTCYER 65  
XX  
RESULT 12  
XX  
AAB56449 standard; protein; 132 AA.  
XX  
ID AAB56449  
XX  
AC AAB56449;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Human prostate cancer antigen protein sequence SEQ ID NO:1027.  
XX  
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
KW neuroprotective; cytosolic; cardioactive; immunomodulatory; muscular;  
KW vulnerability; gastrointestinal; nephrotoxic; antiinfective; gynaecological;  
KW antibacterial; gene therapy; neutral; immune; reproductive; renal;  
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
KW wound; infectious disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200055174-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 08-MAR-2000; 2000WO-US005988.  
XX  
PR 12-MAR-1999; 99US-0124270P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI (ROSE/) ROSEN C A.  
XX  
PI Rosen CA, Ruben SM;  
XX  
DR WPI; 2000-587513/55.  
XX  
DR N-PSDB; AAF15652.  
XX



PT Prostate cancer associated gene sequences, referred to as prostate cancer  
PT antigens, useful for treatment, prevention, and diagnosis of disorders  
PT such as prostate cancer.

XX Claim 11; Page 1457; 2338bp; English.

XX AAF1566 to AAF1650 encode the human prostate cancer associated  
CC proteins, called prostate cancer antigens, given in AAB5633 to AAB57302.  
CC The prostate cancer antigens can have neuroprotective, cytostatic,  
CC cardiocactive, immunomodulatory, muscular, vulnary, gastrointestinal,  
CC nephrotoxic, antineoplastic, gynecological and antibacterial activities,  
CC and can be used in gene therapy. The prostate cancer antigen  
CC polynucleotides may be used for detection of prostate cancer, chromosome  
CC identification, as chromosome markers, and for numerous other diagnostic  
CC or research purposes. The prostate cancer antigens may be used to treat  
CC disorders such as neural, immune, muscular, reproductive,  
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to  
CC AAB57303 represent sequences used in the exemplification of the present  
CC invention.

XX Sequence 132 AA;

Query Match 100.0%; Score 45; DB 3; Length 132;  
Best Local Similarity 100.0%; Pred. No. 6.2e-39;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPGDSTRKMDLKGKHPINSEWQDNCECTCYET 45  
DB 39 SCYFIPNEGVPGDSTRKMDLKGKHPINSEWQDNCECTCYET 83

RESULT 13  
AA017994  
ID AA017994 standard; protein; 44 AA.

XX AA017994;

XX 30-AUG-2002 (first entry)

XX Human prostate secretory protein of 94 amino acids PSP94 analogue #83.

XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
XX beta-microseminoprotein; human seminal plasma inhibin; analogue;  
XX prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
XX stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
XX benign prostate hyperplasia; cytostatic.

XX Homo sapiens.

XX WO200233090-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-CA001463.

XX 16-OCT-2000; 2000CA-02321256.

XX 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC.

XX PI Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;  
XX WPI; 2002-471401/50.

XX New human prostate secretory protein of 94 amino acids, useful for  
XX inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
XX gastrointestinal, breast, endometrial, and ovarian cancers.

XX Claim 2; Page 103; 185pp; English.

XX The present invention relates to analogues of the human prostate  
XX secretory protein of 94 amino acids (PSP94, also known as prostatic

CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-  
CC microseminoprotein (beta-MSP). The analogues are useful for inhibiting  
CC growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal  
CC cancer, breast cancer, endometrial, ovarian or other cancers of  
CC epithelial secretion, or benign prostate hyperplasia and for treating  
CC patients with a disease characterized by elevated levels of FSH. The  
CC present sequence is an analogue of the invention

XX Sequence 44 AA;

Query Match 97.8%; Score 44; DB 5; Length 44;  
Best Local Similarity 100.0%; Pred. No. 2.8e-38;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CYFIPNEGVPGDSTRKMDLKGKHPINSEWQDNCECTCYET 45  
DB 1 CYFIPNEGVPGDSTRKMDLKGKHPINSEWQDNCECTCYET 44

RESULT 14  
AA017993  
ID AA017993 standard; protein; 43 AA.

XX AA017993;

XX 30-AUG-2002 (first entry)

XX Human prostate secretory protein of 94 amino acids PSP94 analogue #82.

XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;  
XX beta-microseminoprotein; human seminal plasma inhibin; analogue;  
XX prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
XX stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
XX benign prostate hyperplasia; cytostatic.

XX Homo sapiens.

XX WO200233090-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-CA001463.

XX 16-OCT-2000; 2000CA-02321256.

XX 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC.

XX PI Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;  
XX WPI; 2002-471401/50.

XX New human prostate secretory protein of 94 amino acids, useful for  
XX inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
XX gastrointestinal, breast, endometrial, and ovarian cancers.

XX Claim 2; Page 103; 185pp; English.

XX The present invention relates to analogues of the human prostate  
XX secretory protein of 94 amino acids (PSP94, also known as prostatic  
XX inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-  
XX microseminoprotein (beta-MSP)). The analogues are useful for inhibiting  
XX growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal  
XX cancer, breast cancer, endometrial, ovarian or other cancers of  
XX epithelial secretion, or benign prostate hyperplasia and for treating  
XX patients with a disease characterized by elevated levels of FSH. The  
XX present sequence is an analogue of the invention

XX Sequence 43 AA;

Query Match 95.6%; Score 43; DB 5; Length 43;  
Best Local Similarity 100.0%; Pred. No. 3e-37;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 YFIPNEGVPDSTRKMDLKGKHPINSEWQTNCECTCYET 45  
 |||||  
 DB 1 YFIPNEGVPDSTRKMDLKGKHPINSEWQTNCECTCYET 43  
 |||||

## RESULT 15

AA017992  
 ID AA017992 standard; protein, 42 AA.

XX AA017992;  
 AC

XX 30-AUG-2002 (first entry)  
 DT

XX Human prostate secretory protein of 94 amino acids PSP94 analogue #81.  
 DE

XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSF;  
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;  
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;  
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;  
 KW benign prostate hyperplasia; cytostatic.

XX Homo sapiens.  
 OS

XX W0200233090-A2.  
 PN

XX 25-APR-2002.  
 PD

XX 15-OCT-2001; 2001MO-CA001463.  
 PE

XX 16-OCT-2000; 2000CA-02321256.  
 PR

XX 20-AUG-2001; 2001CA-02355334.  
 PR

XX (PROC-) PROCYON BIOPHARMA INC.  
 PA

XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;  
 PI

XX WPI; 2002-471401/50.  
 DR

XX New human prostate secretory protein of 94 amino acids, useful for  
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,  
 PT gastrointestinal, breast, endometrial, and ovarian cancers.

XX Claim 2; Page 103; 185PP; English.  
 PS

XX The present invention relates to analogues of the human prostate  
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic  
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-  
 CC microseminoprotein (beta-MSF)). The analogues are useful for inhibiting  
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal  
 CC cancer, breast cancer, endometrial, ovarian or other cancers of  
 CC epithelial secretion, or benign prostate hyperplasia and for treating  
 CC patients with a disease characterized by elevated levels of FSH. The  
 CC present sequence is an analogue of the invention

XX Sequence 42 AA;  
 SQ

Query March 93.3%; Score 42; DB 5; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-36;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 FIPNEGVPDSTRKMDLKGKHPINSEWQTNCECTCYET 45  
 |||||  
 DB 1 FIPNEGVPDSTRKMDLKGKHPINSEWQTNCECTCYET 42  
 |||||

Search completed: March 11, 2004, 18:10:33  
 Job time : 52.2581 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2004, 18:05:52 ; Search time 35.5645 Seconds  
(without alignments)  
399.227 Million cell updates/sec

Title: US-09-977-406a-88

Sequence: 1 SCFFINRGVPGDSTRKCMD.....HPINSEWDNCTCTCTCT 45

Scoring table: Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

SPTREMBL\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_procent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriopl:\*
- 17: sp\_archaeop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.6	93	16	Q8XFD6	Q8XFD6 salmonella
2	15.6	186	12	Q64859	Q64859 human adeno
3	15.6	494	5	Q9VWP1	Q9VWP1 dirosophila
4	15.6	502	16	O53551	O53551 mycobacteri
5	15.6	502	16	Q7WVC5	Q7WVC5 mycobacteri
6	15.6	758	5	Q26125	Q26125 plasmodium
7	15.6	759	5	Q26128	Q26128 plasmodium
8	13.3	40	5	Q9TXA3	Q9TXA3 caenorhabdi
9	13.3	83	5	Q95881	Q95881 dirosophila
10	13.3	96	16	Q8XW65	Q8XW65 ralsionia s
11	13.3	97	5	Q7WVY3	Q7WVY3 caenorhabdi
12	13.3	105	2	Q62097	Q62097 pseudomonas
13	13.3	143	16	Q88AB7	Q88AB7 pseudomonas
14	13.3	146	5	Q86DE9	Q86DE9 heterodera
15	13.3	160	16	Q9C1Q2	Q9C1Q2 lactococcus
16	13.3	185	4	Q86T25	Q86T25 homo sapien

17	6	13.3	185	5	Q8TJ32	Q8TJ32 heterodera
18	6	13.3	196	11	Q9AD8Y1	Q9AD8Y1 mus musculu
19	6	13.3	215	3	Q74897	Q74897 schizosach
20	6	13.3	219	13	Q91151	Q91151 notophtalm
21	6	13.3	232	3	Q86ZT8	Q86ZT8 hypocrea me
22	6	13.3	233	16	Q89ZT2	Q89ZT2 bacteroides
23	6	13.3	235	16	Q89ZV0	Q89ZV0 bacteroides
24	6	13.3	235	16	Q7UEV4	Q7UEV4 bacteroides
25	6	13.3	243	5	Q818X2	Q818X2 entamoeba h
26	6	13.3	269	17	Q97512	Q97512 sulfolobus
27	6	13.3	277	16	Q9XZRO	Q9XZRO streptomyce
28	6	13.3	277	17	Q8PVA1	Q8PVA1 methanosarc
29	6	13.3	280	3	Q7Z908	Q7Z908 saccharomyc
30	6	13.3	280	3	Q7Z821	Q7Z821 zygosaachar
31	6	13.3	281	3	Q7Z8Y4	Q7Z8Y4 zygosaachar
32	6	13.3	283	3	Q86ZT7	Q86ZT7 hypocrea av
33	6	13.3	293	4	Q9SVQ3	Q9SVQ3 homo sapien
34	6	13.3	306	3	Q7Z8Y8	Q7Z8Y8 zygosaachar
35	6	13.3	319	4	Q9NRG7	Q9NRG7 homo sapien
36	6	13.3	324	16	Q8Y6P6	Q8Y6P6 listeria mo
37	6	13.3	325	13	Q9W6C6	Q9W6C6 brachydanio
38	6	13.3	329	3	Q876P4	Q876P4 rotiferoph
39	6	13.3	329	3	Q870K6	Q870K6 escovopsis
40	6	13.3	329	3	Q870X1	Q870X1 escovopsis
41	6	13.3	329	3	Q870J8	Q870J8 escovopsis
42	6	13.3	329	16	Q7VWLS	Q7VWLS haemophilus
43	6	13.3	333	3	Q876P8	Q876P8 collectotric
44	6	13.3	333	3	Q876P7	Q876P7 collectotric
45	6	13.3	333	3	Q876P6	Q876P6 metarhizium

## ALIGNMENTS

### RESULT 1

Q8XFD6 PRELIMINARY; PRT; 93 AA.

AC Q8XFD6;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Hypothetical protein yehh (putative outer membrane protein)  
 GN (Hypothetical protein STY2382)  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=601, 602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S. typhi; STRAIN=Ty2 / ATCC 700931;  
 RX MEDLINE=22531367; PubMed=12644504;  
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,  
 RA Burdand V., Kodoyanni V., Schwartz D.C., Blattner F.R.,  
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2  
 and CT18";  
 RL J. Bacteriol. 185:2330-2337(2003).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S. typhimurium; STRAIN=LT2 / SCS1412 / ATCC 700720;  
 RX MEDLINE=21534948; PubMed=11677609;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney S., Nguyen C., Scott K., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoenking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
 LT2";  
 RL Nature 413:852-856(2001).  
 RL [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S. typhi; STRAIN=CT18;

RA MEDLINE=21534947; PubMed=11677608;  
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,  
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
 RA Croft A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jacobs K.,  
 RA Krogh A., Larsen T.S., Leach S., Moul S., O'Gaora P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrall B.G.,  
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*  
 RT enterica serovar Typhimurium CT18.";  
 RL Nature 413:848-852(2001).  
 DR EMBL: AE016836; AAC68400.1; -;  
 DR EMBL: AE008796; AAL21056.1; -;  
 DR EMBL: AL627273; CAP02532.1; -;  
 KW Hypothetical protein, complete proteome  
 SQ SEQUENCE 93 AA; 9929 MW; B2FCE9D9F079E298 CRC64;  
 Query Match 15.6%; Score 7; DB 16; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 4;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 VPGDSTR 16  
 DB 79 VPGDSTR 85  
 RESULT 2  
 ID Q64859 PRELIMINARY; PRT; 186 AA.  
 AC Q64859;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE L4 22K.  
 GN L4 22K.  
 OS Human adenovirus type 40.  
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
 OX NCBI\_TaxID=28284;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dugan;  
 RX MEDLINE=87122182; PubMed=3811242;  
 RA Ishino M., Sawada Y., Yaegashi T., Demura M., Fujinaga K.;  
 RT "Nucleotide sequence of the adenovirus type 40 inverted terminal  
 RT repeat: Close relation to that of adenovirus type 5.";  
 RL Virology 156:414-416(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dugan;  
 RX MEDLINE=8808437; PubMed=2961652;  
 RA van Loon A.E., Ligtgenberg M., Reemst A.M.C.B., Sussenbach J.S.,  
 RA Rozijn T.H.;  
 RT "Structure and organization of the left-terminal DNA regions of  
 RT fastidious adenovirus types 40 and 41.";  
 RL Gene 58:109-126(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dugan;  
 RA Ishino M.;  
 RT "Analysis of structure and function of human adenovirus type 40  
 RT leftmost 1.85 kb region including transforming E1a gene.";  
 RL Sapporo Igaku Zasshi 57:59-66(1988).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dugan;  
 RX MEDLINE=88265890; PubMed=2968714;  
 RA Ishino M., Ohashi Y., Emoto T., Sawada Y., Fujinaga K.;  
 RT "Characterization of Adenovirus type 40 E1 region.";  
 RL Virology 165:95-102(1988).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dugan;

RA MEDLINE=88160034; PubMed=3279700;  
 RA Vos H.L., van der Lee F.M., Reemst A.M.C.B., van Loon A.E.,  
 RA Sussenbach J.S.;  
 RT "The genes encoding the DNA binding protein and the 23K protease of  
 RT adenovirus types 40 and 41.";  
 RL Virology 163:1-10(1988).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dugan;  
 RX MEDLINE=89370295; PubMed=2773314;  
 RA Kidd A.H., Erasmus M.C.;  
 RT "Sequence characterization of the adenovirus 40 fiber gene.";  
 RL Virology 172:134-144(1989).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dugan;  
 RX MEDLINE=9011698; PubMed=2481711;  
 RA Toogood C.I., Murali R., Burnett R.M., Hay R.T.;  
 RT "The adenovirus type 40 hexon: sequence, predicted structure and  
 RT relationship to other adenovirus hexons.";  
 RL J. Gen. Virol. 70:3203-3214(1989).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dugan;  
 RX MEDLINE=94087748; PubMed=8263936;  
 RA Davison A.J., Telford E.A., Watson M.S., McBride K., Mautner V.;  
 RT "The DNA sequence of adenovirus type 40.";  
 RL J. Mol. Biol. 234:1308-1316(1993).  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dugan;  
 RA Pieniazek N.J., Siemenda S.B., Pieniazek D., Luftig R.B.;  
 RT "The VA region of human enteric adenovirus type 40 shows homology to  
 RT the VA region of simian adenovirus type 7.";  
 RL Submitted (JUN-1993) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: L19443; AAC13971.1; -;  
 SQ SEQUENCE 186 AA; 21302 MW; 15C19FD4B723E7B5 CRC64;  
 Query Match 15.6%; Score 7; DB 13; Length 186;  
 Best Local Similarity 100.0%; Pred. No. 7.4;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 22 KGNKHPI 28  
 DB 4 KGNKHPI 10  
 RESULT 3  
 ID Q9VWP1 PRELIMINARY; PRT; 494 AA.  
 AC Q9VWP1; Q95RE2;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE CG7288 Protein (LD38070p).  
 GN CG7288.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkely;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Adams W.D., Celniker S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-C., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolhakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Dommes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodet A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ikegami C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mostreft A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson W., Skupski M.P., Smith T.,  
 RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RA "The genome sequence of *Drosophila melanogaster*.";  
 RA Science 287:2185-2195(2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Celinker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Goeckye J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,  
 RA Gonzalez M., Horck J., Hoskins R.A., Hostin D., Howland T.J.,  
 RA Ikegami C., Jalali M., Kruse D., Li P., Mattei B., Mostreft A.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuno J.,  
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,  
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RA "Sequencing of *Drosophila melanogaster* genome.";  
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RP SEQUENCE FROM N.A.  
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celinker S.E.,  
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Searle S.M., Smith E., Shu S., Smutnak F., Whitfield E.,  
 RA Asburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RA "Annotation of *Drosophila melanogaster* genome.";  
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;  
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [5]  
 RP SEQUENCE FROM N.A.  
 RA FlyBase;  
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarini H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,

RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;  
 RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AE003510; AAF4897.2; -;  
 DR EMBL; AY061442; AAL28990.1; -;  
 DR FlyBase; F590030969; CG7288.  
 DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.  
 DR GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.  
 DR GO; GO:0005111; F:ubiquitin-dependent protein catabolism; IEA.  
 DR InterPro; IPR001394; Peptidase\_C19.  
 DR InterPro; IPR001607; ZnF\_UBP.  
 DR Pfam; PF00443; UCH; 1.  
 DR SMART; SM00290; ZnF\_UBP; 1.  
 DR PROSITE; PS00235; UCH 2.3; 1.  
 SQ SEQUENCE 494 AA; 57503 MW; D7C9B515ECBC8397 CAC64;  
 Query Match 15.6%; Score 7; DB 5; Length 494;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 21 LKGNHP 27  
 DB 268 LKGNHP 274  
 RESULT 4  
 ID 053551 PRELIMINARY; PRT; 502 AA.  
 AC 053551;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Putative COA-ligase (4-comarnate-COA ligase, putative).  
 GN FAD017 OR RV3506 OR MT3610 OR MTV023.13.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 CC NCBI\_Taxid=1773;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=3379;  
 RX MEDLINE=98293987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Petwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares K.,  
 RA Rulston J.E., Taylor K., Whitehead S., Barrall B.G.;  
 RA "Deciphering the biology of *Mycobacterium tuberculosis* from the  
 RT complete genome sequence.";  
 RL Nature 393:537-544 (1998).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwinn M., Hatt D., Hickey E.,  
 RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,  
 RA Delcher A., Uterback T., Weidman J., Kouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RA "Whole genome comparison of *Mycobacterium tuberculosis* clinical and  
 RT laboratory strains.";  
 RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AL022022; CAI17743.1; -;  
 DR EMBL; AE007163; AAK47969.1; -;  
 DR PIR; D70806; D70806.  
 DR TIGR; WT3610; -;  
 DR Tuberculist; RV3506; -;  
 DR GO; GO:001674; F:ligase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR000873; AMP-bind.  
 DR Pfam; PF00501; AMP-binding; 1.  
 DR PROSITE; PS00455; AMP\_BINDING; 1.

KM Ligase; Complete proteome.  
 FT CONFLICT 282 282 F -> V (IN REF. 2).  
 SQ SEQUENCE 502 AA; 53738 MW; 0AF9A7B3B9C3A4D CRC64;

Query Match  
 Best Local Similarity 15.6%; Score 7; DB 16; Length 502;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 NEGVPGD 13  
 DB 272 NEGVPGD 278

## RESULT 5

OTWCS  
 ID Q7WC5 PRELIMINARY; PRT; 502 AA.  
 AC Q7WC5;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Possible fatty-acid-CoA synthetase FAD17 (Fatty-acid-CoA synthase)  
 DE (Fatty-acid-CoA ligase) (EC 6.2.1.-).  
 GN FAD17 OR MB3536.  
 OS Mycobacterium bovis.  
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1765;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AF2122/97;  
 RX MEDLINE=22709107; PubMed=12788972;  
 RA Garnier T., Eglmeier K., Camus J.-C., Medina N., Mansoor H.,  
 RA Fryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,  
 RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,  
 RA Parhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.,  
 RT "The complete genome sequence of Mycobacterium bovis."  
 RT Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).  
 RU EMBL; BX248346; CAD5722.1;  
 KW Ligase; Complete proteome.  
 SQ SEQUENCE 502 AA; 53738 MW; 0AF9A7B3B9C3A4D CRC64;

Query Match  
 Best Local Similarity 15.6%; Score 7; DB 16; Length 502;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NEGVPGD 13  
 DB 272 NEGVPGD 278

## RESULT 6

ID Q26125 PRELIMINARY; PRT; 758 AA.  
 AC Q26125;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Microneme protein-1 (Fragment).  
 OS Plasmodium vivax.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5855;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ENG 50;  
 RX MEDLINE=95048797; PubMed=7960140;  
 RA Tsudoi T., Kappe S.H., al-Yaman F., Prickett M.D., Alpers M.,  
 RA Adams J.H.,  
 RT "Natural variation within the principal adhesion domain of the  
 RT Plasmodium vivax Duffy binding protein."  
 RT Infect. Immun. 62:5581-5586(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ENG 50;

RX MEDLINE=91187056; PubMed=1849231;  
 RA Pang X.D., Kaslow D.C., Adams J.H., Miller L.H.,  
 RT "Cloning of the Plasmodium vivax Duffy receptor."  
 RT Mol. Biochem. Parasitol. 44:125-132(1991).  
 DR EMBL; U10103; AAA61633.1;  
 DR InterPro; IPR008602; Duffy\_binding.  
 DR Pfam; PF05424; Duffy\_binding; 1.  
 FT NON\_TER 1  
 FT NON\_TER 758  
 SQ SEQUENCE 758 AA; 83869 MW; 7580C5D047271CA9 CRC64;

Query Match  
 Best Local Similarity 15.6%; Score 7; DB 5; Length 758;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VPQDSTR 16  
 DB 307 VPQDSTR 313

## RESULT 7

ID Q26128 PRELIMINARY; PRT; 759 AA.  
 AC Q26128;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Microneme protein-1 (Fragment).  
 OS Plasmodium vivax.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5855;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ENG 50;  
 RX MEDLINE=95048797; PubMed=7960140;  
 RA Tsudoi T., Kappe S.H., al-Yaman F., Prickett M.D., Alpers M.,  
 RA Adams J.H.,  
 RT "Natural variation within the principal adhesion domain of the  
 RT Plasmodium vivax Duffy binding protein."  
 RT Infect. Immun. 62:5581-5586(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ENG 50;  
 RX MEDLINE=91187056; PubMed=1849231;  
 RA Pang X.D., Kaslow D.C., Adams J.H., Miller L.H.,  
 RT "Cloning of the Plasmodium vivax Duffy receptor."  
 RT Mol. Biochem. Parasitol. 44:125-132(1991).  
 DR EMBL; U10106; AAA61636.1;  
 DR InterPro; IPR008602; Duffy\_binding.  
 DR Pfam; PF05424; Duffy\_binding; 1.  
 FT NON\_TER 1  
 FT NON\_TER 759  
 SQ SEQUENCE 759 AA; 83900 MW; F61BBE94F577640 CRC64;

Query Match  
 Best Local Similarity 15.6%; Score 7; DB 5; Length 759;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VPQDSTR 16  
 DB 306 VPQDSTR 312

## RESULT 8

ID Q9TXA3 PRELIMINARY; PRT; 40 AA.  
 AC Q9TXA3;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE GTP-1 protein (Fragment).  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditiidae; Peloderinae; Caenorhabditis.  
 NCBI\_Taxid=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=93091267; PubMed=1457827;  
 RA Kodyanski V., Maine E.M., Kimble J.,  
 RT "Molecular basis of loss-of-function mutations in the gfp-1 gene of  
 Caenorhabditis elegans."  
 RL Mol. Biol. Cell 3:1199-1213 (1992).  
 DR GO; GO:0016020; P:cell differentiation; IEA.  
 DR GO; GO:0030154; P:cell differentiation; IEA.  
 DR InterPro; IPR000800; Notch\_dom.  
 DR Pfam; PF00066; notch; 1.  
 DR SMART; SM00004; NU; 1.  
 SQ SEQUENCE 40 AA; 4357 MW; E71837429A62B680 CRC64;

Query Match 13.3%; Score 6; DB 5; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 RKCMDL 21  
 Db 4 RKCMDL 9

RESULT 9  
 ID Q95S81 PRELIMINARY; PRT; 83 AA.

AC Q95S81;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE GM06310P.  
 GN BCDNA:GM06310.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscordera;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Steadton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise R., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuno J., Paclio J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.,  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY060920; AAL28468.1;  
 DR FlyBase; FBgn0047271; BCDNA:GM06310.  
 SQ SEQUENCE 83 AA; 9157 MW; 0C4D47380D6B4846 CRC64;

Query Match 13.3%; Score 6; DB 5; Length 83;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 NSEWOT 34  
 Db 33 NSEWOT 38

RESULT 10  
 ID Q8XW65 PRELIMINARY; PRT; 96 AA.

AC Q8XW65;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Putative transcription regulator protein.  
 GN RSC610 OR RS00859.  
 OS Ralstonia solanacearum (Pseudomonas solanacearum).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Burkholderiaceae; Ralstonia.  
 NCBI\_Taxid=305;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GM11000;  
 RM MEDLINE=21681879; PubMed=11823852;  
 RA Salanoubat M., Genin S., Attiguenave F., Gouzy J., Mangenot S.,  
 RA Ariat M., Billault A., Broctier P., Camus J.C., Cattolico L.,  
 RA Chardier M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,  
 RA Gaspin C., Lavie W., Moisan A., Robert C., Saurin W., Schlex T.,  
 RA Sigler P., Thebaud P., Whalen M., Winkler P., Levy M.,  
 RA Weissenbach J., Boucher C.A.,  
 RT Genome sequence of the plant pathogen Ralstonia solanacearum."  
 RL Nature 415:497-502 (2002).  
 DR EMBL; AL646071; CAD16317.1;  
 DR GO; GO:0006677; F:DNA binding; IEA.  
 DR InterPro; IPR013877; HTH\_3.  
 DR Pfam; PF01381; HTH\_3; 1.  
 DR SMART; SM00530; HTH\_XRE; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 96 AA; 10597 MW; BD977C3AB0AD9A47 CRC64;

Query Match 13.3%; Score 6; DB 16; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GDSTRK 17  
 Db 70 GDSTRK 75

RESULT 11  
 ID Q7YVY3 PRELIMINARY; PRT; 97 AA.

AC Q7YVY3;  
 DT 01-OCT-2003 (TREMBlrel. 25, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Hypothetical protein K09C8.7.  
 GN K09C8.7.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiidae; Rhabditoidea;  
 OC Rhabditiidae; Peloderinae; Caenorhabditis.  
 OC NCBI\_Taxid=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=Bristol N2;  
 RC MEDLINE=99069613; PubMed=9851916;  
 RX none.  
 RA none.  
 RT "Genome sequence of the nematode C. elegans: A platform for  
 investigating biology."  
 RL Science 282:2012-2018 (1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=Bristol N2;  
 RC Kerstew J.K.,  
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z68006; CAE17869.1;  
 DR Hypothetical protein; Metalloprotease; Peroxidase.  
 KW Hypothetical protein; Metalloprotease; Peroxidase.  
 SQ SEQUENCE 97 AA; 10874 MW; E403BC9B7FCA0D7F CRC64;

Query Match 13.3%; Score 6; DB 5; Length 97;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TRKCMD 20  
 Db 65 TRKCMD 70

RESULT 12  
 ID Q52097 PRELIMINARY; PRT; 105 AA.  
 AC Q52097;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE ORF (Fragment).  
 OS Pseudomonas putida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 CC Pseudomonadaceae; Pseudomonas.  
 NCBI\_TaxId=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ICR3460;  
 RX MEDLINE=96172583; PubMed=8586629;  
 RA Inoue H., Inagaki K., Sugimoto M., Sakai N., Soda K., Tanaka H.;  
 RT "Structural analysis of the L-methionine gamma-lyase gene from  
 Pseudomonas putida.";  
 RL J. Biochem. 117:1120-1125 (1996).  
 DR EMBL; D88554; BAA13643.1; -;  
 DR PIR; PC4046; PC4046.  
 DR HSSP; P06358; 118A.  
 FT NON TER  
 SQ SEQUENCE 105 AA; 11575 MW; 294E908303B579C2 CRC64;  
 QY  
 Db 9 GVPGDS 14  
 12 GVPGDS 17  
 RESULT 13  
 ID 088AB7 PRELIMINARY; PRT; 143 AA.  
 AC 088AB7;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DE Hypothetical protein.  
 GN PSPPO0475.  
 OS Pseudomonas syringae (pv. tomato).  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 CC Pseudomonadaceae; Pseudomonas.  
 NCBI\_TaxId=323;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DC3000;  
 RA Buell R., Joeris V., Khouri H., Fedorova N., Tran B., Russell D.,  
 RA Berry K., Utechtack T., Van Aken S., Feldblyum T., Gwin M.,  
 RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,  
 RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidson T.,  
 RA White O., Fraser C., Collier A.;  
 RT "Complete sequence of Pseudomonas syringae.";  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF016957; A054019.1; -;  
 DR TIGR; PSPPO0475; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 143 AA; 16031 MW; 30BD418D955F43C CRC64;  
 QY  
 Db 6 PNEGVP 11  
 68 PNEGVP 73  
 Query Match 13.3%; Score 6; DB 16; Length 143;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 14  
 ID 086DB9 PRELIMINARY; PRT; 146 AA.  
 AC 086DB9;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Putative gland protein G24A12.  
 OS Heterodera glycines (Soybean cyst nematode).  
 OC Nematoda; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchima;  
 CC Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.  
 NCBI\_TaxId=51029;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Gao B., Maier T., Allen R., Davis E.L., Baum T.J., Huesey R.S.;  
 RT "A comprehensive profile of putative parasitism genes expressed in the  
 esophageal gland cells of the soybean cyst nematode, Heterodera  
 glycines.";  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF500034; AAP30773.1; -;  
 SQ SEQUENCE 146 AA; 14992 MW; D6D7AB455AD1C61C CRC64;  
 QY  
 Db 29 NSEWOT 34  
 84 NSEWOT 89  
 Query Match 13.3%; Score 6; DB 5; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 15  
 ID 09CIQ2 PRELIMINARY; PRT; 160 AA.  
 AC 09CIQ2;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Thiol peroxidase (1.11.1.1).  
 GN TPX OR L0304.  
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
 CC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.  
 NCBI\_TaxId=1360;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LI1403;  
 RX MEDLINE=21235186; PubMed=11337471;  
 RA Bolotin A., Wincker P., Manger S., Jallion O., Malarme K.,  
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;  
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus  
 lactis ssp. lactis LI1403.";  
 RL Genome Res. 11:731-753 (2001).  
 DR EMBL; AB036267; AAK04402.1; -;  
 DR PIR; H86662; H86662.  
 DR GO; GO:0004601; F:peroxidase activity; IEA.  
 DR InterPro; IPR000866; AMP-C-TSA.  
 DR Pfam; PF00578; AMP-C-TSA; 1.  
 KW Peroxidase; Complete proteome.  
 SQ SEQUENCE 160 AA; 17437 MW; B7C788B4585D0AA CRC64;  
 QY  
 Db 20 DLKGNK 25  
 30 DLKGNK 35  
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 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Job time : 37.5645 secs



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OM protein - protein search, using sw model

Run on: March 11, 2004, 18:13:08 ; Search time 29.7581 Seconds  
(without alignments)  
319.305 Million cell updates/sec

Title: US-09-977-406A-88  
Perfect score: 45  
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Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 809742 seqs, 21153259 residues

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Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

Database:

Published Applications AA:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	45	US-09-977-406A-88	Sequence 88, Appl
2	45	100.0	94	US-09-977-406A-1	Sequence 1, Appl
3	45	100.0	94	US-10-291-360-1	Sequence 1, Appl
4	45	100.0	102	US-09-977-406A-2	Sequence 2, Appl
5	45	100.0	102	US-10-291-360-2	Sequence 2, Appl
6	45	100.0	114	US-10-012-896-1003	Sequence 1003, Ap
7	45	100.0	114	US-10-295-823-271	Sequence 271, Ap
8	45	100.0	114	US-10-144-678A-1003	Sequence 1003, Ap
9	45	100.0	114	US-10-294-025-1003	Sequence 1003, Ap
10	45	100.0	114	US-10-291-172-236	Sequence 236, Ap
11	45	100.0	132	US-09-925-300-1027	Sequence 1027, Ap
12	44	97.8	44	US-09-977-406A-87	Sequence 87, Appl
13	43	95.6	43	US-09-977-406A-86	Sequence 86, Appl
14	42	93.3	42	US-09-977-406A-85	Sequence 85, Appl

16	40	88.9	40	US-09-977-406A-83	Sequence 83, Appl
17	39	86.7	39	US-09-977-406A-82	Sequence 82, Appl
18	38	84.4	38	US-09-977-406A-81	Sequence 81, Appl
19	37	82.2	37	US-09-977-406A-80	Sequence 80, Appl
20	36	80.0	36	US-09-977-406A-79	Sequence 79, Appl
21	35	77.8	35	US-09-977-406A-78	Sequence 78, Appl
22	34	75.6	34	US-09-977-406A-77	Sequence 77, Appl
23	33	73.3	33	US-09-977-406A-76	Sequence 76, Appl
24	32	71.1	32	US-09-977-406A-75	Sequence 75, Appl
25	31	68.9	31	US-09-977-406A-74	Sequence 74, Appl
26	30	66.7	30	US-09-977-406A-73	Sequence 73, Appl
27	29	64.4	29	US-09-977-406A-72	Sequence 72, Appl
28	28	62.2	28	US-09-977-406A-71	Sequence 71, Appl
29	27	60.0	27	US-09-977-406A-70	Sequence 70, Appl
30	26	57.8	26	US-09-977-406A-69	Sequence 69, Appl
31	25	55.6	25	US-09-977-406A-68	Sequence 68, Appl
32	24	53.3	24	US-09-977-406A-67	Sequence 67, Appl
33	23	51.1	23	US-09-977-406A-66	Sequence 66, Appl
34	22	48.9	22	US-09-977-406A-65	Sequence 65, Appl
35	21	46.7	21	US-09-977-406A-64	Sequence 64, Appl
36	20	44.4	20	US-09-977-406A-63	Sequence 63, Appl
37	19	42.2	19	US-09-977-406A-62	Sequence 62, Appl
38	18	40.0	18	US-09-977-406A-61	Sequence 61, Appl
39	17	37.8	17	US-09-977-406A-60	Sequence 60, Appl
40	16	35.6	16	US-09-977-406A-59	Sequence 59, Appl
41	15	33.3	15	US-09-977-406A-58	Sequence 58, Appl
42	14	31.1	14	US-09-977-406A-57	Sequence 57, Appl
43	13	28.9	13	US-09-977-406A-56	Sequence 56, Appl
44	12	26.7	12	US-09-977-406A-55	Sequence 55, Appl
45	11	24.4	11	US-09-977-406A-54	Sequence 54, Appl

#### ALIGNMENTS

RESULT 1  
US-09-977-406A-88  
; Sequence 88, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCTON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 88  
; LENGTH: 45  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rhPSP94 sequence (polypeptide analog)  
US-09-977-406A-88

Query Match  
Best Local Similarity 100.0%  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 SCYFIPNEGVPDSTRKCMDLKGNKRPINSEWQDNCETCTCYET 45  
US-09-977-406A-1  
; Sequence 1, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:

APPLICANT: PROCTON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 94  
TYPE: PRT  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
AUTHORS: Uvsvack, M., Lindstrom, C., Weiber, H., Abrahamson, P.A., Lilja, H., and  
AUTHORS: Lundwall, A.  
TITLE: Molecular cloning of a small prostate protein, known as beta-  
TITLE: microsemoprotein, PSP4 or beta-inhibin, and demonstration of transcripts  
TITLE: non-genital tissues.  
JOURNAL: Biochem. Biophys. Res Commun.  
VOLUME: 164  
ISSUE: 3  
PAGES: 1310-1315  
DATE: 1989  
DATABASE ACCESSION NUMBER: GI 131436  
DATABASE ENTRY DATE: 1988-08-01  
US-09-977-406A-1

Query Match 100.0%; Score 45; DB 10; Length 94;  
Best Local Similarity 100.0%; Pred. No. 3.6e-41;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNKGVPDSTKCMCLKGNKHPINSEWQTDNCECTCYET 45  
DB 1 SCYFIPNKGVPDSTKCMCLKGNKHPINSEWQTDNCECTCYET 45

RESULT 3  
US-10-291-360-1  
Sequence 1, Application US/10291360  
Publication No. US20030119744A1  
GENERAL INFORMATION:  
APPLICANT: PROCTON BIOPHARMA INC.  
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis  
FILE REFERENCE: 06508-051-US-02  
CURRENT APPLICATION NUMBER: US/10/291,360  
CURRENT FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: CA 2,361,736  
PRIOR FILING DATE: 2001-11-08  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 94  
TYPE: PRT  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
AUTHORS: Uvsvack, M., Lindstrom, C., Weiber, H., Abrahamson, P.A., Lilja, H., and  
AUTHORS: Lundwall, A.  
TITLE: Molecular cloning of a small prostate protein, known as beta-  
TITLE: microsemoprotein, PSP4 or beta-inhibin, and demonstration of transcripts  
TITLE: non-genital tissues.  
JOURNAL: Biochem. Biophys. Res Commun.  
VOLUME: 164  
ISSUE: 3  
PAGES: 1310-1315  
DATE: 1989  
DATABASE ACCESSION NUMBER: GI 131436  
DATABASE ENTRY DATE: 1988-08-01  
US-10-291-360-1

Query Match 100.0%; Score 45; DB 14; Length 94;

Best Local Similarity 100.0%; Pred. No. 3.6e-41;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNKGVPDSTKCMCLKGNKHPINSEWQTDNCECTCYET 45  
DB 1 SCYFIPNKGVPDSTKCMCLKGNKHPINSEWQTDNCECTCYET 45

RESULT 4  
US-09-977-406A-2  
Sequence 2, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCTON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 102  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: recombinant human PSP4 (rHSP4) produced from yeast  
US-09-977-406A-2

Query Match 100.0%; Score 45; DB 10; Length 102;  
Best Local Similarity 100.0%; Pred. No. 3.8e-41;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNKGVPDSTKCMCLKGNKHPINSEWQTDNCECTCYET 45  
DB 9 SCYFIPNKGVPDSTKCMCLKGNKHPINSEWQTDNCECTCYET 53

RESULT 5  
US-10-291-360-2  
Sequence 2, Application US/10291360  
Publication No. US20030119744A1  
GENERAL INFORMATION:  
APPLICANT: PROCTON BIOPHARMA INC.  
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis  
FILE REFERENCE: 06508-051-US-02  
CURRENT APPLICATION NUMBER: US/10/291,360  
CURRENT FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: CA 2,361,736  
PRIOR FILING DATE: 2001-11-08  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 102  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: recombinant human PSP4 (rHSP4) produced from yeast  
US-10-291-360-2

Query Match 100.0%; Score 45; DB 14; Length 102;  
Best Local Similarity 100.0%; Pred. No. 3.8e-41;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNKGVPDSTKCMCLKGNKHPINSEWQTDNCECTCYET 45  
DB 9 SCYFIPNKGVPDSTKCMCLKGNKHPINSEWQTDNCECTCYET 53

RESULT 6

US-10-012-896-1003

```
/ Sequence 1003, Application US/10012896
/ Publication No. US20020183251A1
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, David C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yugu
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darriek
/ APPLICANT: Li, Samuel X.
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Hepler, William T.
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Hurai, John
/ APPLICANT: McNeill, Patricia D.
/ APPLICANT: Houghton, Raymond L.
/ APPLICANT: Vinals de Bassols, Carlota
/ APPLICANT: Foy, Teresa
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Mantanabe, Yoshihiro
/ APPLICANT: Meagher, Madeleine Joy
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.427C27
/ CURRENT APPLICATION NUMBER: US/10/012.896
/ CURRENT FILING DATE: 2001-12-10
/ NUMBER OF SEQ ID NOS: 1011
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1003
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-012-896-1003
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Query Match 100.0%; Score 45; DB 13; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.2e-41;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 SCYFIPEGVPGDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 45
DB 21 SCYFIPEGVPGDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 65
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RESULT 7

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US-10-205-823-271
/ Sequence 271, Application US/10205823
/ Publication No. US20030108963A1
```

GENERAL INFORMATION:

```
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbacheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Monsey, Angela M.
APPLICANT: Glatz, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Anderson, Dustin
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
/ TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ FILE REFERENCE: MRI-044
/ CURRENT APPLICATION NUMBER: US/10/205.823
/ CURRENT FILING DATE: 2002-07-25
/ PRIOR APPLICATION NUMBER: 60/307,982
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PRIOR FILING DATE: 2001-07-25

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/ PRIOR APPLICATION NUMBER: 60/314,356
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/325,020
/ PRIOR FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: 60/341,746
/ PRIOR FILING DATE: 2001-12-12
/ PRIOR APPLICATION NUMBER: 60/362,158
/ PRIOR FILING DATE: 2002-03-05
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 271
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-205-823-271
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Query Match 100.0%; Score 45; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.2e-41;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SCYFIPEGVPGDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 45
DB 21 SCYFIPEGVPGDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 65
```

RESULT 8

```
US-10-144-678A-1003
/ Sequence 1003, Application US/10144678A
/ Publication No. US20030157089A1
```

GENERAL INFORMATION:

```
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Jennifer L.
APPLICANT: Mitcham, David C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William T.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Foy, Teresa M.
APPLICANT: Matanabe, Yoshihiro
APPLICANT: Deng, Ta
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.427C28
/ CURRENT APPLICATION NUMBER: US/10/144.678A
/ CURRENT FILING DATE: 2002-08-12
/ NUMBER OF SEQ ID NOS: 1033
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1003
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-144-678A-1003
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```
Query Match 100.0%; Score 45; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.2e-41;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SCYFIPEGVPGDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 45
```

Db 21 SCYFIPEGVPGDSTRKCMDLKGKHPINSEWQTDNCECTCYET 65

RESULT 9  
US-10-294-025-1003  
Sequence 1003, Application US/10294025  
Publication No. US20030185830A1

GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Stolk, John A.  
APPLICANT: Kalos, Michael D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C29  
CURRENT APPLICATION NUMBER: US/10/294,025  
CURRENT FILING DATE: 2002-11-12  
NUMBER OF SEQ ID NOS: 1038  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1003  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-294-025-1003

Query Match 100.0%; Score 45; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 4,2e-41;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPEGVPGDSTRKCMDLKGKHPINSEWQTDNCECTCYET 45  
Db 21 SCYFIPEGVPGDSTRKCMDLKGKHPINSEWQTDNCECTCYET 65

RESULT 10  
US-10-291-172-236  
Sequence 236, Application US/10291172  
Publication No. US20030228584A1

GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc  
TITLE OF INVENTION: No. US20030228584A1 Nucleic Acids and Polypeptides  
FILE REFERENCE: 21272-045  
CURRENT APPLICATION NUMBER: US/10/291,172  
CURRENT FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 09/693,267  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 09/665,363  
PRIOR FILING DATE: 2000-09-19  
PRIOR APPLICATION NUMBER: 09/616,847  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 09/596,193  
PRIOR FILING DATE: 2000-06-17  
PRIOR APPLICATION NUMBER: 09/574,454  
PRIOR FILING DATE: 2000-05-19  
PRIOR APPLICATION NUMBER: 09/519,705  
PRIOR FILING DATE: 2000-03-07  
NUMBER OF SEQ ID NOS: 752  
SEQ ID NO 236  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-291-172-236

Query Match 100.0%; Score 45; DB 15; Length 114;  
Best Local Similarity 100.0%; Pred. No. 4,2e-41;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPEGVPGDSTRKCMDLKGKHPINSEWQTDNCECTCYET 45  
Db 21 SCYFIPEGVPGDSTRKCMDLKGKHPINSEWQTDNCECTCYET 65

RESULT 11

US-09-925-300-1027  
Sequence 1027, Application US/09925300  
Patent No. US20020151681A1  
GENERAL INFORMATION:  
APPLICANT: Craig Rosen,  
APPLICANT: Steve Ruben,  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA101  
CURRENT APPLICATION NUMBER: US/09/925,300  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05988  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1890  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1027  
LENGTH: 132  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-925-300-1027

Query Match 100.0%; Score 45; DB 9; Length 132;  
Best Local Similarity 100.0%; Pred. No. 4,8e-41;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPEGVPGDSTRKCMDLKGKHPINSEWQTDNCECTCYET 45  
Db 39 SCYFIPEGVPGDSTRKCMDLKGKHPINSEWQTDNCECTCYET 83

RESULT 12  
US-09-977-406A-87  
Sequence 87, Application US/09977406A  
Publication No. US20030170220A1

GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 87  
LENGTH: 44  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)  
US-09-977-406A-87

Query Match 97.8%; Score 44; DB 10; Length 44;  
Best Local Similarity 100.0%; Pred. No. 2,2e-40;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CYFIPEGVPGDSTRKCMDLKGKHPINSEWQTDNCECTCYET 45  
Db 1 CYFIPEGVPGDSTRKCMDLKGKHPINSEWQTDNCECTCYET 44

RESULT 13  
US-09-977-406A-86  
Sequence 86, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A

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; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406A-86

```

```

Query Match          95.6%; Score 43; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 2,6e-39;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 YFIPNEGVPDSTRKCMCLKGNKHPINSEWQTDNCETCTCYET 45
DB 1 YFIPNEGVPDSTRKCMCLKGNKHPINSEWQTDNCETCTCYET 43

```

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RESULT 14
US-09-977-406A-85
; Sequence 85, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406A-85

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Query Match          93.3%; Score 42; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.1e-38;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 FIPNEGVPDSTRKCMCLKGNKHPINSEWQTDNCETCTCYET 45
DB 1 FIPNEGVPDSTRKCMCLKGNKHPINSEWQTDNCETCTCYET 42

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RESULT 15
US-09-977-406A-84
; Sequence 84, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 84
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406A-84

```

```

Query Match          91.1%; Score 41; DB 10; Length 41;
Best Local Similarity 100.0%; Pred. No. 3.6e-37;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 IPNEGVPDSTRKCMCLKGNKHPINSEWQTDNCETCTCYET 45
DB 1 IPNEGVPDSTRKCMCLKGNKHPINSEWQTDNCETCTCYET 41

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Job time : 30.7581 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2004, 18:05:52 ; Search time 50.5806 Seconds  
(without alignments)  
399.227 Million cell updates/sec

Title: US-09-977-406A-58  
Perfect score: 64  
Sequence: 1 EMTGDMCECTCTCTETISCC.....YIVVEKDDPKTCVSEWII 64

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	12.5	368	16	Q891V1	Q891V1	Clostridium
2	10.9	143	2	Q840A4	Q840A4	listeria mo
3	10.9	143	2	Q840A3	Q840A3	listeria mo
4	10.9	143	2	Q83UB6	Q83UB6	listeria mo
5	10.9	143	2	Q83UT3	Q83UT3	listeria mo
6	10.9	288	5	Q9VH00	Q9VH00	dirosophila
7	10.9	529	2	Q9LSB9	Q9LSB9	listeria mo
8	10.9	848	10	Q9AYE2	Q9AYE2	oryza sativ
9	10.9	1378	10	Q9LTA4	Q9LTA4	arabidopsis
10	9.4	30	12	Q86B18	Q86B18	influenzavi
11	9.4	33	10	Q945D4	Q945D4	castranea sa
12	9.4	43	2	Q8GFS6	Q8GFS6	zymomonas m
13	9.4	50	12	Q80UB6	Q80UB6	influenza a
14	9.4	50	12	Q8JMV5	Q8JMV5	influenza a
15	9.4	66	12	Q82553	Q82553	influenzavi
16	9.4	71	12	Q67237	Q67237	influenzavi

17	6	9.4	71	12	Q67239	Q67239	influenzavi
18	6	9.4	71	12	Q67242	Q67242	influenzavi
19	6	9.4	71	12	Q67234	Q67234	influenzavi
20	6	9.4	71	12	Q67236	Q67236	influenzavi
21	6	9.4	71	12	Q67240	Q67240	influenzavi
22	6	9.4	71	12	Q67241	Q67241	influenzavi
23	6	9.4	71	12	Q67235	Q67235	influenzavi
24	6	9.4	71	12	Q67238	Q67238	influenzavi
25	6	9.4	71	12	Q67243	Q67243	influenzavi
26	6	9.4	71	12	Q67244	Q67244	influenzavi
27	6	9.4	72	12	Q82554	Q82554	influenzavi
28	6	9.4	92	7	Q9VXB1	Q9VXB1	barbus inte
29	6	9.4	92	12	Q91U43	Q91U43	influenza a
30	6	9.4	94	16	Q8EMP4	Q8EMP4	mycoplasma
31	6	9.4	102	12	Q91U47	Q91U47	influenza a
32	6	9.4	102	12	Q91U45	Q91U45	influenza a
33	6	9.4	102	11	Q8C982	Q8C982	mus. musculi
34	6	9.4	110	11	Q91198	Q91198	influenza a
35	6	9.4	110	12	Q91196	Q91196	influenza a
36	6	9.4	110	12	Q911A0	Q911A0	influenza a
37	6	9.4	110	12	Q911A6	Q911A6	influenza a
38	6	9.4	110	12	Q911A4	Q911A4	influenza a
39	6	9.4	110	12	Q91195	Q91195	influenza a
40	6	9.4	110	12	Q911A7	Q911A7	influenza a
41	6	9.4	110	12	Q911A3	Q911A3	influenza a
42	6	9.4	110	12	Q91197	Q91197	influenza a
43	6	9.4	110	12	Q91199	Q91199	influenza a
44	6	9.4	110	12	Q911A5	Q911A5	influenza a
45	6	9.4	110	12	Q911A1	Q911A1	influenza a

## ALIGNMENTS

## RESULT 1

Q891V1

PRELIMINARY;

PRT; 368 AA.

AC Q891V1; Q891V1; PRELIMINARY; PRT; 368 AA.  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Glycosyl transferase (EC 2.4.1.-).  
 GN CTC02262.  
 OS Clostridium tetani.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1513;  
 RX STRAIN=Massachusetts / E88;  
 RX MEDLINE=22457253; PubMed=12552129;  
 RA Bruggemann H., Bauner S., Fricke W.F., Wieser A., Liesegang H.,  
 RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,  
 RA Gottschalk G.;  
 RT "The genome sequence of Clostridium tetani, the causative agent of  
 tetanus disease".  
 RT Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).  
 RL EMBL; A015943; A036744.1; -;  
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . . ; IEA.  
 DR GO; GO:0009058; P:biogenesis; IEA.  
 DR InterPro; IPR001296; Glyco. Trans. 1.  
 DR Pfam; PF00534; Glycos. trans. 1; I.  
 KW Glycosyltransferase; Transferase; Complete proteome.  
 SQ SEQUENCE 368 AA; 42864 MW; E1143720ED1EB7A1 CRC64;

## Query Match

Best Local Similarity 12.5%; Score 8; DB 16; Length 368;  
 Pred. No. 1.9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 KKEDCKYI 46  
 DB 209 KKEDCKYI 216

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RESULT 2
Q840A4 PRELIMINARY; PRT; 143 AA.
AC Q840A4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Listeriolysin O (Fragment).
GN HLXA.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CECT 934;
RA Rodriguez-Lazaro D., Hernandez M., Esteve T., Pla M.;
RT "Development of real-time PCR systems based in Amplifluor and TaqMan
RT technologies for specific quantitative detection of Listeria
RT monocytogenes and Listeria innocua."
RL Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY174659; AAC46017.1; -.
DR GO; GO:0015485; F:cholesterol binding; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001869; Thiol_cytolysin.
DR PRINTS; PRO1400; TACYTOLYSIN.
DR ProDom; PD007062; Thiol_cytolysin; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 15693 MW; 5F01FC159234FE8 CRC64;

Query Match 10.9%; Score 7; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIWEKK 51
DB 98 YIWEKK 104

RESULT 3
Q840A3 PRELIMINARY; PRT; 143 AA.
AC Q840A3;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Listeriolysin O (Fragment).
GN HLXA.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CECT 937;
RA Rodriguez-Lazaro D., Hernandez M., Esteve T., Pla M.;
RT "Development of real-time PCR systems based in Amplifluor and TaqMan
RT technologies for specific quantitative detection of Listeria
RT monocytogenes and Listeria innocua."
RL Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY174662; AAC46020.1; -.
DR GO; GO:0015485; F:cholesterol binding; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR InterPro; IPR001869; Thiol_cytolysin.
DR PRINTS; PRO1400; TACYTOLYSIN.
DR ProDom; PD007062; Thiol_cytolysin; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 15728 MW; 432FAE14DB7F7799 CRC64;

Query Match 10.9%; Score 7; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 45 YIWEKK 51
DB 98 YIWEKK 104

RESULT 4
Q83U86 PRELIMINARY; PRT; 143 AA.
AC Q83U86;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Listeriolysin O (Fragment).
GN HLXA.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CECT 935, CECT 936, CECT 940, CTC 1034, and CECT 4032;
RA Rodriguez-Lazaro D., Hernandez M., Esteve T., Pla M.;
RT "Development of real-time PCR systems based in Amplifluor and TaqMan
RT technologies for specific quantitative detection of Listeria
RT monocytogenes and Listeria innocua."
RL Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY174660; AAC46018.1; -.
DR EMBL; AY174664; AAC46022.1; -.
DR EMBL; AY174667; AAC46025.1; -.
DR EMBL; AY174669; AAC46027.1; -.
DR GO; GO:0015485; F:cholesterol binding; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001869; Thiol_cytolysin.
DR PRINTS; PRO1400; TACYTOLYSIN.
DR ProDom; PD007062; Thiol_cytolysin; 1.
FT NON TER 143
SQ SEQUENCE 143 AA; 15705 MW; 71BD03A20012C5D0 CRC64;

Query Match 10.9%; Score 7; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIWEKK 51
DB 98 YIWEKK 104

RESULT 5
Q83T23 PRELIMINARY; PRT; 143 AA.
AC Q83T23;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Listeriolysin O (Fragment).
GN HLXA.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CECT 911, CECT 932, CECT 938, CTC 1010, CTC 1011, and CECT
RC 4031;
RA Rodriguez-Lazaro D., Hernandez M., Esteve T., Pla M.;
RT "Development of real-time PCR systems based in Amplifluor and TaqMan
RT technologies for specific quantitative detection of Listeria
RT monocytogenes and Listeria innocua."
RL Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY174657; AAC46015.1; -.
DR EMBL; AY174658; AAC46016.1; -.
DR EMBL; AY174663; AAC46021.1; -.

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DR EMBL; AY174665; AA046023.1; -  
 DR EMBL; AY174666; AA046024.1; -  
 DR EMBL; AY174668; AA046026.1; -  
 DR GO; GO:0015485; F:cholesterol binding; IEA.  
 DR GO; GO:0015070; F:coxin activity; IEA.  
 DR GO; GO:0009405; P:patogenesis; IEA.  
 DR InterPro; IPR001869; Thiol\_cytolysin.  
 DR PRINTS; PR01400; TACTOLYSIN.  
 DR ProDom; PD007062; Thiol\_cytolysin; 1.  
 FT NON TER 143 143  
 SQ SEQUENCE 143 AA; 15679 MW; 90CBDFD3C9244FF8 CRC64;

Query Match 10.9%; Score 7; DB 2; Length 143;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIVVEKK 51  
 Db 98 YIVVEKK 104

RESULT 6  
 Q9VH00 PRELIMINARY; PRT; 288 AA.  
 AC Q9VH00;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE CG12818 protein.  
 GN CG12818  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCB1\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20136006; PubMed=10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang X., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA War K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-U., Andrews-Plannkoch C., Baldwin D.,  
 RA Ballew R.M., Baau A., Bakendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cateley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Palcos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser X.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ileguam C.,  
 RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kesterson J.A., Ketchum K.A.,  
 RA Kamei B.E., Kodira C.D., Kraat C., Kravitz S., Kulp D., Lai Z.,  
 RA Liao X., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mohrson D.,  
 RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Mostreft A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazcolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Snie B.C., Sinden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E.H., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RA "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195 (2000).  
 DR EMBL; AE003686; AAF54521.1; -  
 DR FlyBase; FBgn0037809; CG12818.  
 SQ SEQUENCE 288 AA; 33386 MW; 821B776FF7E126C2 CRC64;

Query Match 10.9%; Score 7; DB 5; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 EKKDPKK 55  
 Db 168 EKKDPKK 174

RESULT 7  
 Q9LSB9 PRELIMINARY; PRT; 529 AA.  
 AC Q9LSB9;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Listeriolysin O.  
 GN HLVA.  
 OS Listeria monocytogenes.  
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.  
 OC NCB1\_TaxID=1639;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 9525;  
 RA Giammarini C., Andreoni F., Amagliani G., Magnani M.,  
 RA "Expression in E. coli and sequence analysis of the listeriolysin O  
 (hlyA) gene of Listeria monocytogenes";  
 RL Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF253320; AAF64524.1; -  
 DR HSP; P13995; IPR0.  
 DR GO; GO:0015485; F:cholesterol binding; IEA.  
 DR GO; GO:0015070; F:toxin activity; IEA.  
 DR GO; GO:0009405; P:patogenesis; IEA.  
 DR InterPro; IPR001869; Thiol\_cytolysin.  
 DR Pfam; PF01289; Thiol\_cytolysin; 1.  
 DR PRINTS; PR01400; TACTOLYSIN.  
 DR ProDom; PD007062; Thiol\_cytolysin; 1.  
 DR PROSITE; PS00481; THIOL\_CYTOLYSINS; 1.  
 SQ SEQUENCE 529 AA; 58755 MW; 897041D9ED8D0D4D CRC64;

Query Match 10.9%; Score 7; DB 2; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIVVEKK 51  
 Db 98 YIVVEKK 104

RESULT 8  
 Q9AYE2 PRELIMINARY; PRT; 848 AA.  
 AC Q9AYE2;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN OSJNB0003623.16.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 NC NCB1\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=cv. Nipponbare;  
 RA Buehl C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,  
 RA Zisman V., Pai G., Bowman C.L., Fujii C.Y., Vankken S.E.,  
 RA Bowman C.L., Craven B., Uterback T.R., Khaliq H., Feldblum T.V.,  
 RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;  
 RT "Oryza sativa chromosome 3 BAC OSUNBA003G23 genomic sequence."  
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC079736; AAK00966.1; -  
 DR Gramene; Q9AYE2; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 848 AA; 93068 MW; 36166A59E62723F6 CRC64;

Query Match 10.9%; Score 7; DB 10; Length 848;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 DMCORIF 38  
 DB 606 DMCORIF 612

RESULT 9  
 O9LTA4 PRELIMINARY; PRT; 1378 AA.  
 ID O9LTA4  
 AC O9LTA4  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE Gb|AAC49734.1.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 ON NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Columbia;  
 RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI";  
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB025613; BAA98156.1; -  
 SQ SEQUENCE 1378 AA; 156840 MW; AF8D028F0F4E865E CRC64;

Query Match 10.9%; Score 7; DB 10; Length 1378;  
 Best Local Similarity 100.0%; Pred. No. 72;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 DMCORIF 38  
 DB 469 DMCORIF 475

RESULT 10  
 ID O86818 PRELIMINARY; PRT; 30 AA.  
 AC O86818;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Hemagglutinin (Fragment).  
 GN HA-NP.  
 OS Influenzavirus A.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza A viruses.  
 CC NCBI\_TaxID=197911;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 MEDLINE=94378528; PubMed=8091560;  
 RA Orlich M., Gottwald H., Rott R.;  
 RT "Nonhomologous recombination between the hemagglutinin gene and the  
 RT nucleoprotein gene of an influenza virus."  
 RL Virology 204:462-465(1994).

DR EMBL; S73497; AAB31976.1; -  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR002141; F1u\_NP.  
 DR Pfam; PF00506; F1u\_NP; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 30 AA; 3329 MW; B96AACAT015A78DE CRC64;

Query Match 9.4%; Score 6; DB 12; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 KDPKKT 56  
 DB 13 KDPKKT 18

RESULT 11  
 O94SD4 PRELIMINARY; PRT; 33 AA.  
 ID O94SD4  
 AC O94SD4  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Translation elongation factor 1 alpha-like protein (Fragment).  
 OS Castanea sativa (Sweet chestnut).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Fagales; Fagaceae; Castanea.  
 ON NCBI\_TaxID=21020;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Schafleitner R., Wilhelm E.;  
 RT "Wound-responsive genes of chestnut";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF417301; AAL15889.1; -  
 DR GO; GO:0003746; F:translation elongation factor activity; IEA.  
 KW Elongation factor.  
 FT NON\_TER 1  
 SQ SEQUENCE 33 AA; 3393 MW; 6C3B7346A23E1A8 CRC64;

Query Match 9.4%; Score 6; DB 10; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 48 VEKXDP 53  
 DB 15 VEKXDP 20

RESULT 12  
 O8GF56 PRELIMINARY; PRT; 43 AA.  
 ID O8GF56  
 AC O8GF56;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Hypothetical protein.  
 OS Zymomonas mobilis.  
 OG Plasmid 1.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;  
 OC Sphingomonadaceae; Zymomonas.  
 ON NCBI\_TaxID=542;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ZM4;  
 RA Seo J., Park H., Kim H., Wang K., Yoon K., Rhee H., Kang J., Jung C.,  
 RA Kim M., Park C., An Y., Choi E.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY057845; AAL36112.1; -  
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
 KW Hypothetical protein; Plasmid.  
 SQ SEQUENCE 43 AA; 4726 MW; 57059E16BCEC2DF CRC64;

Query Match 9.4%; Score 6; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 KTCVS 60  
13 KTCVS 18

## RESULT 13

080JB6 PRELIMINARY; PRT; 50 AA.  
AC 080JB6;  
DT 01-JUN-2003 (TRENBLREL. 24, Created)  
DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)  
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)  
DE Nucleoprotein (Fragment).  
OS Influenza A virus (A/Cinnamon Teal/1/1916).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza A viruses; Influenzavirus A.  
OX NCBI\_TaxID=224211;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/Cinnamon Teal/1/1916;  
RA Reid A.H., Fanning T.G., Slemmons R.D., Janczewski T.A., Dean J.,  
RT Taubenberger J.K.;  
RT "Relationship of Pre-1918 Avian Influenza HA and NP Sequences to  
Subsequent Avian Influenza Strains.";  
RL Avian Dis. 0:0-0(2003).  
DR EMBL; AY220475; AAC62906.1; -  
DR GO; GO:0019013; C:Viral nucleocapsid; IEA.  
KM Nucleocapsid. 1  
FT NON\_TER 1  
FT SEQUENCE 50 AA; 5823 MW; D8FEBF46C75DBD59 CRC64;  
SQ  
Query Match 9.4%; Score 6; DB 12; Length 50;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 51 KDPKKT 56  
38 KDPKKT 43  
Db  
RESULT 14  
080JMV5 PRELIMINARY; PRT; 50 AA.  
AC 080JMV5;  
DT 01-OCT-2002 (TRENBLREL. 22, Created)  
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)  
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)  
DE Nucleoprotein (Fragment).  
GN NP  
OS Influenza A virus (A/Brant Goose/1/1917(H1N1)).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza A viruses; Influenzavirus A.  
OX NCBI\_TaxID=194387;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/Brant Goose/1/1917;  
RX MEDLINE=22092538; PubMed=12097598;  
RA Fanning T.G., Slemmons R.D., Reid A.H., Janczewski T.A., Dean J.,  
RT Taubenberger J.K.;  
RT "1917 Avian Influenza Virus Sequences Suggest that the 1918 Pandemic  
Virus Did Not Acquire Its Hemagglutinin Directly from Birds.";  
RL J. Virol. 76:7860-7862(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/Brant Goose/1/1917;  
RA Fanning T.G., Slemmons R.D., Reid A.H., Janczewski T.A., Dean J.,  
RT Taubenberger J.K.;  
RT "Relationship of Pre-1918 Avian Influenza HA and NP Sequences to

RT Subsequent Avian Influenza Strains.";

RL Avian Dis. 0:0-0(2002).  
DR EMBL; AY095228; NAM2279.1; -  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR002141; Flu\_NP.  
DR Pfam; PF00506; Flu\_NP; 1.  
FT NON\_TER 1  
FT NON\_TER 50  
FT SEQUENCE 50 AA; 5823 MW; D8FEBF46C75DBD59 CRC64;  
SQ

Query Match 9.4%; Score 6; DB 12; Length 50;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 KDPKKT 56  
38 KDPKKT 43  
Db

## RESULT 15

082553 PRELIMINARY; PRT; 66 AA.  
AC 082553;  
DT 01-NOV-1996 (TRENBLREL. 01, Created)  
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)  
DE Strain A/WI/4754/94 NP (Fragment).  
GN NP.  
OS Influenzavirus A.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza A viruses.  
OX NCBI\_TaxID=197911;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/WI/4754/94;  
RA Wentworth D.E., McGregor M.W., Macklin M.D., Neumann V., Hinshaw V.S.;  
RT "Transmission of Swine Influenza Virus To Humans After Exposure To  
Experimentally Infected Pigs.";  
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.  
DR EMBL; U53164; AAB03293.1; -  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR002141; Flu\_NP.  
DR Pfam; PF00506; Flu\_NP; 1.  
FT NON\_TER 1  
FT NON\_TER 66  
FT SEQUENCE 66 AA; 7676 MW; 30B359393741F866 CRC64;  
SQ  
Query Match 9.4%; Score 6; DB 12; Length 66;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 51 KDPKKT 56  
5 KDPKKT 10  
Db  
Search completed: March 11, 2004, 18:13:02  
Job time : 52.5806 secs

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Fri Mar 12 09:42:18 2004

us-09-977-406a-58.olig.rapb

Page 1

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OM protein - protein search, using sw model

Run on: March 11, 2004, 18:13:08 ; Search time 42.3226 Seconds  
(without alignments)  
319.305 Million cell updates/sec

Title: US-09-977-406A-58  
Perfect score: 64  
Sequence: 1 EMQTNCECTCYETETISCC.....YIVKXDPKTKTSVSEWII 64

Scoring table: Gapop 60.0, Gapext 60.0

Searched: 809742 seqs, 21153259 residues

Word size : 0

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA:\*  
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2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/prodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/prodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
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17: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	100.0	64	US-09-977-406A-58	Sequence 58, Appl
2	64	100.0	94	US-09-977-406A-1	Sequence 1, Appl
3	64	100.0	94	US-10-291-360-1	Sequence 1, Appl
4	64	100.0	102	US-09-977-406A-2	Sequence 2, Appl
5	64	100.0	102	US-10-291-360-2	Sequence 2, Appl
6	64	100.0	114	US-10-012-896-1003	Sequence 1003, Ap
7	64	100.0	114	US-10-205-823-271	Sequence 271, Ap
8	64	100.0	114	US-10-144-678A-1003	Sequence 1003, Ap
9	64	100.0	114	US-10-294-025-1003	Sequence 1003, Ap
10	64	100.0	114	US-10-294-172-236	Sequence 236, Ap
11	64	100.0	132	US-09-925-300-1027	Sequence 1027, Ap
12	64	98.4	63	US-09-977-406A-57	Sequence 57, Appl
13	62	96.9	62	US-09-977-406A-56	Sequence 56, Appl
14	61	95.3	61	US-09-977-406A-55	Sequence 55, Appl
15	60	93.8	60	US-09-977-406A-54	Sequence 54, Appl

16	59	92.2	59	10	US-09-977-406A-53	Sequence 53, Appl
17	58	90.6	58	10	US-09-977-406A-52	Sequence 52, Appl
18	57	89.1	57	10	US-09-977-406A-51	Sequence 51, Appl
19	56	87.5	56	10	US-09-977-406A-50	Sequence 50, Appl
20	55	85.9	55	10	US-09-977-406A-49	Sequence 49, Appl
21	54	84.4	54	10	US-09-977-406A-48	Sequence 48, Appl
22	53	82.8	53	10	US-09-977-406A-47	Sequence 47, Appl
23	52	81.2	52	10	US-09-977-406A-46	Sequence 46, Appl
24	51	79.7	51	10	US-09-977-406A-45	Sequence 45, Appl
25	50	78.1	50	10	US-09-977-406A-44	Sequence 44, Appl
26	49	76.6	49	10	US-09-977-406A-43	Sequence 43, Appl
27	48	75.0	48	10	US-09-977-406A-42	Sequence 42, Appl
28	47	73.4	47	10	US-09-977-406A-41	Sequence 41, Appl
29	46	71.9	46	10	US-09-977-406A-40	Sequence 40, Appl
30	45	70.3	45	10	US-09-977-406A-39	Sequence 39, Appl
31	44	68.8	44	10	US-09-977-406A-38	Sequence 38, Appl
32	43	67.2	43	10	US-09-977-406A-37	Sequence 37, Appl
33	42	65.6	42	10	US-09-977-406A-36	Sequence 36, Appl
34	41	64.1	41	10	US-09-977-406A-35	Sequence 35, Appl
35	40	62.5	40	10	US-09-977-406A-34	Sequence 34, Appl
36	39	60.9	39	10	US-09-977-406A-33	Sequence 33, Appl
37	38	59.4	38	10	US-09-977-406A-32	Sequence 32, Appl
38	37	57.8	37	10	US-09-977-406A-31	Sequence 31, Appl
39	36	56.2	36	10	US-09-977-406A-30	Sequence 30, Appl
40	35	54.7	35	10	US-09-977-406A-29	Sequence 29, Appl
41	34	53.1	34	10	US-09-977-406A-28	Sequence 28, Appl
42	33	51.6	33	10	US-09-977-406A-27	Sequence 27, Appl
43	32	50.0	32	10	US-09-977-406A-26	Sequence 26, Appl
44	31	48.4	31	10	US-09-977-406A-25	Sequence 25, Appl
45	30	46.9	30	10	US-09-977-406A-24	Sequence 24, Appl

#### ALIGNMENTS

RESULT 1  
US-09-977-406A-58  
Sequence 58, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCTON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 58  
LENGTH: 64  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-58

Query Match 100.0%; Score 64; DB 10; Length 64;  
Best Local Similarity 100.0%; Pred. No. 5.9e-59;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQTNCECTCYETETISCCITVSTPVGYDKNCCRIFFKEDCKYIVKXDPKTKTSV 60  
DB 1 EMQTNCECTCYETETISCCITVSTPVGYDKNCCRIFFKEDCKYIVKXDPKTKTSV 60

QY 61 EWTI 64  
DB 61 EWTI 64

RESULT 2

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US-09-977-406A-1
; Sequence 1, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Urvashak, M., Lindstrom, C., Weiber, H., Abrahamson, P.A., Lilja, H., and
; AUTHORS: Lundwall, A.
; TITLE: Molecular cloning of a small prostate protein, known as beta-
; TITLE: microsemoprotein, PSP94 or beta-inhibin, and demonstration of transcripts
; JOURNAL: Biochem. Biophys. Res Commun.
; VOLUME: 164
; ISSUE: 3
; PAGES: 1310-1315
; DATE: 1989
; DATABASE ACCESSION NUMBER: GI 131436
; DATABASE ENTRY DATE: 1988-08-01
US-09-977-406A-1

Query Match
Best Local Similarity 100.0%; Score 64; DB 10; Length 94;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKKTCSVS 60
Db 31 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKKTCSVS 90
Qy 61 EMII 64
Db 91 EMII 94

RESULT 3
US-10-291-360-1
; Sequence 1, Application US/10291360
; Publication No. US20030119744A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis
; FILE REFERENCE: 06508-051-US-02
; CURRENT APPLICATION NUMBER: US/10/291,360
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: CA 2,361,736
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Urvashak, M., Lindstrom, C., Weiber, H., Abrahamson, P.A., Lilja, H., and
; AUTHORS: Lundwall, A.
; TITLE: Molecular cloning of a small prostate protein, known as beta-
; TITLE: microsemoprotein, PSP94 or beta-inhibin, and demonstration of transcripts
; JOURNAL: Biochem. Biophys. Res Commun.
; VOLUME: 164

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; ISSUE: 3
; PAGES: 1310-1315
; DATE: 1989
; DATABASE ACCESSION NUMBER: GI 131436
; DATABASE ENTRY DATE: 1988-08-01
US-10-291-360-1

Query Match
Best Local Similarity 100.0%; Score 64; DB 14; Length 94;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 31 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKKTCSVS 90
Qy 61 EMII 64
Db 91 EMII 94

RESULT 4
US-09-977-406A-2
; Sequence 2, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: recombinant human PSP94 (rhPSP94) produced from yeast
US-09-977-406A-2

Query Match
Best Local Similarity 100.0%; Score 64; DB 10; Length 102;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKKTCSVS 60
Db 39 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKKTCSVS 98
Qy 61 EMII 64
Db 99 EMII 102

RESULT 5
US-10-291-360-2
; Sequence 2, Application US/10291360
; Publication No. US20030119744A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis
; FILE REFERENCE: 06508-051-US-02
; CURRENT APPLICATION NUMBER: US/10/291,360
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: CA 2,361,736
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 102

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TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: recombinant human PSP94 (rHSP94) produced from yeast  
 US-10-291-360-2

Query Match 100.0%; Score 64; DB 14; Length 102;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-59;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 39 EMQTDNCETCTCYETEISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKKTCSVS 98  
 QY 61 EWII 64  
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 DB 99 EWII 102

RESULT 6  
 US-10-012-896-1003  
 Sequence 1003, Application US/10012896  
 Publication No. US20020183251A1  
 GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
 APPLICANT: Dillon, Davin C.  
 APPLICANT: Mitcham, Jennifer L.  
 APPLICANT: Harlocker, Susan L.  
 APPLICANT: Jiang, Yugu  
 APPLICANT: Kalos, Michael D.  
 APPLICANT: Retter, Marc W.  
 APPLICANT: Stolk, John A.  
 APPLICANT: Day, Craig H.  
 APPLICANT: Vedvick, Thomas S.  
 APPLICANT: Carter, Derrick  
 APPLICANT: Li, Samuel X.  
 APPLICANT: Wang, Aljun  
 APPLICANT: Skeiky, Yasir A.W.  
 APPLICANT: Hepler, William T.  
 APPLICANT: Henderson, Robert A.  
 APPLICANT: Hural, John  
 APPLICANT: McNeill, Patricia D.  
 APPLICANT: Houghlon, Raymond L.  
 APPLICANT: Vinals de Bassols, Carlota  
 APPLICANT: Foy, Teresa  
 APPLICANT: Fanger, Gary R.  
 APPLICANT: Mantanabe, Yoshihiro  
 APPLICANT: Mesgher, Madeleine Joy  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 FILE REFERENCE: 210121.427C27  
 CURRENT APPLICATION NUMBER: US/10/012.896  
 CURRENT FILING DATE: 2001-12-10  
 NUMBER OF SEQ ID NOS: 1011  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 1003  
 LENGTH: 114  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-012-896-1003

Query Match 100.0%; Score 64; DB 13; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-59;  
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 QY 61 EWII 64  
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 DB 111 EWII 114

RESULT 7  
 US-10-205-823-271

Sequence 271, Application US/10205823  
 Publication No. US20030108963A1  
 GENERAL INFORMATION:

APPLICANT: Schlegel, Robert  
 APPLICANT: Monahan, John E.  
 APPLICANT: Endege, Wilson O.  
 APPLICANT: Gannavarapu, Manjula  
 APPLICANT: Gorbacheva, Bella  
 APPLICANT: Hoersch, Sebastian  
 APPLICANT: Kamatkar, Shubhangi  
 APPLICANT: Monsey, Angela M.  
 APPLICANT: Glatz, Karen  
 APPLICANT: Zhao, Xumei

APPLICANT: Anderson, Dustin  
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
 TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 TITLE OF INVENTION: THERAPY OF PROSTATE CANCER  
 FILE REFERENCE: MRI-044

CURRENT APPLICATION NUMBER: US/10/205.823  
 CURRENT FILING DATE: 2002-07-25  
 PRIOR APPLICATION NUMBER: 60/307,982  
 PRIOR FILING DATE: 2001-07-25  
 PRIOR APPLICATION NUMBER: 60/314,356  
 PRIOR FILING DATE: 2001-08-22  
 PRIOR APPLICATION NUMBER: 60/325,020  
 PRIOR FILING DATE: 2001-09-25  
 PRIOR APPLICATION NUMBER: 60/341,746  
 PRIOR FILING DATE: 2001-12-12  
 PRIOR APPLICATION NUMBER: 60/362,158  
 PRIOR FILING DATE: 2002-03-05  
 NUMBER OF SEQ ID NOS: 455  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 271  
 LENGTH: 114  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-205-823-271

Query Match 100.0%; Score 64; DB 14; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-59;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQTDNCETCTCYETEISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKKTCSVS 60  
 |||||  
 DB 51 EMQTDNCETCTCYETEISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKKTCSVS 110  
 QY 61 EWII 64  
 |||||  
 DB 111 EWII 114

RESULT 8

US-10-144-678A-1003

Sequence 1003, Application US/10144678A  
 Publication No. US20030157089A1  
 GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
 APPLICANT: Dillon, Davin C.  
 APPLICANT: Mitcham, Jennifer L.  
 APPLICANT: Harlocker, Susan L.  
 APPLICANT: Jiang, Yugu  
 APPLICANT: Henderson, Robert A.  
 APPLICANT: Fanger, Gary R.  
 APPLICANT: Kalos, Michael D.  
 APPLICANT: Retter, Marc W.  
 APPLICANT: Stolk, John A.  
 APPLICANT: Day, Craig H.  
 APPLICANT: Vedvick, Thomas S.  
 APPLICANT: Carter, Derrick  
 APPLICANT: Li, Samuel X.

APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A. W.  
APPLICANT: Hepler, William T.  
APPLICANT: Hural, John  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Vinals Y de Bassols, Carleca  
APPLICANT: Foy, Teresa M.  
APPLICANT: Matanabe, Yoshihiro  
APPLICANT: Deng, Ta  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C28  
CURRENT APPLICATION NUMBER: US/10/44,678A  
CURRENT FILING DATE: 2002-08-12  
NUMBER OF SEQ ID NOS: 1033  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1003  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-144-678A-1003

Query Match 100.0%; Score 64; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 9.9e-59;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60  
DB 51 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 110  
CY 61 EWII 64  
DB 111 EWII 114

RESULT 9  
US-10-294-025-1003  
Sequence 1003, Application US/10294025  
Publication No. US20030185830A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Katos, Michael D.  
APPLICANT: Stol, John A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C29  
CURRENT APPLICATION NUMBER: US/10/294,025  
CURRENT FILING DATE: 2002-11-12  
NUMBER OF SEQ ID NOS: 1038  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1003  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-294-025-1003

Query Match 100.0%; Score 64; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 9.9e-59;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60  
DB 51 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 110  
CY 61 EWII 64  
DB 111 EWII 114

RESULT 10  
US-10-291-172-236  
Sequence 236, Application US/10291172

Publication No. US20030228584A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc  
TITLE OF INVENTION: No. US20030228584A1 Nucleic Acids and Polypeptides  
FILE REFERENCE: 21272-045  
CURRENT APPLICATION NUMBER: US/10/291,172  
CURRENT FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 09/693,267  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 09/665,363  
PRIOR FILING DATE: 2000-09-19  
PRIOR APPLICATION NUMBER: 09/616,847  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 09/596,193  
PRIOR FILING DATE: 2000-06-17  
PRIOR APPLICATION NUMBER: 09/574,454  
PRIOR FILING DATE: 2000-05-19  
PRIOR APPLICATION NUMBER: 09/519,705  
PRIOR FILING DATE: 2000-03-07  
NUMBER OF SEQ ID NOS: 752  
SEQ ID NO 236  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-291-172-236

Query Match 100.0%; Score 64; DB 15; Length 114;  
Best Local Similarity 100.0%; Pred. No. 9.9e-59;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60  
DB 51 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 110  
CY 61 EWII 64  
DB 111 EWII 114

RESULT 11  
US-09-925-300-1027  
Sequence 1027, Application US/09925300  
Patent No. US20020151681A1  
GENERAL INFORMATION:  
APPLICANT: Craig Rosen,  
APPLICANT: Steve Ruben  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA101  
CURRENT APPLICATION NUMBER: US/09/925,300  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05988  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1890  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1027  
LENGTH: 132  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-925-300-1027

Query Match 100.0%; Score 64; DB 9; Length 132;  
Best Local Similarity 100.0%; Pred. No. 1.1e-58;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60  
DB 69 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 128  
CY 61 EWII 64  
DB 129 EWII 132



## RESULT 12

US-09-977-406A-57  
; Sequence 57, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCTON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 57  
; LENGTH: 63  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-57

## Query Match

Best Local Similarity 98.4%; Score 63; DB 10; Length 63;  
Best Local Similarity 100.0%; Pred. No. 6.3e-58;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKDPKKTCSVS 60  
DB 1 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKDPKKTCSVS 60

QY 61 EWI 63  
DB 61 EWI 63

## RESULT 13

US-09-977-406A-56  
; Sequence 56, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCTON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 56  
; LENGTH: 62  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-56

Query Match 96.9%; Score 62; DB 10; Length 62;  
Best Local Similarity 100.0%; Pred. No. 6.8e-57;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKDPKKTCSVS 60  
DB 1 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKDPKKTCSVS 60

QY 61 EW 62  
DB 61 EW 62

DB 61 EW 62

## RESULT 14

US-09-977-406A-55  
; Sequence 55, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCTON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 55  
; LENGTH: 61  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-55

Query Match 95.3%; Score 61; DB 10; Length 61;  
Best Local Similarity 100.0%; Pred. No. 7.3e-56;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKDPKKTCSVS 60  
DB 1 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKDPKKTCSVS 60

QY 61 E 61  
DB 61 E 61

## RESULT 15

US-09-977-406A-54  
; Sequence 54, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCTON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 54  
; LENGTH: 60  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-54

Query Match 93.8%; Score 60; DB 10; Length 60;  
Best Local Similarity 100.0%; Pred. No. 7.8e-55;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKDPKKTCSVS 60  
DB 1 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKDPKKTCSVS 60

Search completed: March 11, 2004, 18:25:48  
Job time : 42.3226 secs

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OM protein - protein search, using sw model

Run on: March 11, 2004, 18:05:52 ; Search time 11.8548 Seconds

(without alignments)  
399.227 Million cell updates/sec

Title: US-09-977-406a-5

Perfect score: 15

Sequence: 1 EMQDNCNCTCYET 15

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1017041 segs, 315518202 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SPTREMBL\_25:\*

1: sp.archaea:\*

2: sp.bacteria:\*

3: sp.fungi:\*

4: sp.human:\*

5: sp.invertebrate:\*

6: sp.mammal:\*

7: sp.mhc:\*

8: sp.organelle:\*

9: sp.phage:\*

10: sp.plant:\*

11: sp.rodent:\*

12: sp.virus:\*

13: sp.vertibrate:\*

14: sp.unclassified:\*

15: sp.virus:\*

16: sp.bacteriophage:\*

17: sp.archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	40.0	196	11 Q9D8Y1	Q9D8Y1 mus musculus
2	6	40.0	459	16 Q88V80	Q88V80 lactobacilli
3	6	40.0	601	10 Q9C7H2	Q9C7H2 arabidopsis
4	6	40.0	1068	5 Q81A75	Q81A75 caenorhabditis
5	6	40.0	1075	5 Q81A75	Q81A75 caenorhabditis
6	6	40.0	1870	12 Q905A0	Q905A0 fowlpox vir
7	5	33.3	51	9 Q7Y3N1	Q7Y3N1 enterobacte
8	5	33.3	54	5 Q24985	Q24985 giardia lam
9	5	33.3	58	16 Q8RCX2	Q8RCX2 escherichia
10	5	33.3	74	5 Q86015	Q86015 dermatocor
11	5	33.3	74	5 Q861E4	Q861E4 boophilus m
12	5	33.3	75	12 Q8UX66	Q8UX66 sen virus
13	5	33.3	75	12 Q8UX67	Q8UX67 sen virus
14	5	33.3	83	10 Q39465	Q39465 cicier arlet
15	5	33.3	105	11 Q8BU77	Q8BU77 mus musculu
16	5	33.3	110	10 Q42169	Q42169 arabidopsis

17	5	33.3	111	14 Q9UH97	Q9UH97 unclassified
18	5	33.3	112	9 Q854B7	Q854B7 mycobacteri
19	5	33.3	113	10 Q22079	Q22079 nicotiana t
20	5	33.3	131	11 Q8CFP4	Q8CFP4 mus musculu
21	5	33.3	132	5 Q97442	Q97442 giardia lam
22	5	33.3	137	5 Q9W101	Q9W101 drosophila
23	5	33.3	137	5 Q24987	Q24987 giardia lam
24	5	33.3	151	4 Q9UG32	Q9UG32 homo sapien
25	5	33.3	151	4 Q9F184	Q9F184 arabidopsis
26	5	33.3	161	2 Q93146	Q93146 bacteroides
27	5	33.3	164	10 Q8LRJ3	Q8LRJ3 oryza sativ
28	5	33.3	167	10 Q8LDL5	Q8LDL5 arabidopsis
29	5	33.3	167	10 Q9SAC5	Q9SAC5 arabidopsis
30	5	33.3	178	5 Q8T864	Q8T864 dictyosteli
31	5	33.3	188	5 Q9NIS7	Q9NIS7 babesia bov
32	5	33.3	195	4 Q9H061	Q9H061 homo sapien
33	5	33.3	206	10 Q9AXW5	Q9AXW5 brassica ol
34	5	33.3	209	10 Q9AXW7	Q9AXW7 brassica na
35	5	33.3	210	15 Q8PY88	Q8PY88 anabena sp
36	5	33.3	218	14 Q9TH85	Q9TH85 unclassified
37	5	33.3	223	5 Q9NSA3	Q9NSA3 caenorhabdi
38	5	33.3	226	10 Q8LQC2	Q8LQC2 oryza sativ
39	5	33.3	231	16 Q8NLX0	Q8NLX0 corynebacte
40	5	33.3	233	5 Q8MP13	Q8MP13 patella vul
41	5	33.3	246	16 Q9PK11	Q9PK11 chlamydia m
42	5	33.3	253	10 Q8W311	Q8W311 zea mays (m
43	5	33.3	253	16 Q811Y9	Q811Y9 bacillus ce
44	5	33.3	256	10 Q8L876	Q8L876 arabidopsis
45	5	33.3	258	2 Q8G9S5	Q8G9S5 bacteroides

# ALIGNMENTS

RESULT 1

ID Q9D8Y1 PRELIMINARY; PRT; 196 AA.

AC Q9D8Y1; 01-JUN-2001 (TREMREL. 17, Created)

DT 01-JUN-2001 (TREMREL. 17, Last sequence update)

DT 01-JUN-2002 (TREMREL. 21, Last annotation update)

DE 1810020E01RIK protein (RIKEN CDNA 1810020E01 gene).

GN 1810020E01RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_Taxid=10090;

[1]

SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=Pancreas;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K., Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H., Kuehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J., Schmitt L.M., Steinhilber F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., But C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F., Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilmink L., Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontsuki S., Hayashizaki Y.,

RT "Functional annotation of a full-length mouse cDNA collection."

RL Nature 409:685-690(2001).

[2]

SEQUENCE FROM N.A.

RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK007559; BAB25107.1; -  
 DR EMBL; BC023171; AAB23171.1; -  
 DR MGI; MGI:1913521; 1810020E01R1K.  
 SQ SEQUENCE 196 AA; 21539 MW; 994DF5E2251C5FEB CRC64;

Query Match 40.0%; Score 6; DB 11; Length 196;  
 Best Local Similarity 100.0%; Pred. No. 6.6;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11  
 DB 98 NCERTCT 103

# RESULT 2

Q88V80 PRELIMINARY; PRT; 459 AA.  
 AC Q88V80;  
 DT 01-JUN-2003 (TRENBLrel. 24, Created)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE UDP-N-acetylmutamoylalanine-D-glutamate ligase (EC 6.3.2.9).  
 GN MORD OR LP 2197.  
 OS Lactobacillus plantarum.  
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 OC Lactobacillus.  
 NCBI\_TaxID=1590;  
 RX NCBI\_TaxID=1590;  
 RX SEQUENCE FROM N.A.  
 RC STRAIN=NCIMB 8826 / WCF51;  
 RX MEDLINE=22480296; PubMed=12566566;  
 RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,  
 RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandring H.M.,  
 RA Hoffer M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,  
 RA Raaijmakers W.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Uuring B.,  
 RA De Vos W.M., Stezen R.J.;  
 RT "Complete genome sequence of Lactobacillus plantarum WCF51";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).  
 DR EMBL; AL935258; CAD64544.1; -  
 DR GO; GO:0005524; P-ATP binding; IEA.  
 DR GO; GO:0016874; P-ligase activity; IEA.  
 DR GO; GO:0008764; F:UDP-N-acetylmuramoylalanine-D-glutamate lig. .; IEA.  
 DR GO; GO:0009058; P:biogenesis; IEA.  
 DR InterPro; IPR000713; Mur\_ligase.  
 DR InterPro; IPR004101; Mur\_ligase\_C.  
 DR Pfam; PF01225; Mur\_ligase\_1.  
 DR Pfam; PF02875; Mur\_ligase\_C; 1.  
 DR Ligase; Complete proteome.  
 SQ SEQUENCE 459 AA; 50137 MW; 083AB3B45C599DC9 CRC64;

Query Match 40.0%; Score 6; DB 16; Length 459;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDNCET 9  
 DB 403 TDNCET 408

# RESULT 3

Q9C7H2 PRELIMINARY; PRT; 601 AA.  
 AC Q9C7H2;  
 DT 01-JUN-2001 (TRENBLrel. 17, Created)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE Hypothetical protein (At1g72090/F28P5\_4).  
 GN F28P5.4.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016719; PubMed=11130712;  
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
 RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Euehlert E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 RA Dunn P., Eftu P., Feldlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizlar L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzilli A.,  
 RA Miltner J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
 RA Uteback T., Van Aken S., Vaysberg M., Vayotskaia V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 thaliana".  
 RL Nature 408:816-820 (2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Shin P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,  
 RA Bower L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,  
 RA Ishida J., Jones T., Kamiya A., Karlin-Neuman G., Kawai J., Lam B.,  
 RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,  
 RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,  
 RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinzaki K.,  
 RA Davis R.W., Theologis A., Ecker J.R.;  
 RT "Arabidopsis cDNA clones".  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Cheuk R., Chen H., Kim C.J., Shin P., Bower L., Carninci P.,  
 RA Chan M.W., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan W.W.,  
 RA Ishida J., Jones T., Kamiya A., Karlin-Neuman G., Kawai J., Lam B.,  
 RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Onodera C.S.,  
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
 RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,  
 RA Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;  
 RT "Arabidopsis ORF clones".  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC069273; AAG51137.1; -  
 DR EMBL; AF367274; AAK56263.1; -  
 DR EMBL; BF002712; AAO11628.1; -  
 DR PIR; B96744; B96744.  
 DR InterPro; IPR006638; E1P3.  
 DR InterPro; IPR006466; M1AB-like\_B.  
 DR InterPro; IPR007197; Radical\_S1M.  
 DR InterPro; IPR007922; TRAM.  
 DR InterPro; IPR005839; UPF0004.  
 DR Pfam; PF04055; Radical\_SAM; 1.  
 DR Pfam; PF01938; TRAM; 1.  
 DR Pfam; PF00919; UPF0004; 1.  
 DR SMART; SM00729; E1P3; 1.  
 DR TIGRPFAMs; TIGR01578; M1AB-like-B; 1.  
 DR TIGRPFAMs; TIGR00089; TIGR00089; 1.  
 DR PROSITE; PS01278; UPF0004; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 601 AA; 65496 MW; AAC13F7EFC3DA3D CRC64;

Query Match 40.0%; Score 6; DB 10; Length 601;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CECTC 12  
 DB 514 CECTC 519

## RESULT 4

ID 081A76 PRELIMINARY; PRT; 1068 AA.

AC 081A76; 01-MAR-2003 (TRENBLREL. 23, Created)

DT 01-MAR-2003 (TRENBLREL. 23, last sequence update)

DE 01-OCT-2003 (TRENBLREL. 25, last annotation update)

GN K10F12.3.

DE Hypothetical protein K10F12.3b.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI\_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RX MEDLINE=99069613; PubMed=9851916;

RA Waterston R.;

RT "Genome sequence of the nematode C. elegans: a platform for

RL Investigating biology. The C. elegans Sequencing Consortium.";

RN Science 282:2012-2018(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Wohldmann P., Beck C.;

RT "The sequence of C. elegans cosmid K10F12.";

RN Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Waterston R.;

RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF025462; AN72423.1; -.

DR WormPep; K10F12.3b; CE31037.

DR GO; GO:0004435; F:phospholipase C activity; IEA.

DR GO; GO:0007242; P:intracellular signaling cascade; IEA.

DR GO; GO:0006629; P:lipid metabolism; IEA.

DR InterPro; IPR000008; C2.

DR InterPro; IPR008973; C2\_CaLB.

DR InterPro; IPR001849; PH.

DR InterPro; IPR001192; PI\_PLC.

DR InterPro; IPR000909; PI\_PLC\_Xdom.

DR InterPro; IPR001711; PI\_PLC\_Y.

DR Pfam; PF00388; C2; 1.

DR Pfam; PF00388; PI\_PLC-X; 1.

DR Pfam; PF00387; PI\_PLC-Y; 1.

DR PRINTS; PR00390; PPHPLIPASEC.

DR PRODOM; PD001202; PI\_PLC\_Y; 1.

DR SMART; SM00239; C2; 1.

DR SMART; SM00233; PH; 1.

DR SMART; SM00148; PLCC; 1.

DR SMART; SM00149; PLCC; 1.

DR PROSITE; PS50004; C2\_DOMAIN\_2; 1.

DR PROSITE; PS50007; PI\_PLC\_X\_DOMAIN; 1.

DR PROSITE; PS50008; PI\_PLC\_Y\_DOMAIN; 1.

KW Hypothetical protein.

SQ SEQUENCE 1068 AA; 120042 MW; 98F7CFCFFD7EC221 CRC64;

QY

DB 310 TNCERT 315

ID 081A75 PRELIMINARY; PRT; 1075 AA.

AC 081A75;

RESULT 5

ID 081A75;

AC 081A75;

DT 01-MAR-2003 (TRENBLREL. 23, Created)

DT 01-MAR-2003 (TRENBLREL. 23, last sequence update)

DT 01-OCT-2003 (TRENBLREL. 25, last annotation update)

DE Hypothetical protein K10F12.3a.

GN K10F12.3.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI\_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RX MEDLINE=99069613; PubMed=9851916;

RA Waterston R.;

RT "Genome sequence of the nematode C. elegans: a platform for

RL Investigating biology. The C. elegans Sequencing Consortium.";

RN Science 282:2012-2018(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Wohldmann P., Beck C.;

RT "The sequence of C. elegans cosmid K10F12.";

RN Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Waterston R.;

RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF025462; AN72422.1; -.

DR WormPep; K10F12.3a; CE31036.

DR GO; GO:0004435; F:phospholipase C activity; IEA.

DR GO; GO:0007242; P:intracellular signaling cascade; IEA.

DR GO; GO:0006629; P:lipid metabolism; IEA.

DR InterPro; IPR000008; C2.

DR InterPro; IPR008973; C2\_CaLB.

DR InterPro; IPR001849; PH.

DR InterPro; IPR001192; PI\_PLC.

DR InterPro; IPR000909; PI\_PLC\_Xdom.

DR InterPro; IPR001711; PI\_PLC\_Y.

DR Pfam; PF00388; C2; 1.

DR Pfam; PF00388; PI\_PLC-X; 1.

DR Pfam; PF00387; PI\_PLC-Y; 1.

DR PRINTS; PR00390; PPHPLIPASEC.

DR PRODOM; PD001202; PI\_PLC\_Y; 1.

DR SMART; SM00239; C2; 1.

DR SMART; SM00233; PH; 1.

DR SMART; SM00148; PLCC; 1.

DR PROSITE; PS50004; C2\_DOMAIN\_2; 1.

DR PROSITE; PS50007; PI\_PLC\_X\_DOMAIN; 1.

DR PROSITE; PS50008; PI\_PLC\_Y\_DOMAIN; 1.

KW Hypothetical protein.

SQ SEQUENCE 1075 AA; 121112 MW; 6102111ABF78AFD4 CRC64;

QY

DB 317 TNCERT 322

ID 09J5A0 PRELIMINARY; PRT; 1870 AA.

AC 09J5A0;

DT 01-OCT-2000 (TRENBLREL. 15, Created)

DT 01-OCT-2000 (TRENBLREL. 15, last sequence update)

DT 01-JUN-2003 (TRENBLREL. 24, last annotation update)

DE ORF FV122 variola B22R gene family protein.

GN FV122.

OS Fowlpox virus (FPV).

RESULT 6

ID 09J5A0 PRELIMINARY; PRT; 1870 AA.

AC 09J5A0;

DT 01-OCT-2000 (TRENBLREL. 15, Created)

DT 01-OCT-2000 (TRENBLREL. 15, last sequence update)

DT 01-JUN-2003 (TRENBLREL. 24, last annotation update)

DE ORF FV122 variola B22R gene family protein.

GN FV122.

OS Fowlpox virus (FPV).

Query Match

Best Local Similarity 40.0%; Score 6; DB 5; Length 1068;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

DB 310 TNCERT 315

ID 081A75 PRELIMINARY; PRT; 1075 AA.

AC 081A75;

RESULT 5

ID 081A75;

AC 081A75;

Query Match

Best Local Similarity 100.0%; Pred. No. 29;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

DB 317 TNCERT 322

ID 09J5A0 PRELIMINARY; PRT; 1870 AA.

AC 09J5A0;

DT 01-OCT-2000 (TRENBLREL. 15, Created)

DT 01-OCT-2000 (TRENBLREL. 15, last sequence update)

DT 01-JUN-2003 (TRENBLREL. 24, last annotation update)

DE ORF FV122 variola B22R gene family protein.

GN FV122.

OS Fowlpox virus (FPV).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Avipoxvirus.  
 OX NCBI\_TaxID=10261;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20193820; PubMed=10729156;  
 RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;  
 RT "The genome of fowlpox virus";  
 RL J. Virol. 74:3815-3831(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF198100; AAF44466.1; -  
 DR InterPro; IPR007490; Poxvirus\_B22R.  
 DR Pfam; PF04395; Poxvirus\_B22R; 1.  
 SQ SEQUENCE 1870 AA; 211756 MW; 2423D319743D3F2F CRC64;  
 QY Query Match 40.0%; Score 6; DB 12; Length 1870;  
 Best Local Similarity 100.0%; Pred. No. 46;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 241 NCERTCT 246

RESULT 7  
 QY3N1 PRELIMINARY; PRT; 51 AA.  
 ID QY3N1.  
 AC QY3N1.  
 DT 01-OCT-2003 (TRENBLrel. 25. Created)  
 DT 01-OCT-2003 (TRENBLrel. 25. Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25. Last annotation update)  
 DE Hypothetical protein.  
 GN RB49ORF140M.  
 OS Enterobacteria phage RB49.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
 CC T4-like viruses.  
 OX NCBI\_TaxID=50948;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97250366; PubMed=9096222;  
 RA Monod C., Repollet F., Kutateladze M., Tetaert F., Kirsch H.M.;  
 RT "The genome of the pseudo-T-even bacteriophages, a diverse group that  
 resembles T4";  
 RL J. Mol. Biol. 267:237-249(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21062343; PubMed=11092834;  
 RA Ang D., Keppel F., Klein G., Richardson A., Georgopoulos C.;  
 RT "Genetic analysis of bacteriophage-encoded coheserons";  
 RL Annu. Rev. Genet. 34:439-456(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21972795; PubMed=11976309;  
 RA Desplats C., Dez C., Tetaert F., Eleaume H., Kirsch H.M.;  
 RT "Snapshot of the genome of the pseudo-T-even bacteriophage RB49";  
 RL J. Bacteriol. 184:2789-2804(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Tetaert F., Desplats C., Kutateladze M., Monod C., Ackermann H.-W.,  
 RA Kirsch H.M.;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Kirsch H.M.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Ang D., Richardson A., Mayer M.P., Keppel F., Kirsch H.,  
 RA Georgopoulos C.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Zhao L., Tetaert F., Kirsch H.M., Arita F.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RA Desplats C., Dez C., Tetaert F., Eleaume H., Kirsch H.M.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RA Thieme C.A., Desplats C., Dez C., Tetaert F., Eleaume H., Kirsch H.M.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP SEQUENCE FROM N.A.  
 RA Desplats C., Dez C., Tetaert F., Eleaume H., Kirsch H.M.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 RN [11]  
 RP SEQUENCE FROM N.A.  
 RA Kirsch H.M.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RA Desplats C., Kirsch H.M.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 RN [13]  
 RP SEQUENCE FROM N.A.  
 RA Letarov A.V., Kirsch H.M., Tetaert P.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 RN [14]  
 RP SEQUENCE FROM N.A.  
 RA Bertrand C., Petrov V., Nolan J., Letarov A., Desplats C., Chin D.,  
 RA Karam J.D., Kirsch H.M.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY343333; AAQ15386.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 51 AA; 5832 MW; C0E64565345F8A58 CRC64;  
 QY Query Match 33.3%; Score 5; DB 9; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 7 TDNCE 11

RESULT 8  
 Q24985 PRELIMINARY; PRT; 54 AA.  
 ID Q24985.  
 AC Q24985.  
 DT 01-NOV-1996 (TRENBLrel. 01. Created)  
 DT 01-NOV-1996 (TRENBLrel. 01. Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21. Last annotation update)  
 DE Surface protein (Fragment).  
 GN TSP11-1A2.  
 OS Giardia lamblia (Giardia intestinalis).  
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.  
 OX NCBI\_TaxID=5741;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bris-768;  
 RA Ey P.L., Darby J.M., Mayrhofer G.;  
 RT "Three homologous surface antigen genes identified in the protozoan  
 parasite Giardia intestinalis by multiple sequence alignment of  
 RT polymerase chain reaction products";  
 RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U16809; AAB59196.1; -  
 DR InterPro; IPR005127; Giardia\_VSP.  
 DR Pfam; PF03302; VSP; 1.  
 FT NON TER 1  
 FT 54  
 SQ SEQUENCE 54 AA; 5558 MW; 3EDC76CC784B2A9 CRC64;

Query Match 33.3%; Score 5; DB 5; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CECT 11  
 |||||  
 Db 48 CECT 52

## RESULT 9

08FCX2 PRELIMINARY; PRT; 58 AA.  
 ID 08FCX2;  
 AC 08FCX2;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 GN C4140.  
 OS Escherichia coli O6.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OC NCBI\_TaxID=217992;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=06:H1 / CFT073 / ATCC 700928;  
 RX MEDLINE=22386234; PubMed=12471157;  
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,  
 RA Raeko D., Buckles E.L., Lou S.-R., Boutin A., Hackett J., Stroud D.,  
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
 RA Mobley H.L.T., Donenberg M.S., Blattner F.R.;  
 RT "Extensive mosaic structure revealed by the complete genome sequence  
 of uropathogenic Escherichia coli."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).  
 DR EMBL; AE016767; AAN82578.1; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 58 AA; 6635 MW; 842E4509412386F3 CRC64;

Query Match 33.3%; Score 5; DB 16; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDNCE 8  
 |||||  
 Db 7 TDNCE 11

RESULT 10

086Q15 PRELIMINARY; PRT; 74 AA.  
 ID 086Q15;  
 AC 086Q15;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Varsin A.  
 GN VSNAL.  
 OS Dermacentor variabilis.  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
 OC Parasitiformes; Ixodida; Ixodidae; Dermacentor.  
 OC NCBI\_TaxID=34621;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ceruti S.M., Sonenshine D.E., Hynes W.L.;  
 RT "cDNA sequence of the defensin (Varsin A1) from the hemocytes of the  
 hard tick Dermacentor variabilis."  
 RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY181027; AAO24323.1; -.  
 DR GO; GO:0005576; C:extracellular; IDA.  
 DR GO; GO:0003797; P:antibacterial peptide activity; IDA.  
 DR GO; GO:0006961; P:antibacterial humoral response (sensu Inver. . .); IDA.  
 DR InterPro; IPR001542; Defensin\_anod.  
 DR Pfam; PF01097; Arthro\_defensin; 1.  
 DR PROSITE; PS00425; ARTHROPOD\_DEFENSINS; 1.  
 SQ SEQUENCE 74 AA; 8040 MW; A5A29AF4E70DD0B8 CRC64;

Query Match 33.3%; Score 5; DB 5; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCTCY 13  
 |||||  
 Db 68 TCTCY 72

## RESULT 11

086LE4 PRELIMINARY; PRT; 74 AA.  
 ID 086LE4;  
 AC 086LE4;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Preprodefensin.  
 GN Boophilus microplus (Cattle tick).  
 OS Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
 OC Parasitiformes; Ixodida; Ixodidae; Boophilus.  
 OC NCBI\_TaxID=6941;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Fogaca A.C., Lorenzini D.M., Kaku L.M., Bulet P., Daffre S.;  
 RT "Cysteine-rich antimicrobial peptides of the cattle tick Boophilus  
 microplus: Isolation, structural characterization and biological  
 properties."  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY232213; AAO48943.1; -.  
 DR InterPro; IPR001542; Defensin\_anod.  
 DR Pfam; PF01097; Arthro\_defensin; 1.  
 DR PROSITE; PS00425; ARTHROPOD\_DEFENSINS; 1.  
 SQ SEQUENCE 74 AA; 8271 MW; 38931B0222930752 CRC64;

Query Match 33.3%; Score 5; DB 5; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCTCY 13  
 |||||  
 Db 68 TCTCY 72

RESULT 12

08UX66 PRELIMINARY; PRT; 75 AA.  
 ID 08UX66;  
 AC 08UX66;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE ORF1 protein (Fragment).  
 GN SEN virus.  
 OS Viruses; ssDNA viruses; Circoviridae; Anellovirus.  
 OC NCBI\_TaxID=136966;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SENV-C;  
 RA Tanaka Y., Pfeiffer R., Yeo A.E., Mizokami M., Edlin B.R.,  
 O'Brien T.R., Alter H.J., Shih J.W.;  
 RT "PCR-probe capture hybridization assay and statistical mixture  
 modeling for SEN virus prevalence estimation."  
 RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB075276; BAB97346.1; -.  
 DR InterPro; IPR004219; TTvirus\_Unk.  
 DR Pfam; PF02956; TT\_ORF1; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 75 75  
 SQ SEQUENCE 75 AA; 8652 MW; 5C17B13802FB179 CRC64;

Query Match 33.3%; Score 5; DB 12; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 46;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QTDNC 7  
 |||||  
 Db 28 QTDNC 32

## RESULT 13

08JX67 PRELIMINARY; PRT; 75 AA.  
 AC 08JX67;  
 DT 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE ORF1 protein (Fragment).  
 OS SEN virus.  
 CC Viruses; ssDNA viruses; Circoviridae; Anelloviruses.  
 GN NCB1\_TaxID=136966;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SEN-C;  
 RA Tanaka Y., Pfeiffer R., Yeo A.E., Mizokami M., Edlin B.R.,  
 O'Brien T.R., Alter H.J., Shih J.W.;  
 "PCR-probe capture hybridization assay and statistical mixture  
 RT modeling for SEN virus prevalence estimation".  
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AB075275; BAB7345.1; -.  
 DR InterPro; IPR004219; TVirus\_Unk.  
 DR Pfam; PF02956; TT\_ORF1; 1.  
 FT NON TER 1 75 1  
 FT NON TER 1 75 1  
 SQ SEQUENCE 75 AA; 8700 MW; 5C17BF82DF2C7DB6 CRC64;

Query Match 33.3%; Score 5; DB 12; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QTDNC 7  
 |||||  
 Db 28 QTDNC 32

## RESULT 14

039465 PRELIMINARY; PRT; 83 AA.  
 AC 039465;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE SAM-synthetase (Fragment).  
 GN SAMS.  
 OS Cicier arletium (Chickpea) (Garbanzo).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicier.  
 GN NCB1\_TaxID=3827;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Nicolas C., Cervantes E.;  
 RT "Cloning and nucleotide sequence of CaSAMS (X85252), a cDNA encoding  
 RT SAM synthetase from germinated chickpea seeds.";  
 RL Submitted (MAR-1995) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; X85252; CAA59508.1; -.  
 DR PIR; S53116; S53116.  
 DR HSSP; P04384; IMXB.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.  
 DR GO; GO:0006730; F:one-carbon compound metabolism; IEA.  
 DR InterPro; IPR002133; S-Adomet\_synth.  
 DR Pfam; PF00438; S-Adomet\_synth; 1.  
 FT NON TER 83 83  
 FT NON TER 83 83  
 SQ SEQUENCE 83 AA; 9201 MW; 3FF9D594A16CA998 CRC64;

Query Match 33.3%; Score 5; DB 10; Length 83;

Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 CERTCT 11  
 |||||  
 Db 43 CERTCT 47

## RESULT 15

08BU77 PRELIMINARY; PRT; 105 AA.  
 AC 08BU77;  
 DT 01-MAR-2003 (TRENBLrel. 23, Created)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE LIPOMA PREFERRED partner.  
 GN LPP OR B13005510R1K.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 GN NCB1\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPRAIN-C57BL/6J; TISSUE=lung;  
 RX MEDLINE=22354683; PubMed=1246851;  
 RA The FANTOM Consortium,  
 "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RT Nature 420:563-573 (2002).  
 RL Nature 420:563-573 (2002).  
 DR EMBL; AK087122; BAC39809.1; -.  
 DR WGI; WGI:2441849; Lpp.  
 SQ SEQUENCE 105 AA; 12361 MW; AA8E59DAPD8170B2 CRC64;

Query Match 33.3%; Score 5; DB 11; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 64;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ETCCT 12  
 |||||  
 Db 85 ETCCT 89

Search completed: March 11, 2004, 18:13:00  
 Job time : 12.8548 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2004, 18:13:08 ; Search time 9.91936 Seconds

(without alignments)  
319.305 Million cell updates/sec

Title: US-09-977-406A-5

Perfect score: 15

Sequence: 1 EWQTDNCETCTCYET 15

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 809742 seqs, 21153259 residues

Word size : 0

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/prodata/1/pubppa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/prodata/1/pubppa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/prodata/1/pubppa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/prodata/1/pubppa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/prodata/1/pubppa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/prodata/1/pubppa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/prodata/1/pubppa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/prodata/1/pubppa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/prodata/1/pubppa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/prodata/1/pubppa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/prodata/1/pubppa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/prodata/1/pubppa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/prodata/1/pubppa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/prodata/1/pubppa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/prodata/1/pubppa/US06\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/prodata/1/pubppa/US06\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	10	US-09-977-406A-5
2	15	100.0	15	14	US-10-291-360-5
3	15	100.0	16	10	US-09-977-406A-10
4	15	100.0	16	10	US-09-977-406A-59
5	15	100.0	17	10	US-09-977-406A-11
6	15	100.0	17	10	US-09-977-406A-60
7	15	100.0	18	10	US-09-977-406A-12
8	15	100.0	18	10	US-09-977-406A-61
9	15	100.0	19	10	US-09-977-406A-13
10	15	100.0	19	10	US-09-977-406A-62
11	15	100.0	20	10	US-09-977-406A-14
12	15	100.0	20	10	US-09-977-406A-63
13	15	100.0	21	10	US-09-977-406A-15
14	15	100.0	21	10	US-09-977-406A-64
15	15	100.0	22	10	US-09-977-406A-16

16	15	100.0	22	10	US-09-977-406A-65	Sequence 65, Appl
17	15	100.0	23	10	US-09-977-406A-17	Sequence 17, Appl
18	15	100.0	23	10	US-09-977-406A-66	Sequence 16, Appl
19	15	100.0	24	10	US-09-977-406A-18	Sequence 67, Appl
20	15	100.0	24	10	US-09-977-406A-67	Sequence 18, Appl
21	15	100.0	25	10	US-09-977-406A-19	Sequence 69, Appl
22	15	100.0	25	10	US-09-977-406A-68	Sequence 19, Appl
23	15	100.0	26	10	US-09-977-406A-20	Sequence 20, Appl
24	15	100.0	26	10	US-09-977-406A-69	Sequence 68, Appl
25	15	100.0	27	10	US-09-977-406A-21	Sequence 21, Appl
26	15	100.0	27	10	US-09-977-406A-70	Sequence 70, Appl
27	15	100.0	28	10	US-09-977-406A-22	Sequence 22, Appl
28	15	100.0	28	10	US-09-977-406A-71	Sequence 71, Appl
29	15	100.0	29	10	US-09-977-406A-23	Sequence 23, Appl
30	15	100.0	29	10	US-09-977-406A-72	Sequence 72, Appl
31	15	100.0	30	10	US-09-977-406A-24	Sequence 24, Appl
32	15	100.0	30	10	US-09-977-406A-73	Sequence 73, Appl
33	15	100.0	30	10	US-09-977-406A-90	Sequence 90, Appl
34	15	100.0	31	10	US-09-977-406A-25	Sequence 25, Appl
35	15	100.0	31	10	US-09-977-406A-74	Sequence 74, Appl
36	15	100.0	32	10	US-09-977-406A-26	Sequence 26, Appl
37	15	100.0	32	10	US-09-977-406A-75	Sequence 75, Appl
38	15	100.0	33	10	US-09-977-406A-27	Sequence 27, Appl
39	15	100.0	33	10	US-09-977-406A-76	Sequence 76, Appl
40	15	100.0	34	10	US-09-977-406A-28	Sequence 28, Appl
41	15	100.0	34	10	US-09-977-406A-77	Sequence 77, Appl
42	15	100.0	35	10	US-09-977-406A-29	Sequence 29, Appl
43	15	100.0	35	10	US-09-977-406A-78	Sequence 78, Appl
44	15	100.0	36	10	US-09-977-406A-30	Sequence 30, Appl
45	15	100.0	36	10	US-09-977-406A-79	Sequence 79, Appl

#### ALIGNMENTS

RESULT 1  
US-09-977-406A-5  
; Sequence 5, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCK3145 (polypeptide 31-45)  
US-09-977-406A-5

Query Match 100.0%; Score 15; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1,4e-10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EWQTDNCETCTCYET 15  
|||  
Db 1 EWQTDNCETCTCYET 15

RESULT 2  
US-10-291-360-5  
; Sequence 5, Application US/10291360  
; Publication No. US20030119744A1  
; GENERAL INFORMATION:



OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-60

Query Match 100.0%; Score 15; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 3 EWQDNCETCTCYET 17

RESULT 7

US-09-977-406A-12  
Sequence 12, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:

APPLICANT: PROCYON BIOPHARMA INC.

TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS

FILE REFERENCE: 06508-030-US-03

CURRENT APPLICATION NUMBER: US/09/977,406A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: CA 2,321,256

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: CA 2,355,334

PRIOR FILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn version 3.1

SEQ ID NO 12

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)

US-09-977-406A-12

Query Match 100.0%; Score 15; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e-10;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 1 EWQDNCETCTCYET 15

RESULT 8

US-09-977-406A-61  
Sequence 61, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:

APPLICANT: PROCYON BIOPHARMA INC.

TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS

FILE REFERENCE: 06508-030-US-03

CURRENT APPLICATION NUMBER: US/09/977,406A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: CA 2,321,256

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: CA 2,355,334

PRIOR FILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn version 3.1

SEQ ID NO 61

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)

US-09-977-406A-61

Query Match 100.0%; Score 15; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e-10;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 4 EWQDNCETCTCYET 18

RESULT 9

US-09-977-406A-13  
Sequence 13, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:

APPLICANT: PROCYON BIOPHARMA INC.

TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS

FILE REFERENCE: 06508-030-US-03

CURRENT APPLICATION NUMBER: US/09/977,406A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: CA 2,321,256

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: CA 2,355,334

PRIOR FILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn version 3.1

SEQ ID NO 13

LENGTH: 19

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)

US-09-977-406A-13

Query Match 100.0%; Score 15; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e-10;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 1 EWQDNCETCTCYET 15

RESULT 10

US-09-977-406A-62  
Sequence 62, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:

APPLICANT: PROCYON BIOPHARMA INC.

TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS

FILE REFERENCE: 06508-030-US-03

CURRENT APPLICATION NUMBER: US/09/977,406A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: CA 2,321,256

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: CA 2,355,334

PRIOR FILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn version 3.1

SEQ ID NO 62

LENGTH: 19

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)

US-09-977-406A-62

Query Match 100.0%; Score 15; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e-10;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 5 EWQDNCETCTCYET 19

RESULT 11

US-09-977-406A-14



Fri Mar 12 09:42:15 2004

us-09-977-406a-5.01ig.rapb

Page 5

; SEQ ID NO 16  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rHUPSP94 sequence (polypeptide analog)  
US-09-977-406a-16

Query Match 100.0%; Score 15; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.9e-10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EQQDNCETCTCYET 15  
|||  
Db 1 EQQDNCETCTCYET 15

Search completed: March 11, 2004, 18:25:48  
Job time : 14.9194 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2004, 17:48:56 ; Search time 36.2903 Seconds  
(without alignments)  
391.243 Million cell updates/sec

Title: US-09-977-406a-88  
Perfect score: 268  
Sequence: 1 SCYFINEGVGSDSTRKMD.....HPINSEWOTDNCETCTCTC 45

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP\_invertebrate:\*  
6: SP\_mammal:\*  
7: SP\_mhc:\*  
8: SP\_Organellae:\*  
9: SP\_phase:\*  
10: SP\_plant:\*  
11: SP\_rodent:\*  
12: SP\_virus:\*  
13: SP\_vertebrate:\*  
14: SP\_unclassified:\*  
15: SP\_rvlinus:\*  
16: SP\_bacteriap:\*  
17: SP\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	29.5	221	4 Q96GF5	Q96GF5 homo sapien
2	79	29.5	1496	4 Q92626	Q92626 homo sapien
3	77	28.7	744	11 Q80SM9	Q80SM9 mus musculu
4	77	28.7	1431	11 Q80U60	Q80U60 mus musculu
5	67	25.0	284	5 Q8MZ70	Q8MZ70 entamoeba h
6	67	25.0	1292	5 Q24835	Q24835 entamoeba h
7	66	24.6	2327	13 Q91BG7	Q91BG7 xenopus lae
8	65	24.3	284	5 Q8MZ59	Q8MZ59 entamoeba h
9	63	23.5	263	4 Q99740	Q99740 homo sapien
10	62.5	23.3	1048	13 Q8AWM5	Q8AWM5 gallus gall
11	62.5	23.3	2214	5 Q20219	Q20219 caenorhabdi
12	62	23.1	2813	11 Q8CIZ8	Q8CIZ8 mus musculu
13	61.5	22.9	685	6 Q9TIS5	Q9TIS5 bos taurus
14	61.5	22.9	1028	11 Q9JUL0	Q9JUL0 mus musculu
15	61.5	22.9	1330	10 Q9SKX5	Q9SKX5 heterosigma
16	61.5	22.9	1477	11 Q8BYW0	Q8BYW0 mus musculu

17	61.5	22.9	1732	6 Q9XSV8	Q9XSV8 bos taurus
18	61.5	22.9	4782	11 Q8K1S6	Q8K1S6 mus musculu
19	61.5	22.9	5146	6 Q8SPM4	Q8SPM4 bos taurus
20	61.5	22.9	5374	11 Q99ND0	Q99ND0 mus musculu
21	61	22.8	1311	5 Q961K8	Q961K8 drosophila
22	61	22.8	1527	5 Q9VZ24	Q9VZ24 drosophila
23	61	22.8	1535	5 Q23991	Q23991 drosophila
24	60.5	22.6	898	5 Q8MQ32	Q8MQ32 caenorhabdi
25	60.5	22.6	909	5 Q17429	Q17429 caenorhabdi
26	60.5	22.6	960	5 Q8MM07	Q8MM07 caenorhabdi
27	60	22.4	377	2 Q9R9M3	Q9R9M3 rhizobium m
28	59.5	22.2	1461	5 Q17909	Q17909 caenorhabdi
29	59.5	22.2	110	4 Q8H4B0	Q8H4B0 homo sapien
30	59.5	22.2	628	10 Q80977	Q80977 arabidopsis
31	59.5	22.2	673	4 Q8GKX8	Q8GKX8 homo sapien
32	59.5	22.2	955	4 Q96DN2	Q96DN2 homo sapien
33	59.5	22.2	1125	5 P92135	P92135 entamoeba d
34	59.5	22.2	1282	5 Q18720	Q18720 entamoeba d
35	59	22.0	314	5 Q9BLX1	Q9BLX1 drosophila
36	59	22.0	325	5 Q9VWP5	Q9VWP5 drosophila
37	59	22.0	415	16 Q98BM3	Q98BM3 rhizobium 1
38	59	22.0	1698	5 Q94438	Q94438 chironomus
39	59	22.0	1704	5 Q94446	Q94446 chironomus
40	58.5	21.8	377	12 Q85389	Q85389 variola maj
41	58.5	21.8	377	12 Q89164	Q89164 variola vir
42	58.5	21.8	377	12 Q8QMT7	Q8QMT7 cowpox viru
43	58.5	21.8	377	12 Q93122	Q93122 vaccinia vi
44	58.5	21.8	377	12 Q8JIS8	Q8JIS8 ectromelia
45	58.5	21.8	377	12 Q8V4W1	Q8V4W1 monkeypox v

## ALIGNMENTS

RESULT 1  
Q96GF5 PRELIMINARY; PRT; 221 AA.  
AC Q96GF5;  
ID 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
ON NCBI\_Taxid=9606;  
RX [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RA Strausberg R.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC009496; AA09496.1; -  
DR GO; GO:0004601; F:peroxidase activity; IEA.  
DR GO; GO:0006979; P:response to oxidative stress; IEA.  
DR InterPro; IPR002007; Annu\_peroxidase.  
DR InterPro; IPR002016; Peroxidase.  
DR InterPro; IPR001007; VWF\_C.  
DR Pfam; PF03098; An\_peroxidase; 1.  
DR SMART; SM00214; VWC; 1.  
DR PROSITE; PS50292; PEROXIDASE\_3; 1.  
KW Hypothetical protein.  
FT NON\_TER  
SQ  
SEQUENCE 221 AA; 24819 MW; 253547681268E CRC64;  
Query Match 29.5%; Score 79; DB 4; Length 221;  
Best Local Similarity 41.4%; Pred. No. 0.011;  
Matches 12; Conservative 5; Mismatches 12; Indels 0; Gaps 0;  
QY 14 STRKMDLKGKHPINSEWOTDNCETCTC 42  
DB -154 STTECVDAEGESHANNTRKWKDACTICGC 182

RESULT 2

Q92626 PRELIMINARY; PRT; 1496 AA.

AC Q92626; 01-FEB-1997 (TREMBlrel. 02, Created)

DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE MYELOBLAST KIAA0230 (Fragment).

GN KIAA0230.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Bone marrow;

RX MEDLINE=97191544; PubMed=9039502;

RA Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayashi Y., Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.

RT "Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain."

RT DNA Res. 3:321-329(1996).

RL [2]

RN SEQUENCE FROM N.A.

RP TISSUE=Melanoma;

RX MEDLINE=95048383; PubMed=7959781;

RA Weiler S.R., Taylor S.M., Deans R.J., Kan-Mitchell J., Mitchell M.S., Trent J.M.

RT "Assignment of a human melanoma associated gene MG50 (D5S448) to chromosome 2p25.3 by fluorescence in situ hybridization."

RL Genomics 22:243-244(1994).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Melanoma;

RT "Identification of a novel melanoma gene (MG50) - likely the gene for IL-1 receptor antagonist - which encodes epitopes recognized by human cytolytic T lymphocytes."

RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RL EMBL; D86983; BA13219.1; -.

DR EMBL; AF200348; AAF06354.1; -.

DR HSPB; P05164; ICKP.

DR GO; GO:0005152; P:interleukin-1 receptor antagonist activity; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR002007; Anim\_peroxidase.

DR InterPro; IPR003598; IG\_c2.

DR InterPro; IPR00110; IG-like.

DR InterPro; IPR00483; LRR.

DR InterPro; IPR000483; LRR\_Cterm.

DR InterPro; IPR000372; LRR\_Nterm.

DR InterPro; IPR003591; LRR\_Typ.

DR InterPro; IPR002016; Peroxidase.

DR InterPro; IPR01007; VWF\_C.

DR Pfam; PF03098; An\_peroxidase; 1.

DR Pfam; PF00047; Ig\_4.

DR Pfam; PF00560; LRR\_5.

DR Pfam; PF01463; LRRCT\_1.

DR Pfam; PF00093; VWC\_1.

DR PRINTS; PR00457; ANPEROXIDASE.

DR SMART; SMO0408; IGC2\_4.

DR SMART; SMO0082; LRCT\_1.

DR SMART; SMO0013; LRNT\_1.

DR SMART; SMO0369; LRR\_Typ\_4.

DR SMART; SMO0214; VWC\_1.

DR PROSITE; PS50835; IG\_LIKE\_4.

DR PROSITE; PS50292; PEROXIDASE\_3; 1.

DR PROSITE; PS01208; VWF\_C\_1; 1.

DR PROSITE; PS0184; VWF\_C\_2; 1.

KW Immunoglobulin domain

FT NON\_TER 1

SEQUENCE 1496 AA; 167209 MW; E9B9A7069BFFABFF CRC64;

Query Match 29.5%; Score 79; DB 4; Length 1496;

Best Local Similarity 41.4%; Pred. No. 0.087;

Matches 12; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 14 STRKMDLKGNGHPINSEMDNCETCTC 42

DB 1428 STTECVDSGESHGNTKWKDPCTVCEC 1456

RESULT 3

Q80SW9 PRELIMINARY; PRT; 744 AA.

AC Q80SW9;

DT 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Similar to hypothetical protein FLJ25471.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_Taxid=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N-3; TISSUE=Breast tumor;

RA Strausberg R.;

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC044828; AAH44828.1; -.

DR EMBL; BC049858; AAH49858.1; -.

DR GO; GO:0004601; P:peroxidase activity; IEA.

DR GO; GO:0006579; P:response to oxidative stress; IEA.

DR InterPro; IPR002007; Anim\_peroxidase.

DR InterPro; IPR002016; Peroxidase.

DR InterPro; IPR01007; VWF\_C.

DR Pfam; PF03098; An\_peroxidase; 1.

DR Pfam; PF00093; VWC\_1.

DR PRINTS; PR00457; ANPEROXIDASE.

DR SMART; SMO0214; VWC\_1.

DR PROSITE; PS50292; PEROXIDASE\_3; 1.

DR PROSITE; PS01208; VWF\_C\_1; 1.

DR PROSITE; PS0184; VWF\_C\_2; 1.

KW Hypothetical protein.

SEQUENCE 744 AA; 84135 MW; 8A81DEE90A587FE CRC64;

Query Match 28.7%; Score 77; DB 11; Length 744;

Best Local Similarity 41.4%; Pred. No. 0.077;

Matches 12; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 14 STRKMDLKGNGHPINSEMDNCETCTC 42

DB 676 STTECVDSGESHGNTKWKDPCTVCEC 704

RESULT 4

Q80U60 PRELIMINARY; PRT; 1431 AA.

AC Q80U60;

DT 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE KIAA0230 protein (Fragment).

GN KIAA0230.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_Taxid=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=22579291; PubMed=12693553;

RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yusa S., Nakajima D., Nagase T., Ohara O., Koga H.

RT "Prediction of the coding sequences of mouse homologues of KIAA gene:



RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous  
RT cDNAs identified by screening of terminal sequences of cDNA clones  
RT randomly sampled from size-fractionated libraries."

RL EMBL; AK122223; BAC65505.1; "

DR GO; GO:0004601; P:peroxidase activity; IEA.

DR GO; GO:0006979; P:response to oxidative stress; IEA.

DR InterPro; IPR002007; Antim\_peroxidase.

DR InterPro; IPR003599; IG\_1-like.

DR InterPro; IPR007110; IG\_1-like.

DR InterPro; IPR003598; IG\_C2.

DR InterPro; IPR003596; IG\_V.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR000483; LRR\_Cterm.

DR InterPro; IPR003591; LRR\_Typ.

DR InterPro; IPR002016; Peroxidase.

DR Pfam; PF03098; An\_peroxidase; 1.

DR Pfam; PF00047; IG\_4.

DR Pfam; PF00560; LRR\_5.

DR Pfam; PF01463; LRRCT; 1.

DR Pfam; PF00093; WWC; 1.

DR PRINTS; PR00457; ANPEROXIDASE.

DR SMART; SM00409; IG\_4.

DR SMART; SM00408; IG2; 4.

DR SMART; SM00406; IG; 3.

DR SMART; SM00082; LRRCT; 1.

DR SMART; SM00366; LRR\_P5; 4.

DR SMART; SM00369; LRR\_Typ; 5.

DR SMART; SM00214; WWC; 1.

DR PROSITE; PSS0835; IG\_LIKE; 4.

DR PROSITE; PSS0292; PEROXIDASE\_3; 1.

DR PROSITE; PSS01208; WWC\_1; 1.

DR PROSITE; PSS0184; WWC\_2; 1.

DR NON\_TER 1

FT SSQUENCE 1431 AA; 160591 MW; 684952436DA54B72 CRC64;

Query March 28.7%; Score 77; DB 11; Length 1431;

Best Local Similarity 41.4%; Pred. No. 0.16;

Matches 12; Conservativity 5; Mismatches 12; Indels 0; Gaps 0;

OY 14 STRCKMDLKGKHPINSEWQCTN-----CETCTCYET 42

DB 1363 STTECVDSGSHGNTKMKDPCIVCEC 1391

RESULT 5

Q8MZTO PRELIMINARY; PRT; 284 AA.

AC Q8MZTO;

DT 01-OCT-2002 (TREMblrel. 22, Created)

DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)

DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)

DE Gal/GalNac lectin heavy subunit region E (Fragment).

HSL.

OC Entamoeba histolytica.

OC Eukaryota; Entamoebidae; Entamoeba.

OX NCBI\_TaxID=5759;

RP SEQUENCE FROM N.A.

RC STRAIN=MS2-3346;

RA Beck D.L., Tanyuksel M., Mackey A.J., Pearson W.R., Loftus B.,

RT "Entamoeba histolytica: cloning and sequence analysis of the

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF501279; AAM2200.1; "

DR GO; GO:0005529; F:sugar binding; IEA.

DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.

KM Lectin.

FT NON\_TER 1

SQ SEQUENCE 284 AA; 31163 MW; B5B708C61C803531 CRC64;

Query March 25.0%; Score 67; DB 5; Length 284;

Best Local Similarity 31.7%; Pred. No. 0.65;

Matches 13; Conservativity 6; Mismatches 10; Indels 12; Gaps 1;

OY 17 KCMDLKGNKHPINSEWQCTN-----CETCTCYET 45

DB 97 KCVESKSGDKITHKWEIDTERSNANPKRNPCEATCNQT 137

RESULT 6

Q24835 PRELIMINARY; PRT; 1292 AA.

AC Q24835;

DT 01-NOV-1996 (TREMblrel. 01, Created)

DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)

DE Galactose-specific adhesin 170kd subunit precursor.

GN HGL3.

OS Entamoeba histolytica.

OC Eukaryota; Entamoebidae; Entamoeba.

OX NCBI\_TaxID=5759;

RP SEQUENCE FROM N.A.

RC STRAIN=HM-1;IMSS;

RX MEDLINE=91195330; PubMed=2014248;

RA Mann B.J., Torian B.E., Vedvick T.S., Petri W.A.Jr.;

RT "Sequence of a cysteine-rich galactose-specific lectin of Entamoeba

histolytica."

RT Proc. Natl. Acad. Sci. U.S.A. 88:3248-3252(1991).

RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=HM-1;IMSS;

RA Purdy J.E., Mann B.J., Shugart E.C., Petri W.A.;

RT "The nucleotide sequence of the 5' flanking, entire signal sequence,

RT and part of the 5' coding region of the galactose binding adhesin

(hgl1) of Entamoeba histolytica."

RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=HM-1;IMSS;

RX MEDLINE=94158976; PubMed=8114826;

RA Purdy J.E., Mann B.J., Shugart E.C., Petri W.A.;

RT "Analysis of the gene family encoding the Entamoeba histolytica

galactose-specific adhesin 170-kDa subunit."

RT Mol. Biochem. Parasitol. 62:53-59(1993).

DR EMBL; L14815; AAA18828.1; "

DR PIR; A31435; A31435.

DR PIR; T09229; T09229.

DR InterPro; IPR006209; EGF\_Like.

DR PROSITE; PSS0022; EGF\_1; 1.

KM Signal.

FT SIGNAL 1

SO SEQUENCE 1292 AA; 145176 MW; E3123F4C7B6FD898 CRC64;

Query Match 25.0%; Score 67; DB 5; Length 1292;

Best Local Similarity 31.7%; Pred. No. 3.3;

Matches 13; Conservativity 6; Mismatches 10; Indels 12; Gaps 1;

OY 17 KCMDLKGNKHPINSEWQCTN-----CETCTCYET 45

DB 1099 KCVESKSGDKITHKWEIDTERSNANPKRNPCEATCNQT 1139

RESULT 7

Q9IBG7 PRELIMINARY; PRT; 2327 AA.

AC Q9IBG7;

DT 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)

DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)

DE Kiehn.

OC Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8335;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryonic floor plate;  
 RX MEDLINE=20266358; PubMed=10779551;  
 RA Matsui M., Mizusaki K., Nakatani J., Nakanishi S., Sasai Y.;  
 RT "Xenopus Kiehn: A dorsaling factor containing multiple chordin-type  
 RT repeats secreted from the embryonic midline."  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:5291-5296(2000).  
 DR EMBL: AB026192; BAA95483.1;  
 DR HSSP: p56682; 1CCV.  
 DR GO: GO:0005198; F:structural molecule activity; IEA.  
 DR GO: GO:0007155; P:cell adhesion; IEA.  
 DR InterPro: IPR006209; EGF-like.  
 DR InterPro: IPR002919; TIL Cys-rich.  
 DR InterPro: IPR003129; TSPN.  
 DR InterPro: IPR001007; VWF\_C.  
 DR InterPro: IPR001846; VWF\_D.  
 DR Pfam: PF01826; TIL; 1.  
 DR Pfam: PF00093; VWC; 22.  
 DR Pfam: PF00094; VWC; 1.  
 DR SMART: SM00210; TSPN; 1.  
 DR SMART: SM00214; VMC; 27.  
 DR SMART: SM00216; VMD; 1.  
 DR PROSITE: PS01186; EGF\_2; 1.  
 DR PROSITE: PS01208; VWF\_C\_1; 20.  
 DR PROSITE: PS0184; VWF\_C\_2; 19.  
 SQ SEQUENCE 2327 AA; 255800 MW; 0293109329209983 CRC64;  
 Query Match 24.6%; Score 66; DB 13; Length 2327;  
 Best Local Similarity 31.6%; Pred. No. 8.5;  
 Matches 12; Conservative 3; Mismatches 17; Indels 6; Gaps 1;  
 QY 11 PGDSTRKCM-----LKNGKHPINSEWQDNCECTTC 42  
 Db 1916 PGTCHEGQASAVSCWYGGFFLSNEHQVDECTACTC 1953  
 RESULT 8  
 Q8WZS9 PRELIMINARY; PRT; 284 AA.  
 ID Q8WZS9  
 AC Q8WZS9  
 DT 01-OCT-2002 (TREMblrel. 22, Created)  
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE Gal/GalNAc lectin heavy subunit region E (fragment).  
 GN HGL.  
 OS Entamoeba histolytica.  
 OC Eukaryota; Entamoebidae; Entamoeba.  
 OX NCBI\_TaxID=5759;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MS24-15;  
 RA Beck D.L., Tanyksel M., Mackey A.J., Pearson W.R., Loftus B.,  
 RA Haque R., Petri W.A. Jr.;  
 RT "Entamoeba histolytica: cloning and sequence analysis of the  
 RT Gal/GalNAc lectin in clinical isolates."  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF01280; AAM22201.1;  
 DR GO: GO:0005529; F:sugar binding; IEA.  
 DR GO: GO:0007157; P:heterophilic cell adhesion; IEA.  
 DR Lectin.  
 KW NON\_TER  
 FT NON\_TER  
 SQ SEQUENCE 284 AA; 31035 MW; AAA67FDB13983224 CRC64;  
 Query Match 24.3%; Score 65; DB 5; Length 284;  
 Best Local Similarity 31.7%; Pred. No. 1.2;  
 Matches 13; Conservative 5; Mismatches 11; Indels 12; Gaps 1;

QY 17 KCMDLKNGKHPINSEWQDN-----CETCTCYET 45  
 Db 97 KCAESKSGSKITHKKEIDTERSNANPKRPMCEATCNCQT 137  
 RESULT 9  
 Q99740 PRELIMINARY; PRT; 263 AA.  
 ID Q99740  
 AC Q99740  
 DT 01-MAY-1997 (TREMblrel. 03, Created)  
 DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE Soluble protein tagged (fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Umbilical vein;  
 RX MEDLINE=9521842; PubMed=7697721;  
 RA Lindsey C.E., Shawber C.J., Boulter J., Weinmaster G.;  
 RT "Tagged: a mammalian ligand that activates Notch1."  
 RL Cell 80:909-917(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Umbilical vein;  
 RX MEDLINE=97115768; PubMed=8955070;  
 RA Zimin A.B., Pepper M.S., McMahon G.A., Nguyen F., Montesano R.,  
 RA Maciag T.;  
 RT "An antisense oligonucleotide to the notch ligand tagged enhances  
 RT fibroblast growth factor-induced angiogenesis in vitro."  
 RL J. Biol. Chem. 271:32499-32502(1996).  
 DR EMBL: U77914; AAC50909.1;  
 DR HSSP: P0743; 1CCF.  
 DR GO: GO:0005509; F:calcium ion binding; IEA.  
 DR InterPro: IPR000152; Asx hydroxyl\_S.  
 DR InterPro: IPR000742; EGF\_2.  
 DR InterPro: IPR001861; EGF\_Ca.  
 DR InterPro: IPR001838; EGF\_Ca.  
 DR InterPro: IPR006209; EGF-like.  
 DR InterPro: IPR001007; VWF\_C.  
 DR Pfam: PF00008; EGF; 3.  
 DR PRINTS: PR0010; EGFCA; 2.  
 DR SMART: SM00179; EGF\_CA; 2.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 2.  
 DR PROSITE: PS00022; EGF\_1; 3.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF\_CA; 2.  
 KW EGF-like domain.  
 FT NON\_TER  
 SQ SEQUENCE 263 AA; 28405 MW; E77235CB8360B620 CRC64;  
 Query Match 23.5%; Score 63; DB 4; Length 263;  
 Best Local Similarity 33.3%; Pred. No. 2.1;  
 Matches 13; Conservative 6; Mismatches 12; Indels 8; Gaps 2;  
 QY 11 PGDSTRKCM-----LKNGKHPINSEWQDNCECTTC 42  
 Db 106 PHSAGAKQEVSGRPCTMGSVIPDAKMD-DDCNTQC 143  
 RESULT 10  
 Q8AWWS PRELIMINARY; PRT; 1048 AA.  
 ID Q8AWWS  
 AC Q8AWWS  
 DT 01-MAR-2003 (TREMblrel. 23, Created)  
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE Cysteine-rich motoneuron 1.  
 GN CRIM1.

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OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22395914; PubMed=12508231;
RA Kolle G., Jansen A., Yamada T., Little M.;
RT "In ovo electroporation of Crim in the developing chick spinal
   cord."
RL Dev. Dyn. 226:107-111(2003).
DR EMBL: AY098584; Fasta: 22395914.1.
DR GO: GO:0005576; Cerebral cellular IEA.
DR GO: GO:0005520; F-actin-like growth factor binding; IEA.
DR GO: GO:0004867; F-actin-like growth factor binding; IEA.
DR GO: GO:0001558; P-regulation of cell growth; IEA.
DR InterPro: IPR000867; Antistatin.
DR InterPro: IPR000867; Insulin-like growth factor binding; IEA.
DR InterPro: IPR000867; VC cut.
DR InterPro: IPR001007; VWF_C.
DR Pfam: PF02822; Antistatin; 4.
DR Pfam: PF00053; VWC; 6.
DR SMART: SM00121; IB; 1.
DR SMART: SM00214; VWC; 6.
DR SMART: SM00215; VWC; 6.
DR PROSITE: PS01208; VWC_1; 6.
DR PROSITE: PS0184; VWC_2; 6.
DR PROSITE: PS0184; VWC_2; 6.
SQ SEQUENCE 1048 AA; 114942 MW; 25E4D82C40B08231 CRC64;

Query Match 23.3%; Score 62.5; DB 13; Length 1048;
Best Local Similarity 29.4%; Pred. No. 11;
Matches 10; Conservative 5; Mismatches 18; Indels 1; Gaps 1;

QY 10 VPGDSTRCKMDLKGKHPINSEWQTDNCTCTCY 43
DB 612 MPVKTGSCLSMDGRHNESESWH-DGCRBCYCH 644

RESULT 11
Q02019 PRELIMINARY; PRT; 2214 AA.
ID Q02019
AC Q02019;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Hypothetical protein.
GN F40F4.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
   investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RA Wilson R.;
RT "The sequence of C. elegans cosmid F40F4."
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
EMBL: U04020; AAA81430.1; -

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DR PIR: T16305; T16305
DR WormRep; F40F4.6; CRO4536.
DR GO: GO:0005529; F-sugar binding; IEA.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR006210; EGF.
DR InterPro: IPR001304; Lectin_C.
DR InterPro: IPR005882; WF.
DR InterPro: IPR002035; VWF_A.
DR Pfam: PF00008; EGF; 1.
DR Pfam: PF00059; Lectin_C; 1.
DR Pfam: PF00092; VWA; 1.
DR SMART: SM00034; CLECT; 1.
DR SMART: SM00181; EGF; 3.
DR SMART: SM00604; MD; 2.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS00041; C-TYPE-LECTIN_2; 1.
DR PROSITE: PS00022; EGF_1; 6.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS0234; VWF; 1.
DR PROSITE: PS0234; VWF; 1.
KM Hypothetical protein; EGF-like domain.
SQ SEQUENCE 2214 AA; 243435 MW; B03387B67013A401 CRC64;

Query Match 23.3%; Score 62.5; DB 5; Length 2214;
Best Local Similarity 38.7%; Pred. No. 24;
Matches 12; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

QY 8 EGVPGDS-TRKMDLKGKHPINSEWQTDNCTC 37
DB 1271 DGEPSDPTROCVFNGRSGDANKWYTDTC 1301

RESULT 12
Q08C1Z8 PRELIMINARY; PRT; 2813 AA.
ID Q08C1Z8
AC Q08C1Z8;
DT 01-MAR-2003 (TRENBLREL. 23, Created)
DT 01-OCT-2003 (TRENBLREL. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Von Willebrand factor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c;
RA Lentin P.J., Weinstein E., de Groot P.G., Denis C.V.;
RT "Murine von Willebrand Factor."
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF539800; AAN07781.2; -
SQ SEQUENCE 2813 AA; 309266 MW; 3EE2C7D8F21FPA6 CRC64;

Query Match 23.1%; Score 62; DB 11; Length 2813;
Best Local Similarity 33.3%; Pred. No. 37;
Matches 12; Conservative 7; Mismatches 11; Indels 6; Gaps 2;

QY 12 GDSRCKMDLKGKHPINSEWQTDNCTCTC 42
DB 2419 GCTTTCPLDKVCVHGTVPVQCFWE-EGDCTCTC 2453

RESULT 13
Q9TTS5 PRELIMINARY; PRT; 685 AA.
ID Q9TTS5
AC Q9TTS5;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE SCO-spondin (Fragment).
GN SCO-SPONDIN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

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OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISUS=Subcommisural organ;  
 RA Gobron S., Crevaux I., Monnerie H., Elbittar F.;  
 RT "Characterization of cattle SCO-spondin.";  
 RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AJ132106; CAB53759.1; -  
 DR InterPro; IPR002919; TIL\_Cystrich.  
 DR InterPro; IPR000884; TSP1.  
 DR InterPro; IPR008085; TSP\_1.  
 DR InterPro; IPR006552; VC\_out.  
 DR Pfam; PF01825; TIL; 2.  
 DR Pfam; PF00090; TSP\_1; 6.  
 DR PRINTS; PRO1705; TSP1REPEAT.  
 DR SMART; SM00209; TSP1; 6.  
 DR SMART; SM00215; VWC\_out; 1.  
 DR PROSITE; PS50092; TSP1; 6.  
 FT NON\_TER 1  
 SO SEQUENCE 685 AA; 71389 MW; A003F80E746D5D3 CRC64;  
 Query Match 22.9%; Score 61.5; DB 6; Length 685;  
 Best Local Similarity 30.8%; Pred. No. 9.5;  
 Matches 16; Conservative 7; Mismatches 20; Indels 9; Gaps 3;  
 OY 2 CYFIPNEGVPDST-----RKCMD-LKGNKHPINSEW-QTNCECTCTCYE 44  
 DB 427 CYCPGQVLSDGTVHVQPHGCSLDLITGERHRFGAQLAKPGCNCVCTSE 478  
 RESULT 14  
 OJULLO PRELIMINARY; PRT; 1028 AA.  
 ID OJULLO  
 AC OJULLO  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Cysteine-rich repeat-containing protein CRIM1 precursor  
 (Fragment).  
 GN CRIM1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20108580; PubMed=10642437;  
 RA Kolle G., Georgasi K., Holmes G.P., Little M.H., Yamada T.;  
 RT "CRIM1, a novel gene encoding a cysteine-rich repeat protein, is  
 RT developmentally regulated and implicated in vertebrate CNS development  
 RT and organogenesis.";  
 RL Mech. Dev. 90:181-193(2000).  
 DR EMBL; AF168680; AAF34410.1; -  
 DR HSSP; P15358; 1SKZ.  
 DR MGD; MGI:1354755; Crim1.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005520; F:insulin-like growth factor binding; IEA.  
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.  
 DR GO; GO:0001558; F:regulation of cell growth; IEA.  
 DR InterPro; IPR004094; Anticristin.  
 DR InterPro; IPR000867; Vns1\_gro\_fac\_pr.  
 DR InterPro; IPR001007; Vns1\_C.  
 DR Pfam; PF02822; Anticristin; 4.  
 DR Pfam; PF00093; VWC; 6.  
 DR SMART; SM00121; IB; 1.  
 DR SMART; SM00214; VWC; 6.  
 DR PROSITE; PS01208; VWC\_1; 6.  
 DR PROSITE; PS50184; VWC\_2; 6.  
 KW Signal  
 FT NON\_TER 1  
 FT SIGNAL <1 25 POTENTIAL.

SO SEQUENCE 1028 AA; 113160 MW; 743058AA481D5BD8 CRC64;  
 Query Match 22.9%; Score 61.5; DB 11; Length 1028;  
 Best Local Similarity 26.2%; Pred. No. 15;  
 Matches 11; Conservative 6; Mismatches 24; Indels 1; Gaps 1;  
 OY 2 CYFIPNEGVPDSTKCMDLKGNKHPINSEWQTNCECTCTCYE 43  
 DB 563 CREVPSAGPVLSTGCTLSMDGHHKNESSH-DGCRCTCYH 623

RESULT 15  
 ID O9SXX5 PRELIMINARY; PRT; 1330 AA.  
 AC O9SXX5  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Na-ATPase.  
 DE HANA.  
 OS Heterosigma akashiwo.  
 OC Eukaryota; stramenopiles; Raphidophyceae; Heterosigma.  
 OX NCBI\_TaxID=2829;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OHE-1;  
 RX MEDLINE=21145113; PubMed=11248217;  
 RA Shono M., Wada M., Hara Y., Fujii T.;  
 RT "Molecular cloning of Na+-ATPase cDNA from a marine alga, Heterosigma  
 RT akashiwo".  
 RL Biochim. Biophys. Acta 1511:193-199(2001).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2  
 CC ATPASES).  
 DR EMBL; AB017481; BAA82752.2; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0015662; F:ATPase activity; coupled to transmembrane m. . .; IEA.  
 DR GO; GO:0016787; F:hydrolyase activity; IEA.  
 DR GO; GO:0015077; F:monovalent inorganic cation transporter act. . .; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR GO; GO:0015672; P:monovalent inorganic cation transport; IEA.  
 DR InterPro; IPR001757; ATPase E1-E2.  
 DR InterPro; IPR006069; Cation\_ATPase.  
 DR InterPro; IPR006068; Cation\_ATPase.  
 DR InterPro; IPR004014; Cation\_ATPase\_N.  
 DR InterPro; IPR008250; E1-E2\_ATPase\_reg.  
 DR InterPro; IPR005834; Hydrolyase.  
 DR InterPro; IPR005775; Na/K\_ATPase\_alpha.  
 DR Pfam; PF00689; Cation\_ATPase\_C; 1.  
 DR Pfam; PF00690; Cation\_ATPase\_N; 1.  
 DR Pfam; PF00122; E1-E2\_ATPase; 1.  
 DR Pfam; PF00702; Hydrolyase; 1.  
 DR PRINTS; PRO0119; CATATPASE.  
 DR PRINTS; PRO0121; NAKATPASE.  
 DR TIGRFAMS; TIGR01106; ATPase-III-X-K; 1.  
 DR TIGRFAMS; TIGR01494; ATPase-P-type; 4.  
 DR PROSITE; PS00154; ATPASE\_E1-E2; 1.  
 KW ATP-binding; Hydrolyase; Phosphorylation; Transmembrane.  
 SO SEQUENCE 1330 AA; 146516 MW; EDPB870FC0949751 CRC64;  
 Query Match 22.9%; Score 61.5; DB 10; Length 1330;  
 Best Local Similarity 27.9%; Pred. No. 19;  
 Matches 12; Conservative 6; Mismatches 24; Indels 1; Gaps 1;  
 OY 2 CYFIPNEGVPDSTKCMDLKGNKHPINSEWQTNCECTCTCYE 44  
 DB 1143 CANNYPHSSGYASGAKPGCEAGANTHPINWVACDSCSQ-ACYE 1184

Search completed: March 11, 2004, 17:55:13  
 Job time : 37.2903 secs

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OM protein - protein search, using sw model

Run on: March 11, 2004, 17:55:17 ; Search time 29.7561 Seconds  
(without alignments)  
319.305 Million cell updates/sec

Title: US-09-977-406a-88

Perfect score: 268  
Sequence: 1 SCYFIPNEGVPDSTRKCMDKGNKHPINSEWQDNCETCTCYET 45

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 21153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Listing first 45 summaries

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubppa/PCUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubppa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	268	100.0	45	US-09-977-406a-88	Sequence 88, Appl
2	268	100.0	94	US-09-977-406a-1	Sequence 1, Appl
3	268	100.0	94	US-10-291-360-1	Sequence 1, Appl
4	268	100.0	102	US-09-977-406a-2	Sequence 2, Appl
5	268	100.0	102	US-10-291-360-2	Sequence 2, Appl
6	268	100.0	114	US-10-012-896-1003	Sequence 1003, Ap
7	268	100.0	114	US-10-205-823-271	Sequence 271, Ap
8	268	100.0	114	US-10-144-678a-1003	Sequence 1003, Ap
9	268	100.0	114	US-10-294-025-1003	Sequence 1003, Ap
10	268	100.0	114	US-10-291-172-236	Sequence 236, App
11	268	100.0	132	US-09-925-300-1027	Sequence 1027, Ap
12	264	98.5	44	US-09-977-406a-87	Sequence 87, Appl
13	255	95.1	43	US-09-977-406a-86	Sequence 86, Appl
14	248	92.5	42	US-09-977-406a-85	Sequence 85, Appl
15	242	90.3	41	US-09-977-406a-84	Sequence 84, Appl

16	238	88.8	40	US-09-977-406a-83	Sequence 83, Appl
17	231	86.2	39	US-09-977-406a-82	Sequence 82, Appl
18	225	84.0	38	US-09-977-406a-81	Sequence 81, Appl
19	221.5	82.6	119	US-10-291-172-612	Sequence 612, App
20	220	82.1	37	US-09-977-406a-80	Sequence 80, Appl
21	214	79.9	36	US-09-977-406a-79	Sequence 79, Appl
22	210	78.4	35	US-09-977-406a-78	Sequence 78, Appl
23	203	75.7	34	US-09-977-406a-77	Sequence 77, Appl
24	197	73.5	33	US-09-977-406a-76	Sequence 76, Appl
25	191	71.3	32	US-09-977-406a-75	Sequence 75, Appl
26	187	69.8	31	US-09-977-406a-74	Sequence 74, Appl
27	182	67.9	30	US-09-977-406a-73	Sequence 73, Appl
28	177	66.0	29	US-09-977-406a-72	Sequence 72, Appl
29	172	64.2	28	US-09-977-406a-71	Sequence 71, Appl
30	163	60.8	27	US-09-977-406a-70	Sequence 70, Appl
31	158	59.0	26	US-09-977-406a-69	Sequence 69, Appl
32	152	56.7	25	US-09-977-406a-68	Sequence 68, Appl
33	148	55.2	24	US-09-977-406a-67	Sequence 67, Appl
34	143	53.4	23	US-09-977-406a-66	Sequence 66, Appl
35	137	51.1	22	US-09-977-406a-65	Sequence 65, Appl
36	131	48.9	21	US-09-977-406a-64	Sequence 64, Appl
37	126	47.0	20	US-09-977-406a-63	Sequence 63, Appl
38	118	44.0	19	US-09-977-406a-62	Sequence 62, Appl
39	111	41.4	18	US-09-977-406a-61	Sequence 61, Appl
40	107	39.9	17	US-09-977-406a-60	Sequence 60, Appl
41	101	37.7	16	US-09-977-406a-59	Sequence 59, Appl
42	98	36.6	30	US-09-977-406a-90	Sequence 90, Appl
43	98	36.6	45	US-09-977-406a-91	Sequence 91, Appl
44	98	36.6	60	US-09-977-406a-92	Sequence 92, Appl
45	97	36.2	15	US-09-977-406a-5	Sequence 5, Appl

## ALIGNMENTS

RESULT 1  
US-09-977-406a-88  
Sequence 88, Application US/09977406a  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCCON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
PRIORITY FILING DATE: 2001-10-15  
PRIORITY APPLICATION NUMBER: CA 2,321,256  
PRIORITY FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIORITY FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 88  
LENGTH: 45  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide derived from RHSP94 sequence (polypeptide analog)  
US-09-977-406a-88

Query Match 100.0%; Score 268; DB 10; Length 45;  
Best Local Similarity 100.0%; Pred. No. 4.4e-27;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKCMDKGNKHPINSEWQDNCETCTCYET 45  
DB 1 SCYFIPNEGVPDSTRKCMDKGNKHPINSEWQDNCETCTCYET 45

RESULT 2  
US-09-977-406a-1  
Sequence 1, Application US/09977406a  
Publication No. US20030170220A1  
GENERAL INFORMATION:

APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 94  
TYPE: PRT  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
AUTHORS: Uivassack, M., Lindstrom, C., Weiber, H., Abrahamson, P.A., Lilja, H., and  
AUTHORS: Lundvall, A.  
TITLE: Molecular cloning of a small prostate protein, known as beta-  
TITLE: microsemoprotein, PSP94 or beta-inhibin, and demonstration of transcripts  
TITLE: non-genital tissues.  
JOURNAL: Biochem. Biophys. Res Commun.  
VOLUME: 164  
ISSUE: 3  
PAGES: 1310-1315  
DATE: 1989  
DATABASE ACCESSION NUMBER: GI 131436  
DATABASE ENTRY DATE: 1988-08-01  
US-09-977-406A-1

Query Match 100.0%; Score 268; DB 10; Length 94;  
Best Local Similarity 100.0%; Pred. No. 1e-26;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKCMCLKGNKHPINSEWQDNCETCTCYET 45  
DB 1 SCYFIPNEGVPDSTRKCMCLKGNKHPINSEWQDNCETCTCYET 45

RESULT 3  
US-10-291-360-1  
Sequence 1, Application US/10291360  
Publication No. US20030119744A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis  
FILE REFERENCE: 06508-051-US-02  
CURRENT FILING DATE: 2002-11-08  
CURRENT APPLICATION NUMBER: US/10/291,360  
PRIOR APPLICATION NUMBER: CA 2,361,736  
PRIOR FILING DATE: 2001-11-08  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 94  
TYPE: PRT  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
AUTHORS: Uivassack, M., Lindstrom, C., Weiber, H., Abrahamson, P.A., Lilja, H., and  
AUTHORS: Lundvall, A.  
TITLE: Molecular cloning of a small prostate protein, known as beta-  
TITLE: microsemoprotein, PSP94 or beta-inhibin, and demonstration of transcripts  
TITLE: non-genital tissues.  
JOURNAL: Biochem. Biophys. Res Commun.  
VOLUME: 164  
ISSUE: 3  
PAGES: 1310-1315  
DATE: 1989  
DATABASE ACCESSION NUMBER: GI 131436  
DATABASE ENTRY DATE: 1988-08-01  
US-10-291-360-1

Query Match 100.0%; Score 268; DB 14; Length 94;

Best Local Similarity 100.0%; Pred. No. 1e-26;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKCMCLKGNKHPINSEWQDNCETCTCYET 45  
DB 1 SCYFIPNEGVPDSTRKCMCLKGNKHPINSEWQDNCETCTCYET 45

RESULT 4  
US-09-977-406A-2  
Sequence 2, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 102  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: recombinant human PSP94 (rHSP94) produced from yeast  
US-09-977-406A-2

Query Match 100.0%; Score 268; DB 10; Length 102;  
Best Local Similarity 100.0%; Pred. No. 1e-26;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKCMCLKGNKHPINSEWQDNCETCTCYET 45  
DB 9 SCYFIPNEGVPDSTRKCMCLKGNKHPINSEWQDNCETCTCYET 53

RESULT 5  
US-10-291-360-2  
Sequence 2, Application US/10291360  
Publication No. US20030119744A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis  
FILE REFERENCE: 06508-051-US-02  
CURRENT FILING DATE: 2002-11-08  
CURRENT APPLICATION NUMBER: US/10/291,360  
PRIOR APPLICATION NUMBER: CA 2,361,736  
PRIOR FILING DATE: 2001-11-08  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 102  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: recombinant human PSP94 (rHSP94) produced from yeast  
US-10-291-360-2

Query Match 100.0%; Score 268; DB 14; Length 102;  
Best Local Similarity 100.0%; Pred. No. 1e-26;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 9 SCYFIPNEGVPDSTRKCMCLKGNKHPINSEWQDNCETCTCYET 53

RESULT 6

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US-10-012-896-1003
; Sequence 1003, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Heppler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Mantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1003
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-1003

Query Match          100.0%; Score 268; DB 13; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-26;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCYFIPEGVPGDSTRKCMCLKGNKHPINSEWQDNCETCTCYET 45
DB      21 SCYFIPEGVPGDSTRKCMCLKGNKHPINSEWQDNCETCTCYET 65

RESULT 7
US-10-205-823-271
; Sequence 271, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982

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; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 271
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-271

Query Match          100.0%; Score 268; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-26;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      21 SCYFIPEGVPGDSTRKCMCLKGNKHPINSEWQDNCETCTCYET 65

RESULT 8
US-10-144-678A-1003
; Sequence 1003, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Heppler, William T.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Mantanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1003
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-678A-1003

Query Match          100.0%; Score 268; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-26;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCYFIPEGVPGDSTRKCMCLKGNKHPINSEWQDNCETCTCYET 45

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Db 21 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 65

RESULT 9  
US-10-294-025-1003  
; Sequence 1003, Application US/10294025  
; Publication No. US20030185830A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Stolk, John A.  
; APPLICANT: Kalos, Michael D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C29  
; CURRENT FILING DATE: 2002-11-12  
; NUMBER OF SEQ ID NOS: 1038  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1003  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-294-025-1003

Query Match 100.0%; Score 268; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.2e-26;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 45  
Db 21 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 65

RESULT 10  
US-10-291-172-236  
; Sequence 236, Application US/10291172  
; Publication No. US20030228584A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: No. US20030228584A1 Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-045  
; CURRENT APPLICATION NUMBER: US/10/291.172  
; CURRENT FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 09/693,267  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/665,363  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 09/616,847  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 09/596,193  
; PRIOR FILING DATE: 2000-06-17  
; PRIOR APPLICATION NUMBER: 09/574,454  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: 09/519,705  
; PRIOR FILING DATE: 2000-03-07  
; NUMBER OF SEQ ID NOS: 752  
; SEQ ID NO 236  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-291-172-236

Query Match 100.0%; Score 268; DB 15; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.2e-26;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 45  
Db 21 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 65

RESULT 11

US-09-925-300-1027  
; Sequence 1027, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen,  
; APPLICANT: Steve Ruben,  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA101  
; CURRENT APPLICATION NUMBER: US/09/925,300  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05988  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1027  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-300-1027

Query Match 100.0%; Score 268; DB 9; Length 132;  
Best Local Similarity 100.0%; Pred. No. 1.5e-26;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 45  
Db 39 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 83

RESULT 12  
US-09-977-406A-87  
; Sequence 87, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCYON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 87  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-87

Query Match 98.5%; Score 264; DB 10; Length 44;  
Best Local Similarity 100.0%; Pred. No. 1.4e-26;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 45  
Db 1 CYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 44

RESULT 13  
US-09-977-406A-86  
; Sequence 86, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCYON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A



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/ CURRENT FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: CA 2,321,256
/ PRIOR FILING DATE: 2000-10-16
/ PRIOR APPLICATION NUMBER: CA 2,355,334
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 92
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 86
/ LENGTH: 43
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-86
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Query Match          95.1%; Score 255; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 1,9e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      3 YFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCECTCTCYET 45
DB      1 YFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCECTCTCYET 43
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```
RESULT 14
US-09-977-406A-85
/ Sequence 85, Application US/09977406A
/ Publication No. US20030170220A1
/ GENERAL INFORMATION:
/ APPLICANT: PROCYON BIOPHARMA INC.
/ TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
/ FILE REFERENCE: 06508-030-US-03
/ CURRENT APPLICATION NUMBER: US/09/977,406A
/ PRIOR FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: CA 2,321,256
/ PRIOR FILING DATE: 2000-10-16
/ PRIOR APPLICATION NUMBER: CA 2,355,334
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 92
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 85
/ LENGTH: 42
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-85
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Query Match          92.5%; Score 248; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-24;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      4 FIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCECTCTCYET 45
DB      1 FIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCECTCTCYET 42
```

```
RESULT 15
US-09-977-406A-84
/ Sequence 84, Application US/09977406A
/ Publication No. US20030170220A1
/ GENERAL INFORMATION:
/ APPLICANT: PROCYON BIOPHARMA INC.
/ TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
/ FILE REFERENCE: 06508-030-US-03
/ CURRENT APPLICATION NUMBER: US/09/977,406A
/ PRIOR FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: CA 2,321,256
/ PRIOR FILING DATE: 2000-10-16
/ PRIOR APPLICATION NUMBER: CA 2,355,334
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 92
/ SOFTWARE: PatentIn version 3.1
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/ SEQ ID NO 84
/ LENGTH: 41
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-84
```

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Query Match          90.3%; Score 242; DB 10; Length 41;
Best Local Similarity 100.0%; Pred. No. 8.5e-24;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      5 IPNEGVPDSTRKCMDLKGKHPINSEWQTDNCECTCTCYET 45
DB      1 IPNEGVPDSTRKCMDLKGKHPINSEWQTDNCECTCTCYET 41
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Search completed: March 11, 2004, 18:07:56
Job time : 29.7561 secs
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Fri Mar 12 09:42:21 2004

us-09-977-406a-58.rsp

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2004, 17:48:56 ; Search time 51.6129 Seconds  
(without alignments)  
391.243 Million cell updates/sec

Title: US-09-977-406a-58

Sequence: 1 EMOJDNCECTCYETETISCC.....YIVVEKKDPKTCVSEWII 64

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL 25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85.5	23.2	898	Q8M0G2	Q8M0G2 caenorhabdi
2	85.5	23.2	909	Q17429	Q17429 caenorhabdi
3	85.5	23.2	960	Q8M0G7	Q8M0G7 caenorhabdi
4	81.5	22.1	2327	Q9IBG7	Q9IBG7 xenopus lae
5	79.5	21.6	1036	Q9NZV1	Q9NZV1 homo sapien
6	77.5	21.1	286	Q8B896	Q8B896 mus musculu
7	77.5	21.1	1028	Q9J110	Q9J110 mus musculu
8	76.5	20.8	186	Q96524	Q96524 caenorhabdi
9	76	20.7	219	Q16406	Q16406 caenorhabdi
10	75	20.4	3198	Q9U868	Q9U868 manduca sex
11	73.5	20.0	1048	Q8AWM5	Q8AWM5 gallus gall
12	73	19.8	104	Q9C6P1	Q9C6P1 arabidopsis
13	73	19.8	154	Q9C6T5	Q9C6T5 arabidopsis
14	73	19.8	766	Q8I192	Q8I192 plasmodium
15	72	19.6	4179	Q9W474	Q9W474 drosophila
16	71.5	19.4	198	Q9I521	Q9I521 caenorhabdi

17	70	19.0	784	11	Q8BM43	Q8BM43 mus musculu
18	70	19.0	816	11	Q8R417	Q8R417 rattus norv
19	70	19.0	819	11	Q8Q1M5	Q8Q1M5 mus musculu
20	70	19.0	858	11	Q8BM06	Q8BM06 mus musculu
21	69.5	18.9	156	5	Q8MXV6	Q8MXV6 cryptospori
22	69.5	18.9	168	5	Q9G222	Q9G222 cryptospori
23	69.5	18.9	429	5	Q09538	Q09538 caenorhabdi
24	69.5	18.9	687	5	Q23729	Q23729 cryptospori
25	69.5	18.9	1027	13	Q7T302	Q7T302 brachydanio
26	69.5	18.9	2841	5	Q8MLU9	Q8MLU9 drosophila
27	69.5	18.9	2931	5	Q9W2C6	Q9W2C6 drosophila
28	69	18.8	1311	5	Q961K8	Q961K8 drosophila
29	69	18.8	1527	5	Q9VZ24	Q9VZ24 drosophila
30	69	18.8	1535	5	Q23991	Q23991 drosophila
31	68.5	18.6	1376	5	Q26637	Q26637 strongyloce
32	68	18.5	496	13	Q7SY84	Q7SY84 xenopus lae
33	67.5	18.3	420	5	P91776	P91776 pacifastacu
34	67.5	18.3	565	4	Q8TF36	Q8TF36 homo sapien
35	67.5	18.3	685	4	Q8N8U9	Q8N8U9 homo sapien
36	66.5	18.1	355	5	P91465	P91465 caenorhabdi
37	66.5	18.1	2108	13	Q8U19	Q8U19 gallus gall
38	66	17.9	1360	5	Q9TYK4	Q9TYK4 caenorhabdi
39	66	17.9	1704	5	Q94446	Q94446 chromomus
40	66	17.9	4599	11	Q8U118	Q8U118 mus musculu
41	65.5	17.8	130	13	Q8U363	Q8U363 piecoglossu
42	65.5	17.8	200	5	Q45153	Q45153 caenorhabdi
43	65.5	17.8	227	5	Q45158	Q45158 caenorhabdi
44	65.5	17.8	550	4	Q8IWC8	Q8IWC8 homo sapien
45	65.5	17.8	580	11	Q8CB23	Q8CB23 mus musculu

## ALIGNMENTS

### RESULT 1

ID	Q8M0G2	PRELIMINARY;	PRT;	898 AA.
AC	Q8M0G2	01-OCT-2002 (Tremblrel. 22, Created)		
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)			
DT	01-JUN-2003 (Tremblrel. 24, Last annotation update)			
DE	B0024.14d protein.			
GN	B0024.14 OR B0024.14D.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Felodermidae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	McMurray A.A.;			
RL	Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	McMurray A.A.;			
RX	MEDLINE=9069613; PubMed=9851916;			
RA	none;			
RT	"Genome sequence of the nematode C.elegans: A platform for			
RT	investigating biology."			
RT	Science 282:2012-2018 (1998).			
DR	EMBL; Z71178; CAD44089.1; -			
DR	EMBL; AL021478; CAD44089.1; JOINED.			
DR	Wormep; B0024.14d; CE31279.			
DR	GO; GO:0004867; F-serine protease inhibitor activity; IEA.			
DR	InterPro; IPR004094; Antifastin.			
DR	InterPro; IPR001007; VWF_C.			
DR	Pfam; PF02822; Antifastin; 3.			
DR	Pfam; PF00093; VWC; 4.			
DR	SMART; SM00214; VWC; 8.			
DR	PROSITE; PS01208; VWC_1; 6.			
DR	PROSITE; PS0184; VWC_2; 2.			
SO	SEQUENCE 898 AA; 98306 MW; F9686C10837AF35C CRC64;			

Query Match 23.2%; Score 85.5; DB 5; Length 898;  
Best Local Similarity 32.3%; Pred. No. 0.082;



DR EMBL; AB026192; BAA95483.1; -.  
 DR HSP; P56682; 1CV.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR GO; GO:0007155; P:cell adhesion; IEA.  
 DR InterPro; IPR006209; EGF like.  
 DR InterPro; IPR002919; TIL\_Cysrich.  
 DR InterPro; IPR003129; TSPN.  
 DR InterPro; IPR001007; VWF\_C.  
 DR InterPro; IPR001846; VWF\_D.  
 DR Pfam; PF00093; VWC; 22.  
 DR Pfam; PF00094; VWD; 1.  
 DR SMART; SM00210; TSPN; 1.  
 DR SMART; SM00214; VWC; 27.  
 DR SMART; SM00216; VWD; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS01208; VWF\_C\_1; 20.  
 DR PROSITE; PS0184; VWF\_C\_2; 19.  
 SQ SEQUENCE 2327 AA; 255800 MW; 0293109329209983 CRC64;

Query Match 22.1%; Score 81.5; DB 13; Length 2327;  
 Best Local Similarity 28.0%; Pred. No. 0.62;  
 Matches 21; Conservative 6; Mismatches 25; Indels 23; Gaps 3;

QY 2 WQDNCETCTCYETEISC-----CTLVSTPVGYDKDNCOR-IFKEDCKYIVVEKKDPK- 45  
 ID 08BS96 PRELIMINARY; PRT; 1036 AA.  
 AC Q9NZV1; Q9H318;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cysteine-rich repeat-containing protein S52 precursor (CRIM1 protein).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20108580; PubMed=10642437;  
 RA Kojima G., Georgas K., Holmes G.P., Little M.H., Yamada T.;  
 RT "CRIM1, a novel gene encoding a cysteine-rich repeat protein, is developmentally regulated and implicated in vertebrate CNS development and organogenesis";  
 RL Mech. Dev. 90:181-193(2000).  
 RU Mech. Dev. 90:181-193(2000).

RESULT 5  
 Q9NZV1 PRELIMINARY; PRT; 1036 AA.

AC Q9NZV1; Q9H318;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cysteine-rich repeat-containing protein S52 precursor (CRIM1 protein).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20108580; PubMed=10642437;  
 RA Kojima G., Georgas K., Holmes G.P., Little M.H., Yamada T.;  
 RT "CRIM1, a novel gene encoding a cysteine-rich repeat protein, is developmentally regulated and implicated in vertebrate CNS development and organogenesis";  
 RL Mech. Dev. 90:181-193(2000).  
 RU Mech. Dev. 90:181-193(2000).  
 RN [2]  
 RP SEQUENCE OF 112-1036 FROM N.A.  
 RA Kojima G., Georgas K., Holmes G.P., Little M.H., Yamada T.;  
 RT "CRIM1, a novel gene encoding a cysteine-rich repeat protein, is developmentally regulated and implicated in vertebrate CNS development and organogenesis";  
 RL Mech. Dev. 90:181-193(2000).  
 RU EMBL; AF167706; AAG34409.1; -.  
 DR EMBL; AF167706; AAG34409.1; -.  
 DR HSSP; P15358; 1SKZ.  
 DR Genew; HGNC:2359; CRIM1.  
 DR GO; GO:0005010; F:insulin-like growth factor receptor activity; TAS.  
 DR GO; GO:0005010; F:insulin-like growth factor receptor activity; TAS.  
 DR GO; GO:0007399; P:neurogenesis; TAS.  
 DR InterPro; IPR004094; Anticapsin.  
 DR InterPro; IPR000867; Insl\_gro\_fac\_pr.  
 DR InterPro; IPR000169; SHPOT\_acsite.  
 DR InterPro; IPR001007; VWF\_C.  
 DR Pfam; PF02822; Anticapsin; 4.

DR Pfam; PF00093; VWC; 6.  
 DR SMART; SM00121; IB; 1.  
 DR SMART; SM00214; VWC; 6.  
 DR PROSITE; PS00139; THIOL\_PROTEASE\_CYS; 1.  
 DR PROSITE; PS01208; VWF\_C\_1; 6.  
 DR PROSITE; PS0184; VWF\_C\_2; 6.  
 KW Signal.  
 FT SIGNAL 1 34  
 SQ SEQUENCE 1036 AA; 113737 MW; 10CBF02A5C579C27 CRC64;

Query Match 21.6%; Score 79.5; DB 4; Length 1036;  
 Best Local Similarity 32.3%; Pred. No. 0.5;  
 Matches 21; Conservative 8; Mismatches 21; Indels 15; Gaps 4;

QY 2 WQDNCETCTCYETEISC-----CTLVSTPVGYDKDNCOR-IFKEDCKYIVVEKKDPK- 55  
 ID 08BS96 PRELIMINARY; PRT; 286 AA.  
 AC Q9BS96;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cysteine-rich motor neuron 1 (Fragment).  
 GN CRIM1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; Tissue=Embryo;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK034889; BAC28869.1; -.  
 DR MGD; MGI:1354756; Crim1.  
 DR InterPro; IPR001007; VWF\_C.  
 DR Pfam; PF00093; VWC; 2.  
 DR SMART; SM00214; VWC; 2.  
 DR PROSITE; PS01208; VWF\_C\_1; 2.  
 DR PROSITE; PS0184; VWF\_C\_2; 2.  
 FT NON TER 1 1  
 SQ SEQUENCE 286 AA; 32314 MW; 7C371BCA5E39270E CRC64;

Query Match 21.1%; Score 77.5; DB 11; Length 286;  
 Best Local Similarity 30.8%; Pred. No. 0.25;  
 Matches 20; Conservative 9; Mismatches 21; Indels 15; Gaps 4;

QY 2 WQDNCETCTCYETEISC-----CTLVSTPVGYDKDNCOR-IFKEDCKYIVVEKKDPK- 55  
 ID 09JUL0 PRELIMINARY; PRT; 1028 AA.  
 AC Q9JUL0;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DB 16 WKPDACTCVCVDSNAISCSSESPVA-----CERPVLRKGGCCPCIEDTIPKVV 66  
 QY 56 TCVS 60  
 DB 67 VCHFS 71  
 RESULT 7  
 Q9JUL0 PRELIMINARY; PRT; 1028 AA.  
 AC Q9JUL0;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)



Db 119 NCBAVYHEDFSDGSDKLTAKKSVCFDNDPDPGHIHLEDEKVEKMKETCKRYRCK 178

QY 41 EDCXYIVKEDPKTKCSVSEW 62  
179 DDCM-----KKEIVETCSQKEN 195

Db 179 DDCM-----KKEIVETCSQKEN 195

RESULT 10

Q9UG8 PRELIMINARY; PRT; 3198 AA.

AC Q9UG8; 09UG8; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Lepidoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingodea;

OC Sphingidae; Sphinginae; Manduca.

NCBI\_TaxID=7130;

OX NCBI\_TaxID=7130;

RP SEQUENCE FROM N.A.

RX MEDLINE=99457716; PubMed=10528409;

RA Nardl J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;

RT "Expression of lacunin, a large multidomain extracellular matrix protein, accompanies morphogenesis of epithelial monolayers in Manduca sexta."

RL Insect Biochem. Mol. Biol. 29:883-897(1999).

DR EMBL; AF078161; AAF04457.1; -.

DR HSP; P12111; 2KNT.

DR GO; GO:000467; F:serine protease inhibitor activity; IEA.

DR InterPro; IPR004094; Antistatin.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig\_C2.

DR InterPro; IPR002223; Kunitz\_BPTI.

DR InterPro; IPR000884; TSP1.

DR InterPro; IPR008197; WAP.

DR Pfam; PF02822; Antistatin; 4.

DR Pfam; PF00047; Ig\_2; 2.

DR Pfam; PF00014; Kunitz\_BPTI; 10.

DR Pfam; PF00090; tsp\_1; 5.

DR Pfam; PF00095; wap; 1.

DR PRINTS; PR00759; BASICPTASE.

DR ProDom; PD000222; Kunitz\_BPTI; 10.

DR SMART; SM00408; IgC2; 2.

DR SMART; SM00131; KU; 10.

DR SMART; SM00209; TSP1; 7.

DR SMART; SM00217; WAP; 1.

DR PROSITE; PS00317; 4-DISULFIDE CORE; 1.

DR PROSITE; PS00280; BPTI KUNITZ\_1; 8.

DR PROSITE; PS00279; BPTI KUNITZ\_2; 10.

DR PROSITE; PS00835; IG LIKE; 2.

DR PROSITE; PS00092; TSP1; 5.

KM Immunoglobulin domain; Protease inhibitor; Serine protease inhibitor;

KW Signal.

FT SIGNAL.

SC SEQUENCE 1 21 POTENTIAL.

Query Match 3198 AA; 349364 MW; AA4ACD453C0D9134 CRC64;

Best Local Similarity 20.4%; Score 75; DB 5; Length 3198;

Matches 19; Conservative 8; Mismatches 18; Indels 14; Gaps 3;

QY 5 DNECTCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVK-KDPKTKSVSE 61  
2807 DGCRCGCGVGEIDCEPL-----KLCERL-----KCGYIVRGVAGDGCRCRCSE 2853

Db 2807 DGCRCGCGVGEIDCEPL-----KLCERL-----KCGYIVRGVAGDGCRCRCSE 2853

RESULT 11

Q8AWWS PRELIMINARY; PRT; 1048 AA.

AC Q8AWWS; 08AWWS; 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Cysteine-rich motoneuron 1.

GN CRIML.

OS Gallus gallus (chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RP SEQUENCE FROM N.A.

RX MEDLINE=22395914; PubMed=12508231;

RA Kolle G., Jansen A., Yamada T., Little M.;

RT "In ovo electroporation of Criml in the developing chick spinal cord".

RL Dev. Dyn. 226:107-111(2003).

DR EMBL; AY098584; AAM28339.1; -.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005520; F:insulin-like growth factor binding; IEA.

DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.

DR GO; GO:0001558; P:regulation of cell growth; IEA.

DR InterPro; IPR004094; Antistatin.

DR InterPro; IPR000867; Insl\_gro\_fac\_pr.

DR InterPro; IPR006552; VC\_out.

DR InterPro; IPR001007; VWF\_C.

DR Pfam; PF02822; Antistatin; 4.

DR Pfam; PF00093; VWC; 6.

DR SMART; SM00121; IB; 1.

DR SMART; SM00214; VMC; 6.

DR SMART; SM00215; VMC\_out; 3.

DR PROSITE; PS01208; VWF\_C\_1; 6.

DR PROSITE; PS0184; VWF\_C\_2; 6.

SC SEQUENCE 1048 AA; 114942 MW; 25E4D82C40B09231 CRC64;

Query Match 20.0%; Score 73.5; DB 13; Length 1048;

Best Local Similarity 29.5%; Pred. No. 2.7;

Matches 18; Conservative 8; Mismatches 28; Indels 7; Gaps 2;

QY 2 WCTDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKED-CKYIVKEDPKTKSV 59  
705 WNIDSCCTCTCHSGRVLCTETVCPPL-----LCQNPRTSDSCCPQCPDEPLQSLSSNV 759

Db 705 WNIDSCCTCTCHSGRVLCTETVCPPL-----LCQNPRTSDSCCPQCPDEPLQSLSSNV 759

QY 60 S 60  
760 S 760

Db 760 S 760

RESULT 12

Q9CGP1 PRELIMINARY; PRT; 104 AA.

AC Q9CGP1; 09CGP1; 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE Hypothetical protein (Fragment).

GN F1736.24

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosoid II; Brassicales; Brassicaceae; Arabidopsids.

NCBI\_TaxID=3702;

OX NCBI\_TaxID=3702;

RP SEQUENCE FROM N.A.

RX STRAIN=CV. Columbia;

RX MEDLINE=21016719; PubMed=1130712;

RA Theologis A., Ecker J.R., Palm C.J., Pedersen N.A., Kaul S., Kaul S., White O., Alonso J., Alami H., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chen Q., Chen R.F., Chin C.W., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Dunn P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y., Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., Kim C.J., Koo H.L., Kremenetskaia I., Kutz D.B., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,  
 RA Miltischer J., Miranda M., Nguyen M., Niernan W.C., Osborne B.I.,  
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambunga G., Totumt M.J., Town C.D.,  
 RA Utecher T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,  
 RT "Sequence and analysis of chromosome 1 of the plant *Arabidopsis*  
 thaliana";  
 RL Nature 408:816-820(2000).  
 DR EMBL: AC079279; AAC51198.1; -  
 DR InterPro: IPR006969; Stigl.  
 DR Pfam: PF04885; Stigl. 1.  
 KW Hypothetical protein.  
 FT NON TER  
 SQ SEQUENCE 104 AA; 11582 MW; A7B7D10ACA7775EB CRC64;  
 Query Match 19.8%; Score 73; DB 10; Length 104;  
 Best Local Similarity 21.4%; Pred. No. 0.34;  
 Matches 15; Conservative 17; Mismatches 26; Indels 12; Gaps 2;  
 QY 7 CETCTCYETETSCCTLVSTPVGDKDNC-----QRIFKEDCKYIVKK---DPK 54  
 DB 28 CKSQGMVNSTMACCNKCVLDAYDNDGACNCKCTGTCTCGECVLAIDKRGCECN 87  
 QY 55 KTCSVSEWII 64  
 DB 88 HSLVGEFCV 97  
 RESULT 13  
 ID Q9C6T5 PRELIMINARY; PRT; 154 AA.  
 AC Q9C6T5;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN F4M15.5.  
 OS *Arabidopsis thaliana* (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 CC NCBI\_TaxID=3702;  
 CX [1]  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016719; PubMed=11130712;  
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
 RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 RA Dunn P., Egan P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,  
 RA Miltischer J., Miranda M., Nguyen M., Niernan W.C., Osborne B.I.,  
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambunga G., Totumt M.J., Town C.D.,  
 RA Utecher T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,  
 RT "Sequence and analysis of chromosome 1 of the plant *Arabidopsis*  
 thaliana";  
 RL Nature 408:816-820(2000).  
 DR EMBL: AC079279; AAC50782.1; -  
 DR PIR: A96544; A96544.  
 DR InterPro: IPR006969; Stigl.  
 DR Pfam: PF04885; Stigl. 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 154 AA; 17073 MW; CEC49A7999AC2DDB CRC64;

Query Match 19.8%; Score 73; DB 10; Length 154;  
 Best Local Similarity 21.4%; Pred. No. 0.49;  
 Matches 15; Conservative 17; Mismatches 26; Indels 12; Gaps 2;  
 QY 7 CETCTCYETETSCCTLVSTPVGDKDNC-----QRIFKEDCKYIVKK---DPK 54  
 DB 78 CKSQGMVNSTMACCNKCVLDAYDNDGACNCKCTGTCTCGECVLAIDKRGCECN 137  
 QY 55 KTCSVSEWII 64  
 DB 138 HSLVGEFCV 147  
 RESULT 14  
 ID Q81L92 PRELIMINARY; PRT; 766 AA.  
 AC Q81L92;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN P14\_0354.  
 OS *Plasmodium falciparum* (isolate 3D7).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 CC NCBI\_TaxID=36329;  
 CX [1]  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN=3D7;  
 RX MEDLINE=22255705; PubMed=12368864;  
 RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,  
 RA Carlton J.M., Patil A., Nelson K.E., Bowman S., Paulsen I.T., James K.,  
 RA Bisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,  
 RA Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Anguilo S.,  
 RA Pereira M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,  
 RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roper D.S., Ralph S.A.,  
 RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall J.C.,  
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,  
 RA Fraser C.M., Barrell B.,  
 RT "Genome sequence of the human malaria parasite *Plasmodium*  
 falciparum";  
 RL Nature 419:498-511(2002).  
 DR EMBL: AE014823; AAN36967.1; -  
 DR InterPro: IPR004567; Pank\_eukar.  
 DR Pfam: PF03630; Fumbie, 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 766 AA; 91041 MW; E7491A912C9F7CCC CRC64;  
 Query Match 19.8%; Score 73; DB 5; Length 766;  
 Best Local Similarity 40.0%; Pred. No. 2.3;  
 Matches 16; Conservative 6; Mismatches 18; Indels 0; Gaps 0;  
 QY 13 YETETSCCTLVSTPVGDKDNCQRIFKEDCKYIVKKD 52  
 DB 436 YENESSCYENVSSCMSTETSESCQEIFETETCIGFEVEKNN 475  
 RESULT 15  
 ID Q9W4Y4 PRELIMINARY; PRT; 4179 AA.  
 AC Q9W4Y4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE CG7981 protein.  
 GN TROL OR EG:BAICR25B3.11 OR CG7981.  
 OS *Drosophila melanogaster* (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 CC NCBI\_TaxID=7227;  
 CX [1]  
 RN RP SEQUENCE FROM N.A.



RC STRAIN-Berkeley;  
 RX MEDLINE=2019606; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amandides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA April J.F., Agbayani A., An H.-U., Andrews-Plambeck C., Baldwin D.,  
 RA Bailew R.M., Baer A., Baxendale J., Bayraktaroglu I., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokva D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Maes A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,  
 RA Posler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,  
 RA Jalali M., Kalush F., Karpem G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., Moleod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye U., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:12165-2195(2000).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Amandides P.G., Brandon R.C., Rogers Y.,  
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
 RA Ferreira S., Frise E., Gale R.F., Garg N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
 RA Idegam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
 RA Idegash T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA Pacleb J., Pargass V., Park S., Patel S., Pfeiffer B.,  
 RA Prounenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RT "Sequencing of *Drosophila melanogaster* genome.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RN SEQUENCE FROM N.A.  
 RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,  
 RA Clamp W., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Kronmiller B., Marshall B., Milburn G., Richter J., Russo S.,  
 RA Searle S.M.J., Smith E., Shu S., Smutnak F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RT "Annotation of *Drosophila melanogaster* genome.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RN SEQUENCE FROM N.A.  
 RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [5]

RP SEQUENCE FROM N.A.  
 RA Flyase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB003424; AAF45786.3; -  
 DR HSSP; P00740; 1EDM.  
 DR Flyase; Pfam0001402; trol.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0005198; F:Structural molecule activity; IEA.  
 DR GO; GO:0006306; F:DNA methylation; IEA.  
 DR InterPro; IPR001525; C5 DNA meth.  
 DR InterPro; IPR008985; ConA like\_1ec\_g1.  
 DR InterPro; IPR000742; EGF 2.  
 DR InterPro; IPR006209; EGF 1like.  
 DR InterPro; IPR003599; IG 1like.  
 DR InterPro; IPR007110; IG 1like.  
 DR InterPro; IPR003598; IG c2.  
 DR InterPro; IPR000034; Laminin\_B.  
 DR InterPro; IPR002049; Laminin\_EG.  
 DR InterPro; IPR001791; Laminin\_G.  
 DR InterPro; IPR002172; LDL receptor\_A.  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR Pfam; PF00047; IG 12.  
 DR Pfam; PF00052; Laminin\_B; 3.  
 DR Pfam; PF00053; Laminin\_BGF; 2.  
 DR Pfam; PF00054; Laminin\_G; 3.  
 DR Pfam; PF00057; ldl receptor a; 23.  
 DR PRINTS; PR00261; LDLRECEPTOR.  
 DR SMART; SM00180; EGF\_Lam; 9.  
 DR SMART; SM00409; IG; 12.  
 DR SMART; SM00408; IGc2; 12.  
 DR SMART; SM00281; Lamb; 3.  
 DR SMART; SM00282; Lamb; 3.  
 DR SMART; SM00192; LDL; 23.  
 DR PROSITE; PS00064; C5\_MTPASE\_1; 1.  
 DR PROSITE; PS00022; EGF\_1; 10.  
 DR PROSITE; PS01186; EGF\_2; 6.  
 DR PROSITE; PS00835; IG\_LIKE; 11.  
 DR PROSITE; PS01248; LAMININ TYPE EGF; 7.  
 DR PROSITE; PS00025; LAM G DOMAIN; 3.  
 DR PROSITE; PS01209; LDLRA\_1; 20.  
 DR PROSITE; PS00068; LDLRA\_2; 23.  
 DR PROSITE; PS00030; RRM\_RNP\_1; 1.  
 DR Immunoglobulin domain; Laminin EGF-like domain.  
 SQ SEQUENCE 4179 AA; 461782 MW; 47804277D0914B63 CRC64;  
 Query Match 19.6%; Score 72; DB 5; Length 4179;  
 Best Local Similarity 30.5%; Pred. No. 15;  
 Matches 18; Conservative 11; Mismatches 22; Indels 8; Gaps 3;  
 QY 6 NCETCTCYETISCCITVSTFGVYDKDNCQRIFFKEDKTYT-----VVEKKDPKTCVSVS 60  
 DB 2292 SCSLPCPCVSVNTESDLVSG--GYVECHCRKARWKGDRCRSDIDTPILS--DPPQICDLS 2346

Search completed: March 11, 2004, 17:55:12  
 UOB time : 52.6129 secs

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Fri Mar 12 09:42:20 2004

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OM protein - protein search, using sw model

Run on: March 11, 2004, 17:55:17 ; Search time 42.3226 Seconds  
(without alignments)

319.305 Million cell updates/sec

Title: US-09-977-406a-58

Perfect score: 368 1 EWQDNCETCTCTCTETETISCC.....YIVKPKDKTKCTGVSEWII 64

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 21153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

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5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*

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16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*

17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	368	100.0	64	10	US-09-977-406a-58
2	368	100.0	94	10	US-09-977-406a-1
3	368	100.0	94	14	US-10-291-360-1
4	368	100.0	102	10	US-09-977-406a-2
5	368	100.0	102	14	US-10-291-360-2
6	368	100.0	114	13	US-10-012-896-1003
7	368	100.0	114	14	US-10-205-823-271
8	368	100.0	114	14	US-10-144-678a-1003
9	368	100.0	114	14	US-10-294-025-1003
10	368	100.0	114	15	US-10-291-172-236
11	368	100.0	132	9	US-09-925-300-1027
12	364	98.9	63	10	US-09-977-406a-57
13	360	97.8	62	10	US-09-977-406a-56
14	349	94.8	61	10	US-09-977-406a-55
15	344	93.5	60	10	US-09-977-406a-54

16	340	92.4	59	10	US-09-977-406a-53	Sequence 53, Appl
17	336	91.3	58	10	US-09-977-406a-52	Sequence 52, Appl
18	332	90.2	57	10	US-09-977-406a-51	Sequence 51, Appl
19	323	87.8	56	10	US-09-977-406a-50	Sequence 50, Appl
20	318	86.4	55	10	US-09-977-406a-49	Sequence 49, Appl
21	313	85.1	54	10	US-09-977-406a-48	Sequence 48, Appl
22	308	83.7	53	10	US-09-977-406a-47	Sequence 47, Appl
23	301	81.8	52	10	US-09-977-406a-46	Sequence 46, Appl
24	295	80.2	51	10	US-09-977-406a-45	Sequence 45, Appl
25	290	78.8	50	10	US-09-977-406a-44	Sequence 44, Appl
26	285	77.4	49	10	US-09-977-406a-43	Sequence 43, Appl
27	280	76.1	48	10	US-09-977-406a-42	Sequence 42, Appl
28	279	75.8	119	15	US-10-291-172-612	Sequence 612, Appl
29	276	75.0	47	10	US-09-977-406a-41	Sequence 41, Appl
30	272	73.9	46	10	US-09-977-406a-40	Sequence 40, Appl
31	268	72.8	45	10	US-09-977-406a-39	Sequence 39, Appl
32	261	70.9	44	10	US-09-977-406a-38	Sequence 38, Appl
33	256	69.6	43	10	US-09-977-406a-37	Sequence 37, Appl
34	247	67.1	42	10	US-09-977-406a-36	Sequence 36, Appl
35	241	65.5	41	10	US-09-977-406a-35	Sequence 35, Appl
36	236	64.1	40	10	US-09-977-406a-34	Sequence 34, Appl
37	231	62.8	39	10	US-09-977-406a-33	Sequence 33, Appl
38	226	61.4	38	10	US-09-977-406a-32	Sequence 32, Appl
39	220	59.8	37	10	US-09-977-406a-31	Sequence 31, Appl
40	216	58.7	36	10	US-09-977-406a-30	Sequence 30, Appl
41	211	57.3	35	10	US-09-977-406a-29	Sequence 29, Appl
42	206	56.0	34	10	US-09-977-406a-28	Sequence 28, Appl
43	197	53.5	33	10	US-09-977-406a-27	Sequence 27, Appl
44	191	51.9	32	10	US-09-977-406a-26	Sequence 26, Appl
45	185	50.3	31	10	US-09-977-406a-25	Sequence 25, Appl

#### ALIGNMENTS

RESULT 1  
US-09-977-406a-58  
Sequence 58, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 58  
LENGTH: 64  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Polypeptide derived from rhupsp94 sequence (polypeptide analog)  
US-09-977-406a-58

Query Match: 100.0%; Score 368; DB 10; Length 64;  
Best Local Similarity 100.0%; Pred. No. 9.7e-35;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCTCTCTCTVGVGDKDNCRIKKEDCKYIVKPKTKTSVS 60  
DB 1 EWQDNCETCTCTCTCTCTVGVGDKDNCRIKKEDCKYIVKPKTKTSVS 60  
QY 61 EWII 64  
DB 61 EWII 64

RESULT 2

US-09-977-406A-1  
; Sequence 1, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCTON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 94  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; AUTHORS: Ulvback, M., Lindstrom, C., Weiber, H., Abrahamson, P.A., Lilja, H., and  
; AUTHORS: Lundvall, A.  
; TITLE: Molecular cloning of a small prostate protein, known as beta-  
; TITLE: microsemoprotein, PSP94 or beta-inhibin, and demonstration of transcripts  
; TITLE: non-genital tissues.  
; JOURNAL: Biochem. Biophys. Res Commun.  
; VOLUME: 164  
; ISSUE: 3  
; PAGES: 1310-1315  
; DATE: 1989  
; DATABASE ACCESSION NUMBER: GI 131436  
; DATABASE ENTRY DATE: 1988-08-01  
US-09-977-406A-1  
Query Match 100.0%; Score 368; DB 10; Length 94;  
Best Local Similarity 100.0%; Pred. No. 1,5e-34;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKKTCSVS 60  
Db 31 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKKTCSVS 90  
Qy 61 EWII 64  
Db 91 EWII 94  
RESULT 3  
US-10-291-360-1  
; Sequence 1, Application US/10291360  
; Publication No. US20030119744A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCTON BIOPHARMA INC.  
; TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis  
; FILE REFERENCE: 06508-051-US-02  
; CURRENT APPLICATION NUMBER: US/10/291,360  
; CURRENT FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: CA 2,361,736  
; PRIOR FILING DATE: 2001-11-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 94  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; AUTHORS: Ulvback, M., Lindstrom, C., Weiber, H., Abrahamson, P.A., Lilja, H., and  
; AUTHORS: Lundvall, A.  
; TITLE: Molecular cloning of a small prostate protein, known as beta-  
; TITLE: microsemoprotein, PSP94 or beta-inhibin, and demonstration of transcripts  
; TITLE: non-genital tissues.  
; JOURNAL: Biochem. Biophys. Res Commun.  
; VOLUME: 164

ISSUE: 3  
; PAGES: 1310-1315  
; DATE: 1989  
; DATABASE ACCESSION NUMBER: GI 131436  
; DATABASE ENTRY DATE: 1988-08-01  
US-10-291-360-1  
Query Match 100.0%; Score 368; DB 14; Length 94;  
Best Local Similarity 100.0%; Pred. No. 1,5e-34;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKKTCSVS 60  
Db 31 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKKTCSVS 90  
Qy 61 EWII 64  
Db 91 EWII 94  
RESULT 4  
US-09-977-406A-2  
; Sequence 2, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCTON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 102  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: recombinant human PSP94 (rhPSP94) produced from yeast  
US-09-977-406A-2  
Query Match 100.0%; Score 368; DB 10; Length 102;  
Best Local Similarity 100.0%; Pred. No. 1,6e-34;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKKTCSVS 60  
Db 39 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKKTCSVS 98  
Qy 61 EWII 64  
Db 99 EWII 102  
RESULT 5  
US-10-291-360-2  
; Sequence 2, Application US/10291360  
; Publication No. US20030119744A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCTON BIOPHARMA INC.  
; TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis  
; FILE REFERENCE: 06508-051-US-02  
; CURRENT APPLICATION NUMBER: US/10/291,360  
; CURRENT FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: CA 2,361,736  
; PRIOR FILING DATE: 2001-11-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 102

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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: recombinant human PSP94 (rHSP94) produced from yeast
US-10-291-360-2
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Query Match      100.0%; Score 368; DB 14; Length 102;
Best Local Similarity 100.0%; Pred. No. 1,6e-34;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1  EMOTDNCETCTCYETETISCTTIVSTPYGDKNCORIFKKEDCKYIVVEKKDPKTKCSVS 60
          |||
DB      39  EMOTDNCETCTCYETETISCTTIVSTPYGDKNCORIFKKEDCKYIVVEKKDPKTKCSVS 98
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```
QY      61  EWII 64
          |||
DB      99  EWII 102
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RESULT 6
US-10-012-896-1003
Sequence 1003, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
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```
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepker, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlot
APPLICANT: Roy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Mantsabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1003
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-012-896-1003
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Query Match      100.0%; Score 368; DB 13; Length 114;
Best Local Similarity 100.0%; Pred. No. 1,8e-34;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1  EMOTDNCETCTCYETETISCTTIVSTPYGDKNCORIFKKEDCKYIVVEKKDPKTKCSVS 60
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DB      51  EMOTDNCETCTCYETETISCTTIVSTPYGDKNCORIFKKEDCKYIVVEKKDPKTKCSVS 110
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```
QY      61  EWII 64
          |||
DB      111  EWII 114
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RESULT 7
US-10-205-823-271
Sequence 271, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:
```

```
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Ganavara, Manjula
APPLICANT: Gorbatcheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Womsey, Angela M.
APPLICANT: Glat, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 271
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-205-823-271
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Query Match      100.0%; Score 368; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 1,8e-34;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1  EMOTDNCETCTCYETETISCTTIVSTPYGDKNCORIFKKEDCKYIVVEKKDPKTKCSVS 60
          |||
DB      51  EMOTDNCETCTCYETETISCTTIVSTPYGDKNCORIFKKEDCKYIVVEKKDPKTKCSVS 110
```

```
QY      61  EWII 64
          |||
DB      111  EWII 114
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RESULT 8
US-10-144-678A-1003
Sequence 1003, Application US/10144678A
Publication No. US20030157083A1
GENERAL INFORMATION:
```

```
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
```

APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A. W.  
APPLICANT: Hepier, William T.  
APPLICANT: Hural, John  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Vinals y de Bassols, Carlota  
APPLICANT: Roy, Teresa M.  
APPLICANT: Matanabe, Yoshihiro  
APPLICANT: Deng, Ta  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C28  
CURRENT APPLICATION NUMBER: US/10/144,678A  
CURRENT FILING DATE: 2002-08-12  
NUMBER OF SEQ ID NOS: 1033  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1003  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-144-678A-1003

Query Match 100.0%; Score 368; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKKTCSVS 60  
DB 51 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKKTCSVS 110

QY 61 EWII 64  
DB 111 EWII 114

RESULT 9  
US-10-294-025-1003

Sequence 1003, Application US/10294025  
Publication No. US20030185830A1  
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Stolk, John A.  
APPLICANT: Kalos, Michael D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C29  
CURRENT APPLICATION NUMBER: US/10/294,025  
CURRENT FILING DATE: 2002-11-12  
NUMBER OF SEQ ID NOS: 1038  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1003  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-294-025-1003

Query Match 100.0%; Score 368; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKKTCSVS 60  
DB 51 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKKTCSVS 110

QY 61 EWII 64  
DB 111 EWII 114

RESULT 10  
US-10-291-172-236  
Sequence 236, Application US/10291172

Publication No. US20030228584A1  
GENERAL INFORMATION:  
APPLICANT: Hysq, Inc  
TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides  
FILE REFERENCE: 21272-045  
CURRENT APPLICATION NUMBER: US/10/291,172  
CURRENT FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 09/653,267  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 09/665,363  
PRIOR FILING DATE: 2000-09-19  
PRIOR APPLICATION NUMBER: 09/616,847  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 09/596,193  
PRIOR FILING DATE: 2000-06-17  
PRIOR APPLICATION NUMBER: 09/574,454  
PRIOR FILING DATE: 2000-05-19  
PRIOR APPLICATION NUMBER: 09/519,705  
PRIOR FILING DATE: 2000-03-07  
NUMBER OF SEQ ID NOS: 752  
SEQ ID NO 236  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-291-172-236

Query Match 100.0%; Score 368; DB 15; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKKTCSVS 60  
DB 51 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKKTCSVS 110

QY 61 EWII 64  
DB 111 EWII 114

RESULT 11  
US-09-925-300-1027

Sequence 1027, Application US/09925300  
Patent No. US20020151681A1  
GENERAL INFORMATION:  
APPLICANT: Craig Rosen,  
APPLICANT: Steve Ruben  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA101  
CURRENT APPLICATION NUMBER: US/09/925,300  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05988  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1998-03-12  
NUMBER OF SEQ ID NOS: 1890  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1027  
LENGTH: 132  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-925-300-1027

Query Match 100.0%; Score 368; DB 9; Length 132;  
Best Local Similarity 100.0%; Pred. No. 2.1e-34;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKKTCSVS 60  
DB 69 EMQDNCETCTCYETEISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKKTCSVS 128

QY 61 EWII 64  
DB 129 EWII 132

RESULT 12  
US-09-977-406A-57  
; Sequence 57, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCYON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 57  
; LENGTH: 63  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-57

Query Match  
Best Local Similarity 98.9%; Score 364; DB 10; Length 63;  
Best Local Similarity 100.0%; Pred. No. 2.7e-34;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKTKCSVS 60  
DB 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKTKCSVS 60

QY 61 EMI 63  
DB 61 EMI 63

RESULT 13  
US-09-977-406A-56  
; Sequence 56, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCYON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 56  
; LENGTH: 62  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-56

Query Match  
Best Local Similarity 97.8%; Score 360; DB 10; Length 62;  
Best Local Similarity 100.0%; Pred. No. 7.6e-34;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKTKCSVS 60  
DB 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKTKCSVS 60

QY 61 EM 62  
DB 61 EM 62

DB 61 EM 62

RESULT 14  
US-09-977-406A-55  
; Sequence 55, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCYON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 55  
; LENGTH: 61  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-55

Query Match  
Best Local Similarity 94.8%; Score 349; DB 10; Length 61;  
Best Local Similarity 100.0%; Pred. No. 1.3e-32;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKTKCSVS 60  
DB 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKTKCSVS 60

QY 61 E 61  
DB 61 E 61

RESULT 15  
US-09-977-406A-54  
; Sequence 54, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCYON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 54  
; LENGTH: 60  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-54

Query Match  
Best Local Similarity 93.5%; Score 344; DB 10; Length 60;  
Best Local Similarity 100.0%; Pred. No. 4.9e-32;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKTKCSVS 60  
DB 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKTKCSVS 60

Search completed: March 11, 2004, 18:07:56  
Job time : 43.3226 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 11, 2004, 17:48:56 ; Search time 12.0968 Seconds  
(without alignments)  
391.243 Million cell updates/sec

Title: US-09-977-406A-5  
Perfect score: 97  
Sequence: 1 EWQTDNCETCTCYET 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_prodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_ivirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	57	58.8	898 5	Q8MQG2
2	57	58.8	909 5	Q8MQG2
3	57	58.8	909 5	Q8MQG2
4	57	58.8	909 5	Q8MQG2
5	57	58.8	909 5	Q8MQG2
6	57	58.8	909 5	Q8MQG2
7	57	58.8	909 5	Q8MQG2
8	57	58.8	909 5	Q8MQG2
9	57	58.8	909 5	Q8MQG2
10	57	58.8	909 5	Q8MQG2
11	57	58.8	909 5	Q8MQG2
12	57	58.8	909 5	Q8MQG2
13	57	58.8	909 5	Q8MQG2
14	57	58.8	909 5	Q8MQG2
15	57	58.8	909 5	Q8MQG2
16	57	58.8	909 5	Q8MQG2

17	49	50.5	1036 4	Q9NZV1	Q9NZV1 homo sapien
18	49	50.5	1048 13	Q8AMW5	Q8AMW5 gallus gall
19	49	50.5	4007 4	Q8EXX4	Q8EXX4 homo sapien
20	48	49.5	4010 11	Q8OT14	Q8OT14 mus musculu
21	47	48.5	330 12	Q86292	Q86292 human herpe
22	47	48.5	347 16	Q8Z4W7	Q8Z4W7 salmonella
23	47	48.5	377 2	Q9R9M3	Q9R9M3 rhizobium m
24	47	48.5	467 4	Q9GZM7	Q9GZM7 homo sapien
25	47	48.5	644 16	Q98CV7	Q98CV7 rhizobium 1
26	47	48.5	1168 5	Q867S8	Q867S8 schistosom
27	47	48.5	1823 5	Q26638	Q26638 paracentrot
28	46.5	47.9	134 5	Q15649	Q15649 plasmodium
29	46	47.4	467 11	Q9EQF5	Q9EQF5 rattus norv
30	46	47.4	647 5	Q9W2M0	Q9W2M0 drosophila
31	46	47.4	1173 16	Q8RCI3	Q8RCI3 thermococ
32	46	47.4	1215 16	Q893R9	Q893R9 clostridium
33	45.5	46.9	384 5	Q893J5	Q893J5 drosophila
34	45.5	46.9	384 5	Q9VPC4	Q9VPC4 drosophila
35	45	46.4	164 4	Q8IXL9	Q8IXL9 homo sapien
36	45	46.4	351 17	Q8PTW2	Q8PTW2 methanocarc
37	45	46.4	772 4	Q96JG9	Q96JG9 homo sapien
38	45	46.4	912 10	Q9SSD8	Q9SSD8 arabidopsis
39	45	46.4	959 10	Q9CA97	Q9CA97 arabidopsis
40	45	46.4	1171 11	Q8CG82	Q8CG82 mus musculu
41	45	46.4	1171 11	Q80YQ1	Q80YQ1 mus musculu
42	44.5	45.9	553 6	Q8HXE2	Q8HXE2 macaca fasc
43	44.5	45.9	784 11	Q8BM43	Q8BM43 mus musculu
44	44.5	45.9	816 11	Q8R4I7	Q8R4I7 rattus norv
45	44.5	45.9	819 11	Q80UM5	Q80UM5 mus musculu

#### ALIGNMENTS

#### RESULT 1

Q8MQG2 PRELIMINARY; PRT; 898 AA.  
AC Q8MQG2;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE B0024.14d protein.  
GN B0024.14 OR B0024.14P.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Pelodexinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA McMurray A.A.;  
RN Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.  
RP [2]  
RX MEDLINE=9069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
investigating biology".  
RT Science 282:2012-2018(1998).  
RL EMBL/ Z71178; CAD44089.1; .  
RL EMBL/ AL021478; CAD44089.1; JOINED.  
DR Wormpep; B0024.14d; CE31279.  
GO GO:0004867; F:serine protease inhibitor activity; IEA.  
DR InterPro; IPR004094; Anticstasin.  
DR InterPro; IPR001007; VWF\_C.  
DR Pfam; PF02822; Anticstasin; 3.  
DR Pfam; PF00093; VWC; 4.  
DR SMART; SMO0214; VWC; 8.  
DR PROSITE; PS01208; VWF\_C\_1; 6.  
DR PROSITE; PS50184; VWF\_C\_2; 2.  
SQ SEQUENCE 898 AA; 98308 MW; F9686C10837AF35C CRC64;  
Query Match 58.8%; Score 57; DB 5; Length 898;  
Best Local Similarity 61.5%; Pred. No. 0.52;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WOTDNCCTCTCYE 14  
 Db 270 WQKDDCTCTCSE 282

RESULT 2  
 017429 PRELIMINARY; PRT; 909 AA.

AC 017429;  
 DT 01-JAN-1999 (TREMBLrel. 09, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE B0024.14 protein.  
 GN B0024.14  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCB1\_TaxID=6239;

RA SEQUENCE FROM N.A.  
 RA Submitted (Apr-1996) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C.elegans: A platform for  
 RT investigating biology."  
 RL Science 282:2012-2018(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Gardner A.E.;  
 RA Submitted (Jan-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; Z71178; CAA94886.2; -.  
 DR EMBL; AL021478; CAA94886.2; JOINED.  
 DR EMBL; AL021478; CAC35857.1; -.  
 DR EMBL; Z71178; CAC35857.1; JOINED.  
 DR PIR; T18649; T18649.  
 DR HSSP; P15358; 1SKZ.  
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.  
 DR InterPro: IPR004094; Anticstasin.  
 DR InterPro: IPR001007; VWF C.  
 DR Pfam; PF02822; Anticstasin; 3.  
 DR Pfam; PF00093; VWC; 4.  
 DR SMART; SMO0214; VWC; 6.  
 DR PROSITE; PS01208; VWF\_C\_1; 6.  
 DR PROSITE; PS0184; VWF\_C\_2; 2.  
 SQ SEQUENCE 909 AA; 99832 MW; 489CFCFF4C39F1AA CRC64;

Query Match 58.8%; Score 57; DB 5; Length 909;  
 Best Local Similarity 61.5%; Pred. No. 0.53;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WOTDNCCTCTCYE 14  
 Db 270 WQKDDCTCTCSE 282

RESULT 3  
 08MM07 PRELIMINARY; PRT; 960 AA.

AC 08MM07;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE B0024.14b protein.  
 GN B0024.14 OR B0024.14B.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCB1\_TaxID=6239;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA McMurray A.A.;  
 RA Submitted (Apr-1996) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C.elegans: A platform for  
 RT investigating biology."  
 RL Science 282:2012-2018(1998).  
 DR EMBL; Z71178; CAA44087.1; -.  
 DR EMBL; Z71181; CAA44087.1; JOINED.  
 DR EMBL; Z71181; CAA44140.1; -.  
 DR EMBL; Z71178; CAA44140.1; JOINED.  
 DR WormRep; B0024.14b; CE31277.  
 DR GO; GO:000576; C:extracellular; IEA.  
 DR GO; GO:0005520; F:insulin-like growth factor binding; IEA.  
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.  
 DR GO; GO:0001558; P:regulation of cell growth; IEA.  
 DR InterPro: IPR004094; Anticstasin.  
 DR InterPro: IPR000867; Insl\_gro\_fac\_pr.  
 DR InterPro: IPR001007; VWF C.  
 DR Pfam; PF02822; Anticstasin; 3.  
 DR Pfam; PF00093; VWC; 4.  
 DR SMART; SMO0121; IB; 1.  
 DR SMART; SMO0214; VWC; 8.  
 DR PROSITE; PS01208; VWF\_C\_1; 6.  
 DR PROSITE; PS0184; VWF\_C\_2; 2.  
 SQ SEQUENCE 960 AA; 104823 MW; C45B48096D7E409 CRC64;

Query Match 58.8%; Score 57; DB 5; Length 960;  
 Best Local Similarity 61.5%; Pred. No. 0.53;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 WOTDNCCTCTCYE 14  
 Db 336 WQKDDCTCTCSE 348

RESULT 4  
 098SU7 PRELIMINARY; PRT; 910 AA.

AC 098SU7;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Spiggin alpha.  
 OS Gasterosteus aculeatus (three spined stickleback).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;  
 OC Gasterosteidae; Gasterosteus.  
 OX NCB1\_TaxID=69293;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21264567; PubMed=11279178;  
 RA Jones T., Lindberg C., Jakobsson S., Hellqvist A., Hellman U.,  
 RA Borg B., Olsson P.E.;  
 RT "Molecular cloning and characterization of spiggin. An androgen-  
 RT regulated extraorganismal adhesive with structural similarities to von  
 RT Willebrand factor-related proteins."  
 RL J. Biol. Chem. 276:17857-17863(2001).  
 DR EMBL; AF323732; AAK15297.1; -.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0015070; F:toxin activity; IEA.  
 DR GO; GO:0009405; P:patogenesis; IEA.  
 DR InterPro: IPR003571; Snake\_toxin.  
 DR InterPro: IPR002919; TIL\_Cysrich.  
 DR InterPro: IPR001846; VWF\_D.  
 DR Pfam; PF00094; vwd; 3.  
 DR SMART; SMO0216; VWD; 2.  
 DR PROSITE; PS00272; SNAKE\_TOXIN; 1.

SO SEQUENCE 910 AA; 102673 MW; 687F6B43ED3A5BD1 CRC64;  
 Query Match 57.7%; Score 56; DB 13; Length 910;  
 Best Local Similarity 80.0%; Pred. No. 0.77; 1; Indels 0; Gaps 0;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 4 TDNCECTCTC 13  
 783 TSNCKTCTCY 792

RESULT 5  
 026637 PRELIMINARY; PRT; 1376 AA.  
 ID 026637; PRELIMINARY; PRT; 1376 AA.  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE 5 alpha fibrillar collagen (Fragment).  
 GN COL5A1PHA.  
 OS Strongylocentrotus purpuratus (Purple sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoida; Echinoidea; Echinacea; Echinoida; Strongylocentrotidae;  
 OC Strongylocentrotus.  
 OC NCB1\_TaxID=7668;  
 RX MEDLINE=96096722; PubMed=8523669;  
 RA Exposito J.Y., Boue N., Delage G., Garrone R.;  
 RT "Characterization of two genes coding for a similar four-cysteine  
 motif of the amino-terminal propeptide of a sea urchin fibrillar  
 collagen.";  
 RT Eur. J. Biochem. 234:59-65 (1995).  
 DR EMBL; X89800; CAA61928.1; .  
 DR EMBL; X89801; CAA61928.1; JOINED.  
 DR EMBL; X89802; CAA61928.1; JOINED.  
 DR EMBL; X89803; CAA61928.1; JOINED.  
 DR EMBL; X89804; CAA61928.1; JOINED.  
 DR EMBL; X89805; CAA61928.1; JOINED.  
 DR PIR; S63986; S63986.  
 DR InterPro; IPR001007; VWF\_C.  
 DR Pfam; PF00093; VWF\_1.  
 DR SMART; SM00214; VWC; 1.  
 DR PROSITE; PS01208; VWF\_C\_1; 1.  
 DR PROSITE; PS50184; VWF\_C\_2; 1.  
 KM Collagen.  
 FT NON TER  
 SQ SEQUENCE 1376 AA; 151182 MW; AF134036781FAAC6 CRC64;

Query Match 55.7%; Score 54; DB 5; Length 1376;  
 Best Local Similarity 58.3%; Pred. No. 2.4;  
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 1 EMOTDNCECTCTC 12  
 28 EMKYDECTTCAC 39

RESULT 6  
 0918G7 PRELIMINARY; PRT; 2327 AA.  
 ID 0918G7; PRELIMINARY; PRT; 2327 AA.  
 AC 0918G7;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Kiehn.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodidae; Xenopus.  
 OC NCB1\_TaxID=8355;  
 RN (1)  
 RP SEQUENCE FROM N.A.

RC TISSUE=Embryonic floor plate;  
 RA MEDLINE=20266358; PubMed=10779551;  
 RX Matsui M., Mizusaki K., Nakatani J., Nakatani S., Sasai Y.;  
 RT "Xenopus Kiehn: A dorso-lateralizing factor containing multiple chordin-type  
 repeats secreted from the embryonic midline."  
 RT Proc. Natl. Acad. Sci. U.S.A. 97:5291-5296 (2000).  
 DR EMBL; AB026192; BAA95483.1; .  
 DR HSSP; P56682; ICCV.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR GO; GO:0007155; P:cell adhesion; IEA.  
 DR InterPro; IPR006209; EGF like.  
 DR InterPro; IPR003129; TSPN.  
 DR InterPro; IPR001007; VWF\_C.  
 DR InterPro; IPR001846; VWF\_D.  
 DR Pfam; PF01826; TIL; 1.  
 DR Pfam; PF00093; VWC; 22.  
 DR Pfam; PF00094; VWD; 1.  
 DR SMART; SM00210; TSPN; 1.  
 DR SMART; SM00214; VWC; 27.  
 DR SMART; SM00216; VWD; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS01208; VWF\_C\_1; 20.  
 DR PROSITE; PS50184; VWF\_C\_2; 19.  
 SQ SEQUENCE 2327 AA; 255800 MW; 0293109329209983 CRC64;

Query Match 54.6%; Score 53; DB 13; Length 2327;  
 Best Local Similarity 63.6%; Pred. No. 5.9;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 2 MOTDNCECTCTC 12  
 451 WRKDTCTCTC 461

RESULT 7  
 0966K0 PRELIMINARY; PRT; 321 AA.  
 ID 0966K0; PRELIMINARY; PRT; 321 AA.  
 AC 0966K0;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Hypothetical protein F35B3.1.  
 GN F35B3.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodermidae; Caenorhabditis.  
 OC NCB1\_TaxID=6239;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 investigating biology. The C. elegans Sequencing Consortium.";  
 RT Science 282:2012-2018 (1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RA Latreil P.;  
 RT "The sequence of C. elegans cosmid F35B3."  
 RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RA Waterston R.;  
 RT "Direct Submission."  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC006633; AAK68372.1; .  
 DR WormPep; F35B3.1; CE07168.  
 DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.  
 DR GO; GO:0004221; Fubitinin thiolesterase activity; IEA.  
 DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.



DT 01-OCT-2003 (Tremblrel. 25, last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, last annotation update)  
 DE Thrombospondin 2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3H/He; Tissue=Mesenchymal Stem Cell;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Krausberg R.L., Feinold E.A., Grouse L.H., Derge J.G.,  
 RA Krausner R.D., Collins F.S., Wagner L., Stemen C.M., Schler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Urdin T.B., Toshiyuki S., Carninci P., Mallory S.J.,  
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mollahy S.J.,  
 RA Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.O., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schmeich A., Schein J.E.,  
 RA Jones S.V., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3H/He; Tissue=Mesenchymal Stem Cell;  
 RA Krausberg R.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC053702; AAHS3702.1;  
 SQ SEQUENCE 1172 AA; 129942 MW; B620EF2B2F5DF0D5 CRC64;

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QY 2 WQDNCCTCTC 12  
 Db 333 WVVDSCCTCTC 343

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 AC Q9E0T9;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, last annotation update)  
 DE ARG1.  
 GN LCN7 OR ARG1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC Kobayashi M., Kinouchi T., Kamikato T., Kuriki K., Suzuki K.,  
 RA Tokue A., Fukayama M., Tanaka A.;  
 RT "Isolation of an Androgen-inducible Novel Lipocarin Protein, Arg1, from  
 RT Androgen-dependent Mouse Mammary Shionogi Carcinoma Cells.";  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB047402; BAB20596.1;  
 DR HSSP; P07688; 10DQ.  
 DR MGI; MGI:2137617; Lcn7.  
 DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.  
 DR GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR000566; Lipocin\_cytrABP.  
 DR InterPro; IPR000668; Peptidase\_C1.  
 DR InterPro; IPR000169; Shpoc\_acsite.  
 DR InterPro; IPR001212; Somatomedin\_B.  
 DR Pfam; PF00112; Peptidase\_C1; 1.  
 DR PRINTS; PR00705; PAPAIN.  
 DR ProDom; PD00158; Peptidase\_C1; 1.  
 DR SMART; SM00645; Pep\_C1; 1.  
 DR SMART; SM00201; SO; 1.  
 DR PROSITE; PS00213; LIPOCALIN; 1.  
 DR PROSITE; PS00639; THIOL PROTEASE HIS; 1.  
 SQ SEQUENCE 415 AA; 46848 MW; AD1147FC759CCB02 CRC64;

Query Match 51.5%; Score 50; DB 11; Length 415;  
 Best Local Similarity 70.0%; Pred. No. 3.5;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 DNCERTCTCE 14  
 Db 68 DNCNCTCTCE 77

RESULT 12  
 ID 009538 PRELIMINARY; PRT; 429 AA.  
 AC 009538;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, last annotation update)  
 DE F19C6.3 protein.  
 GN F19C6.3.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Felodierinae; Caenorhabditis.  
 NCBI\_TaxID=6239;  
 RN  
 RP SEQUENCE FROM N.A.  
 RA Harris B.R.;  
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C. elegans: A platform for  
 RT investigating biology.";  
 RL Science 283:2012-2018(1998).  
 DR EMBL; Z48006; CAA8048.1;  
 DR F1R; T2113; T2113.  
 DR WormPep; F19C6.3; C601556.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR01007; VWF\_C.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00093; vwc; 1.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS01208; VWF\_1; 1.  
 DR PROSITE; PS0184; VWF\_2; 1.  
 KM EGF-like domain.  
 SQ SEQUENCE 429 AA; 48663 MW; 8C2C81FA09AF3D3D CRC64;

Query Match 51.5%; Score 50; DB 5; Length 429;  
 Best Local Similarity 57.1%; Pred. No. 3.6;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EWQDNCCTCTCE 14

DB 227 ETKYVNCNTCTCVD 240

## RESULT 13

Q99UR5 PRELIMINARY; PRT; 466 AA.

AC Q99UR5; 01-JUN-2001 (TRENBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)

DE Hypothetical protein (Tubulointerstitial nephritis antigen-related protein).

GN LCN7 OR TARP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1] SEQUENCE FROM N.A.

RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

RP [2] SEQUENCE FROM N.A.

RC TISSUE=Adrenal cortex; PubMed=12600995;

RA Medline=22615905; PubMed=12600995; Suzuki R., Suzuki T., Suematsu M., Ishimura Y.;

RT "An Inverse Correlation between Expression of a Preprocathepsin B-related Protein with Cysteine-rich Sequences and Steroid 11beta-Hydroxylase in Adrenocortical Cells.";

RU J. Biol. Chem. 278:17084-17092(2003).

DR EMBL; BC005738; AAH05738.1; -

DR EMBL; BC018539; AAH18539.1; -

DR HSSP; P07688; 10DQ.

DR MGD; MGI:2137617; Lcn7.

DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.

DR GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR000668; Lipocln cyFPABP.

DR InterPro; IPR000169; SHprot\_acctle.

DR InterPro; IPR001212; Somatomedin\_B.

DR Pfam; PF00112; Peptidase\_C1; 1.

DR ProDom; PD000158; Peptidase\_C1; 1.

DR SMART; SM00645; Pept\_C1; 1.

DR SMART; SM00201; SO; 1.

DR PROSITE; PS00213; LIPOCALIN; 1.

DR PROSITE; PS00639; THIOL\_PROTEASE\_HIS; 1.

KM Hypothetical protein.

SO SEQUENCE 466 AA; 52664 MW; D12ABDC8F63F36D CRC64;

Query Match 51.5%; Score 50; DB 11; Length 466;

Best Local Similarity 70.0%; Pred. No. 3.9;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 DNCETCTCYE 14

DB 119 DNCNRCCTCHE 128

## RESULT 14

P94804 PRELIMINARY; PRT; 663 AA.

AC P94804; 01-MAY-1997 (TRENBLrel. 03, Created)

DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)

DE Beta-D-galactosidase.

GN BGAH.

OS Haloferax sp. (strain Aa 2.2).

OC Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;

OC Halobacteriaceae; Haloferax.

OX NCBI\_TaxID=2254;

RN [1] SEQUENCE FROM N.A.

RA STRAIN=SB1;

RC MEDLINE=97201076; PubMed=9048905;

RA Holmes M.L., Scopes R.K., Moritz R.L., Simpson R.J., Englert C., Pfeiffer F., Dyall-Smith M.L.;

RT "Purification and analysis of an extremely halophilic beta-galactosidase from Haloferax alkalentel";

RU Biochim. Biophys. Acta 1337:276-286(1997).

DR [2] SEQUENCE FROM N.A.

RA STRAIN=SB1;

RC MEDLINE=20223653; PubMed=10760168;

RA Holmes M.L., Dyall-Smith M.L.;

RT "Sequence and expression of a halobacterial beta-galactosidase gene";

RU Mol. Microbiol. 36:114-122(2000).

DR [3] SEQUENCE FROM N.A.

RA Holmes M.L., Dyall-Smith M.L.;

RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; U70664; AAB40123.2; -

DR PIR; T44793; T44793.

DR GO; GO:0003341; C:beta-galactosidase complex; IEA.

DR GO; GO:0004565; F:beta-galactosidase activity; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR003476; Glyco\_hydro\_42.

DR Pfam; PF02449; Glyco\_hydro\_42; 1.

SO SEQUENCE 663 AA; 74459 MW; 7ADF7634C5D13BE9 CRC64;

Query Match 51.5%; Score 50; DB 1; Length 663;

Best Local Similarity 68.8%; Pred. No. 5.5;

Matches 11; Conservative 0; Mismatches 1; Indels 4; Gaps 2;

QY 2 WOTDN---C-ETCTCY 13

DB 137 WOTDNFQCHETVTCY 152

## RESULT 15

Q77302 PRELIMINARY; PRT; 1027 AA.

AC Q77302; 01-OCT-2003 (TRENBLrel. 25, Created)

DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)

DE Cysteine-rich motor neuron 1.

GN CRIM1.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Osteichthys; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI\_TaxID=7955;

RN [1] SEQUENCE FROM N.A.

RA Kolle G.V., Little M.H.;

RT "Characterization of zebrafish crim1 ortholog.";

RU Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY151045; AAN72833.1; -

SO SEQUENCE 1027 AA; 112222 MW; E831F8CF174344CC CRC64;

Query Match 50.5%; Score 49; DB 13; Length 1027;

Best Local Similarity 50.0%; Pred. No. 12;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 WOTDNCECTCY 13

DB 688 WNDSCCTCTCH 699

Fri Mar 12 09:42:18 2004

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Job time : 14.0968 secs

us-09-977-406a-5.rspt

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

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Title: US-09-977-406a-5

Perfect score: 97

Sequence: 1 EWQDNCETCTCYET 15

Scoring table: BLOSUM62

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:\*  
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2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	97	100.0	15 10 US-09-977-406a-5	Sequence 5, Appl
2	97	100.0	15 14 US-10-291-360-5	Sequence 5, Appl
3	97	100.0	16 10 US-09-977-406a-10	Sequence 10, Appl
4	97	100.0	16 10 US-09-977-406a-59	Sequence 59, Appl
5	97	100.0	17 10 US-09-977-406a-11	Sequence 11, Appl
6	97	100.0	17 10 US-09-977-406a-60	Sequence 60, Appl
7	97	100.0	18 10 US-09-977-406a-12	Sequence 12, Appl
8	97	100.0	18 10 US-09-977-406a-61	Sequence 61, Appl
9	97	100.0	19 10 US-09-977-406a-13	Sequence 13, Appl
10	97	100.0	19 10 US-09-977-406a-62	Sequence 62, Appl
11	97	100.0	20 10 US-09-977-406a-14	Sequence 14, Appl
12	97	100.0	20 10 US-09-977-406a-63	Sequence 63, Appl
13	97	100.0	21 10 US-09-977-406a-15	Sequence 15, Appl
14	97	100.0	21 10 US-09-977-406a-64	Sequence 64, Appl
15	97	100.0	22 10 US-09-977-406a-16	Sequence 16, Appl

15	97	100.0	22	10	US-09-977-406a-65	Sequence 65, Appl
17	97	100.0	23	10	US-09-977-406a-17	Sequence 17, Appl
18	97	100.0	23	10	US-09-977-406a-66	Sequence 66, Appl
19	97	100.0	24	10	US-09-977-406a-18	Sequence 18, Appl
20	97	100.0	24	10	US-09-977-406a-67	Sequence 67, Appl
21	97	100.0	25	10	US-09-977-406a-19	Sequence 19, Appl
22	97	100.0	25	10	US-09-977-406a-68	Sequence 68, Appl
23	97	100.0	26	10	US-09-977-406a-20	Sequence 20, Appl
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27	97	100.0	28	10	US-09-977-406a-22	Sequence 22, Appl
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31	97	100.0	30	10	US-09-977-406a-24	Sequence 24, Appl
32	97	100.0	30	10	US-09-977-406a-73	Sequence 73, Appl
33	97	100.0	31	10	US-09-977-406a-25	Sequence 25, Appl
34	97	100.0	31	10	US-09-977-406a-74	Sequence 74, Appl
35	97	100.0	32	10	US-09-977-406a-26	Sequence 26, Appl
36	97	100.0	32	10	US-09-977-406a-75	Sequence 75, Appl
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44	97	100.0	36	10	US-09-977-406a-79	Sequence 79, Appl
45	97	100.0	36	10	US-09-977-406a-80	Sequence 80, Appl

## ALIGNMENTS

RESULT 1  
US-09-977-406a-5  
; Sequence 5, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCOON BIOPHARMA INC.  
; TITLE OR INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03/977,406A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCK3145 (polypeptide 31-45)  
US-09-977-406a-5  
Query Match 100.0%; Score 97; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 EWQDNCETCTCYET 15  
Db 1 EWQDNCETCTCYET 15  
RESULT 2  
US-10-291-360-5  
; Sequence 5, Application US/10291360  
; Publication No. US20030119744A1  
; GENERAL INFORMATION:

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; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis
; FILE REFERENCE: 06508-051-US-02
; CURRENT APPLICATION NUMBER: US/10/291,360
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: CA 2,361,736
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCK3145 (polypeptide 31-45)
US-10-291-360-5

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DB 1 EMQDNCETCTCYET 15

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; Sequence 10, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-10

Query Match          100.0%; Score 97; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 9,5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYET 15
DB 1 EMQDNCETCTCYET 15

RESULT 4
US-09-977-406A-59
; Sequence 59, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-59
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; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-59

Query Match          100.0%; Score 97; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 9,5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYET 15
DB 2 EMQDNCETCTCYET 16

RESULT 5
US-09-977-406A-11
; Sequence 11, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-11

Query Match          100.0%; Score 97; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYET 15
DB 1 EMQDNCETCTCYET 15

RESULT 6
US-09-977-406A-60
; Sequence 60, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-60
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OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-60

Query Match 100.0%; Score 97; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 3 EWQDNCETCTCYET 17

RESULT 7  
US-09-977-406A-12

Sequence 12, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:

APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS

FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A

PRIOR FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: CA 2,321,256

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: CA 2,355,334

PRIOR FILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn version 3.1

SEQ ID NO 12

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)

US-09-977-406A-12

Query Match 100.0%; Score 97; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 1 EWQDNCETCTCYET 15

RESULT 8  
US-09-977-406A-61

Sequence 61, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:

APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS

FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A

PRIOR FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: CA 2,321,256

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: CA 2,355,334

PRIOR FILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn version 3.1

SEQ ID NO 61

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)

US-09-977-406A-61

Query Match 100.0%; Score 97; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 4 EWQDNCETCTCYET 18

RESULT 9  
US-09-977-406A-13

Sequence 13, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:

APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS

FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A

PRIOR FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: CA 2,321,256

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: CA 2,355,334

PRIOR FILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn version 3.1

SEQ ID NO 13

LENGTH: 19

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)

US-09-977-406A-13

Query Match 100.0%; Score 97; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 1 EWQDNCETCTCYET 15

RESULT 10  
US-09-977-406A-62

Sequence 62, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:

APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS

FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A

PRIOR FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: CA 2,321,256

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: CA 2,355,334

PRIOR FILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn version 3.1

SEQ ID NO 62

LENGTH: 19

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)

US-09-977-406A-62

Query Match 100.0%; Score 97; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 5 EWQDNCETCTCYET 19

RESULT 11  
US-09-977-406A-14

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; Sequence 14, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhHSP94 sequence (polypeptide analog)
US-09-977-406A-14

Query Match
Best Local Similarity 100.0%; Score 97; DB 10; Length 20;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15
DB 1 EWQDNCETCTCYET 15

RESULT 12
US-09-977-406A-63
; Sequence 63, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhHSP94 sequence (polypeptide analog)
US-09-977-406A-63

Query Match
Best Local Similarity 100.0%; Score 97; DB 10; Length 20;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15
DB 6 EWQDNCETCTCYET 20

RESULT 13
US-09-977-406A-15
; Sequence 15, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1

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; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhHSP94 sequence (polypeptide analog)
US-09-977-406A-15

Query Match
Best Local Similarity 100.0%; Score 97; DB 10; Length 21;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15
DB 1 EWQDNCETCTCYET 15

RESULT 14
US-09-977-406A-64
; Sequence 64, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhHSP94 sequence (polypeptide analog)
US-09-977-406A-64

Query Match
Best Local Similarity 100.0%; Score 97; DB 10; Length 21;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15
DB 7 EWQDNCETCTCYET 21

RESULT 15
US-09-977-406A-16
; Sequence 16, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1

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Fri Mar 12 09:42:17 2004

us-09-977-406a-5.rapb

Page 5

SEQ ID NO 16  
LENGTH: 22  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-16

Query Match 100.0%; Score 97; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 EMQTDNCETCTCYET 15

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Job time : 9.91936 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2004, 06:06:42 ; Search time 12.0968 Seconds  
(without alignments)  
321.105 Million cell updates/sec

Title: US-09-977-406A-5  
Perfect score: 97  
Sequence: 1 EMOTDNCECTCYET 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/2/pubpaa/PTI\_NEW\_PUB.pep:\*
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- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
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- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	15	US-09-977-406A-5	Sequence 5, Appl
2	97	100.0	15	US-10-291-360-5	Sequence 5, Appl
3	97	100.0	16	US-09-977-406A-10	Sequence 10, Appl
4	97	100.0	16	US-09-977-406A-59	Sequence 59, Appl
5	97	100.0	17	US-09-977-406A-11	Sequence 11, Appl
6	97	100.0	17	US-09-977-406A-60	Sequence 60, Appl
7	97	100.0	18	US-09-977-406A-12	Sequence 12, Appl
8	97	100.0	18	US-09-977-406A-61	Sequence 61, Appl
9	97	100.0	19	US-09-977-406A-13	Sequence 13, Appl
10	97	100.0	19	US-09-977-406A-62	Sequence 62, Appl
11	97	100.0	20	US-09-977-406A-14	Sequence 14, Appl
12	97	100.0	20	US-09-977-406A-63	Sequence 63, Appl
13	97	100.0	21	US-09-977-406A-15	Sequence 15, Appl
14	97	100.0	21	US-09-977-406A-64	Sequence 64, Appl
15	97	100.0	22	US-09-977-406A-16	Sequence 16, Appl

16	97	100.0	22	US-09-977-406A-65	Sequence 65, Appl
17	97	100.0	23	US-09-977-406A-17	Sequence 17, Appl
18	97	100.0	23	US-09-977-406A-66	Sequence 66, Appl
19	97	100.0	24	US-09-977-406A-18	Sequence 18, Appl
20	97	100.0	24	US-09-977-406A-67	Sequence 67, Appl
21	97	100.0	25	US-09-977-406A-19	Sequence 19, Appl
22	97	100.0	25	US-09-977-406A-68	Sequence 68, Appl
23	97	100.0	26	US-09-977-406A-20	Sequence 20, Appl
24	97	100.0	26	US-09-977-406A-69	Sequence 69, Appl
25	97	100.0	27	US-09-977-406A-71	Sequence 21, Appl
26	97	100.0	27	US-09-977-406A-70	Sequence 20, Appl
27	97	100.0	28	US-09-977-406A-22	Sequence 22, Appl
28	97	100.0	28	US-09-977-406A-71	Sequence 71, Appl
29	97	100.0	29	US-09-977-406A-23	Sequence 23, Appl
30	97	100.0	29	US-09-977-406A-72	Sequence 72, Appl
31	97	100.0	30	US-09-977-406A-24	Sequence 24, Appl
32	97	100.0	30	US-09-977-406A-73	Sequence 73, Appl
33	97	100.0	30	US-09-977-406A-90	Sequence 90, Appl
34	97	100.0	31	US-09-977-406A-25	Sequence 25, Appl
35	97	100.0	31	US-09-977-406A-74	Sequence 74, Appl
36	97	100.0	32	US-09-977-406A-26	Sequence 26, Appl
37	97	100.0	32	US-09-977-406A-75	Sequence 75, Appl
38	97	100.0	33	US-09-977-406A-27	Sequence 27, Appl
39	97	100.0	33	US-09-977-406A-76	Sequence 76, Appl
40	97	100.0	34	US-09-977-406A-28	Sequence 28, Appl
41	97	100.0	34	US-09-977-406A-77	Sequence 77, Appl
42	97	100.0	35	US-09-977-406A-29	Sequence 29, Appl
43	97	100.0	35	US-09-977-406A-78	Sequence 78, Appl
44	97	100.0	36	US-09-977-406A-30	Sequence 30, Appl
45	97	100.0	36	US-09-977-406A-79	Sequence 79, Appl

## ALIGNMENTS

RESULT 1  
US-09-977-406A-5  
Sequence 5, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977, 406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PK3145 (polypeptide 31-45)  
US-09-977-406A-5

Query Match 100.0%; Score 97; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMOTDNCECTCYET 15  
DB 1 EMOTDNCECTCYET 15

RESULT 2  
US-10-291-360-5  
Sequence 5, Application US/10291360  
Publication No. US20030119744A1  
GENERAL INFORMATION:

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; APPLICANT: PROCTON BIOPHARMA INC.
; TITLE OF INVENTION: Psp-94: Use for Treatment of Hypercalcemia and Bone metastasis
; FILE REFERENCE: 06508-051-US-02
; CURRENT APPLICATION NUMBER: US/10/291,360
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: CA 2,361,736
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCK3145 (polypeptide 31-45)
US-10-291-360-5

Query Match      100.0%; Score 97; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EMQDNCETCTCYET 15
DB      1 EMQDNCETCTCYET 15

RESULT 3
US-09-977-406a-10
; Sequence 10, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCTON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-15
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406a-10

Query Match      100.0%; Score 97; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EMQDNCETCTCYET 15
DB      1 EMQDNCETCTCYET 15

RESULT 4
US-09-977-406a-59
; Sequence 59, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCTON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406a-10
```

```

; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406a-59

Query Match      100.0%; Score 97; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EMQDNCETCTCYET 15
DB      2 EMQDNCETCTCYET 16

RESULT 5
US-09-977-406a-11
; Sequence 11, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCTON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406a-11

Query Match      100.0%; Score 97; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EMQDNCETCTCYET 15
DB      1 EMQDNCETCTCYET 15

RESULT 6
US-09-977-406a-60
; Sequence 60, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCTON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406a-10
```



OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-60

Query Match 100.0%; Score 97; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1,3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 3 EWQDNCETCTCYET 17

## RESULT 7

US-09-977-406A-12  
Sequence 12, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT FILING DATE: 2001-10-15  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 12  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-12

Query Match 100.0%; Score 97; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1,4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 1 EWQDNCETCTCYET 15

## RESULT 8

US-09-977-406A-61  
Sequence 61, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT FILING DATE: 2001-10-15  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 61  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-61

Query Match 100.0%; Score 97; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1,4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 4 EWQDNCETCTCYET 18

## RESULT 9

US-09-977-406A-13  
Sequence 13, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT FILING DATE: 2001-10-15  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 13  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-13

Query Match 100.0%; Score 97; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1,5e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 1 EWQDNCETCTCYET 15

## RESULT 10

US-09-977-406A-62  
Sequence 62, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT FILING DATE: 2001-10-15  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 62  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-62

Query Match 100.0%; Score 97; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1,5e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 5 EWQDNCETCTCYET 19

## RESULT 11

US-09-977-406A-14

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; Sequence 14, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-14
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Query Match          100.0%; Score 97; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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CY 1 EMQDNCETCTCYET 15
Db 1 EMQDNCETCTCYET 15
```

```
RESULT 12
US-09-977-406A-63
; Sequence 63, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-63
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```
Query Match          100.0%; Score 97; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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CY 1 EMQDNCETCTCYET 15
Db 6 EMQDNCETCTCYET 20
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RESULT 13
US-09-977-406A-15
; Sequence 15, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
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; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-15
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```
Query Match          100.0%; Score 97; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
CY 1 EMQDNCETCTCYET 15
Db 1 EMQDNCETCTCYET 15
```

```
RESULT 14
US-09-977-406A-64
; Sequence 64, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-64
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```
Query Match          100.0%; Score 97; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
CY 1 EMQDNCETCTCYET 15
Db 7 EMQDNCETCTCYET 21
```

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RESULT 15
US-09-977-406A-16
; Sequence 16, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
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```

; SEQ ID NO 16
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406A-16

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Query Match          100.0%; Score 97; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 EMQDNCETCTCYET 15
Db      1 EMQDNCETCTCYET 15

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Search completed: March 18, 2004, 06:13:00  
 Job time : 12.0968 secs

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Mon Mar 22 13:39:30 2004

us-09-977-406a-58.rapb

Page 1

GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: March 18, 2004, 06:06:42 ; Search time 51.6129 Seconds  
(without alignments)  
321.105 Million cell updates/sec

Title: US-09-977-406A-58

Perfect score: 368  
Sequence: 1 EMQDNCETCTCYETETISCC.....YIVVEKDPKKTCSVSEMI 64

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 14: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	368	100.0	64	10	US-09-977-406A-58
2	368	100.0	94	10	US-09-977-406A-1
3	368	100.0	94	14	US-10-291-360-1
4	368	100.0	102	10	US-09-977-406A-2
5	368	100.0	102	14	US-10-291-360-2
6	368	100.0	114	12	US-10-221-278-236
7	368	100.0	114	12	US-10-012-896-1003
8	368	100.0	114	14	US-10-205-823-271
9	368	100.0	114	14	US-10-244-678A-1003
10	368	100.0	114	14	US-10-294-025-1003
11	368	100.0	114	15	US-10-291-172-236
12	368	100.0	132	9	US-09-925-300-1027
13	364	98.9	63	10	US-09-977-406A-57
14	360	97.8	62	10	US-09-977-406A-56
15	349	94.8	61	10	US-09-977-406A-55

16	344	93.5	60	10	US-09-977-406A-54	Sequence 54, Appl
17	340	92.4	59	10	US-09-977-406A-53	Sequence 53, Appl
18	336	91.3	58	10	US-09-977-406A-52	Sequence 52, Appl
19	332	90.2	57	10	US-09-977-406A-51	Sequence 51, Appl
20	323	87.8	56	10	US-09-977-406A-50	Sequence 50, Appl
21	318	86.4	55	10	US-09-977-406A-49	Sequence 49, Appl
22	313	85.1	54	10	US-09-977-406A-48	Sequence 48, Appl
23	308	83.7	53	10	US-09-977-406A-47	Sequence 47, Appl
24	301	81.6	52	10	US-09-977-406A-46	Sequence 46, Appl
25	295	80.2	51	10	US-09-977-406A-45	Sequence 45, Appl
26	290	78.8	50	10	US-09-977-406A-44	Sequence 44, Appl
27	285	77.4	49	10	US-09-977-406A-43	Sequence 43, Appl
28	280	76.1	48	10	US-09-977-406A-42	Sequence 42, Appl
29	279	75.8	119	12	US-10-221-278-612	Sequence 612, App
30	279	75.8	119	15	US-10-291-172-612	Sequence 612, App
31	275	75.0	47	10	US-09-977-406A-41	Sequence 41, App
32	272	73.9	46	10	US-09-977-406A-40	Sequence 40, Appl
33	268	72.8	45	10	US-09-977-406A-39	Sequence 39, Appl
34	261	70.9	44	10	US-09-977-406A-38	Sequence 38, Appl
35	256	69.6	43	10	US-09-977-406A-37	Sequence 37, Appl
36	247	67.1	42	10	US-09-977-406A-36	Sequence 36, Appl
37	241	65.5	41	10	US-09-977-406A-35	Sequence 35, Appl
38	236	64.1	40	10	US-09-977-406A-34	Sequence 34, Appl
39	231	62.8	39	10	US-09-977-406A-33	Sequence 33, Appl
40	226	61.4	38	10	US-09-977-406A-32	Sequence 32, Appl
41	220	59.8	37	10	US-09-977-406A-31	Sequence 31, Appl
42	216	58.7	36	10	US-09-977-406A-30	Sequence 30, Appl
43	211	57.3	35	10	US-09-977-406A-29	Sequence 29, Appl
44	206	56.0	34	10	US-09-977-406A-28	Sequence 28, Appl
45	197	53.5	33	10	US-09-977-406A-27	Sequence 27, Appl

#### ALIGNMENTS

RESULT 1  
US-09-977-406A-58  
Sequence 58, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCOON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
PRIOR FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 58  
LENGTH: 64  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-58

Query Match 100.0%; Score 368; DB 10; Length 64;  
Best Local Similarity 100.0%; Pred. No. 1.3e-34;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVTPGVYDXDNCQRIKEDCKIYVEKDPKKTCSV 60  
DB 1 EMQDNCETCTCYETETISCTLVTPGVYDXDNCQRIKEDCKIYVEKDPKKTCSV 60  
QY 61 EWII 64  
DB 61 EWII 64

RESULT 2

US-09-977-406A-1  
Sequence 1, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 94  
TYPE: PRT  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
AUTHORS: Ulvback, W., Lindstrom, C., Welber, H., Abrahamson, P.A., Lilja, H., and  
AUTHORS: Lundwall, A.  
TITLE: Molecular cloning of a small prostate protein, known as beta-  
TITLE: microsemoprotein, PSP94 or beta-inhibin, and demonstration of transcripts  
TITLE: non-genital tissues.  
JOURNAL: Biochem. Biophys. Res Commun.  
VOLUME: 164  
ISSUE: 3  
PAGES: 1310-1315  
DATE: 1989  
DATABASE ACCESSION NUMBER: GI 131436  
DATABASE ENTRY DATE: 1988-08-01  
US-09-977-406A-1  
Query Match  
Best Local Similarity 100.0%; Score 368; DB 10; Length 94;  
Pred. No. 1,9e-34;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 61 Ewii 64  
91 Ewii 94  
RESULT 3  
US-10-291-360-1  
Sequence 1, Application US/10291360  
Publication No. US20030119744A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcaemia and Bone metastasis  
FILE REFERENCE: 06508-051-US-02  
CURRENT APPLICATION NUMBER: US/10/291,360  
CURRENT FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: CA 2,361,736  
PRIOR FILING DATE: 2001-11-08  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 94  
TYPE: PRT  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
AUTHORS: Ulvback, W., Lindstrom, C., Welber, H., Abrahamson, P.A., Lilja, H., and  
AUTHORS: Lundwall, A.  
TITLE: Molecular cloning of a small prostate protein, known as beta-  
TITLE: microsemoprotein, PSP94 or beta-inhibin, and demonstration of transcripts  
TITLE: non-genital tissues.  
JOURNAL: Biochem. Biophys. Res Commun.  
VOLUME: 164

ISSUE: 3  
PAGES: 1310-1315  
DATE: 1989  
DATABASE ACCESSION NUMBER: GI 131436  
DATABASE ENTRY DATE: 1988-08-01  
US-10-291-360-1  
Query Match  
Best Local Similarity 100.0%; Score 368; DB 14; Length 94;  
Pred. No. 1,9e-34;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 61 Ewii 64  
91 Ewii 94  
RESULT 4  
US-09-977-406A-2  
Sequence 2, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 102  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: recombinant human PSP94 (rHSP94) produced from yeast  
US-09-977-406A-2  
Query Match  
Best Local Similarity 100.0%; Score 368; DB 10; Length 102;  
Pred. No. 2,1e-34;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 61 Ewii 64  
99 Ewii 102  
RESULT 5  
US-10-291-360-2  
Sequence 2, Application US/10291360  
Publication No. US20030119744A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcaemia and Bone metastasis  
FILE REFERENCE: 06508-051-US-02  
CURRENT APPLICATION NUMBER: US/10/291,360  
CURRENT FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: CA 2,361,736  
PRIOR FILING DATE: 2001-11-08  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 102

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: recombinant human PSP94 (rHSP94) produced from yeast
US-10-291-360-2

Query Match
Best Local Similarity 100.0%; Score 368; DB 14; Length 102;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFKEDCKYIVVEKDPKKTCSVS 60
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DB 39 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFKEDCKYIVVEKDPKKTCSVS 98

QY 61 EWII 64
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DB 99 EWII 102

RESULT 6
US-10-221-278-236
; Sequence 236, Application US/10221278
; Publication No. US20040034208A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20040034208A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT FILING DATE: 2002-09-06
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 236
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-221-278-236

Query Match
Best Local Similarity 100.0%; Score 368; DB 12; Length 114;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFKEDCKYIVVEKDPKKTCSVS 60
   |||||
DB 51 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFKEDCKYIVVEKDPKKTCSVS 110

QY 61 EWII 64
   |||||
DB 111 EWII 114

RESULT 7
US-10-012-896-1003
; Sequence 1003, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
```

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; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hegler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurst, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carloca
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Mantarabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1003
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-1003

Query Match
Best Local Similarity 100.0%; Score 368; DB 13; Length 114;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFKEDCKYIVVEKDPKKTCSVS 60
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DB 51 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFKEDCKYIVVEKDPKKTCSVS 110

QY 61 EWII 64
   |||||
DB 111 EWII 114

RESULT 8
US-10-205-823-271
; Sequence 271, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ganerayaru, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsay, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: NRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
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; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 271
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-271

Query Match
Best Local Similarity 100.0%; Score 368; DB 14; Length 114;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMOTDNCETCTCYETETISCTLVSTPVGDKDNCQRIFKKEDCKYIVVEKKDPKKTCSVS 60
DB 51 EMOTDNCETCTCYETETISCTLVSTPVGDKDNCQRIFKKEDCKYIVVEKKDPKKTCSVS 110

QY 61 EWII 64
DB 111 EWII 114

RESULT 9
US-10-144-678A-1003
; Sequence 1003, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Ajun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hurst, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Roy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1003
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-678A-1003

Query Match
Best Local Similarity 100.0%; Score 368; DB 14; Length 114;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMOTDNCETCTCYETETISCTLVSTPVGDKDNCQRIFKKEDCKYIVVEKKDPKKTCSVS 60
DB 51 EMOTDNCETCTCYETETISCTLVSTPVGDKDNCQRIFKKEDCKYIVVEKKDPKKTCSVS 110
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QY 61 EWII 64
DB 111 EWII 114

RESULT 10
US-10-294-025-1003
; Sequence 1003, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1003
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-025-1003

Query Match
Best Local Similarity 100.0%; Score 368; DB 14; Length 114;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMOTDNCETCTCYETETISCTLVSTPVGDKDNCQRIFKKEDCKYIVVEKKDPKKTCSVS 60
DB 51 EMOTDNCETCTCYETETISCTLVSTPVGDKDNCQRIFKKEDCKYIVVEKKDPKKTCSVS 110

QY 61 EWII 64
DB 111 EWII 114

RESULT 11
US-10-291-172-236
; Sequence 236, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20030228584A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 236
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-172-236

Query Match
Best Local Similarity 100.0%; Score 368; DB 15; Length 114;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMOTDNCETCTCYETETISCTLVSTPVGDKDNCQRIFKKEDCKYIVVEKKDPKKTCSVS 60
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Db 51 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 110  
QY 61 EWTI 64  
111 EWTI 114

RESULT 12  
US-09-925-300-1027  
; Sequence 1027, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen,  
; APPLICANT: Steve Ruben,  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA101  
; CURRENT APPLICATION NUMBER: US/09/925,300  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05998  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1027  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-300-1027

Query Match 100.0%; Score 368; DB 9; Length 132;  
Best Local Similarity 100.0%; Pred. No. 2,8e-34;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 69 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 128  
QY 61 EWTI 64  
111 EWTI 132  
Db 129 EWTI 132

RESULT 13  
US-09-977-406A-57  
; Sequence 57, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCYON BIOPHARMA INC.,  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 57  
; LENGTH: 63  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rhuPSp4 sequence (polypeptide analog)  
US-09-977-406A-57

Query Match 98.9%; Score 364; DB 10; Length 63;  
Best Local Similarity 100.0%; Pred. No. 3.6e-34;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60  
QY 61 EWTI 63  
111 EWTI 63  
Db 61 EWTI 63

RESULT 14  
US-09-977-406A-56  
; Sequence 56, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCYON BIOPHARMA INC.,  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 56  
; LENGTH: 62  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rhuPSp4 sequence (polypeptide analog)  
US-09-977-406A-56

Query Match 97.8%; Score 360; DB 10; Length 62;  
Best Local Similarity 100.0%; Pred. No. 1e-33;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60  
Db 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60  
QY 61 EW 62  
111 EW 62  
Db 61 EW 62

RESULT 15  
US-09-977-406A-55  
; Sequence 55, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCYON BIOPHARMA INC.,  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 55  
; LENGTH: 61  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rhuPSp4 sequence (polypeptide analog)  
US-09-977-406A-55

Query Match 94.8%; Score 349; DB 10; Length 61;  
Best Local Similarity 100.0%; Pred. No. 1.8e-32;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQTDNCEITCTCYETEISCTIIVSTPVGYDKDNCORIFKKEDOKYIIVEKKDPKKTCSYS 60  
Db 1 EMQTDNCEITCTCYETEISCTIIVSTPVGYDKDNCORIFKKEDOKYIIVEKKDPKKTCSYS 60  
QY 61 E 61  
Db 61 E 61

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Job time : 52.6129 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2004, 06:06:42 ; Search time 36.2903 Seconds  
(Without alignments)  
321.105 Million cell updates/sec

Title: US-09-977-406A-88  
Perfect score: 268  
Sequence: 1 SCYFINEGVPGDSTRKMD.....HPINSEWQDNCETCTCYET 45

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/2/pubppa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB.pep.\*
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- 6: /cgn2\_6/ptodata/2/pubppa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubppa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubppa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubppa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubppa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubppa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubppa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubppa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubppa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	268	100.0	45	10	US-09-977-406A-88
2	268	100.0	94	10	US-09-977-406A-1
3	268	100.0	94	14	US-10-291-360-1
4	268	100.0	102	10	US-09-977-406A-2
5	268	100.0	102	14	US-10-291-360-2
6	268	100.0	114	12	US-10-221-278-236
7	268	100.0	114	13	US-10-012-896-1003
8	268	100.0	114	14	US-10-205-823-271
9	268	100.0	114	14	US-10-144-678A-1003
10	268	100.0	114	14	US-10-284-025-1003
11	268	100.0	114	15	US-10-291-172-236
12	268	100.0	132	9	US-09-925-300-1027
13	264	98.5	44	10	US-09-977-406A-87
14	255	95.1	43	10	US-09-977-406A-86
15	248	92.5	42	10	US-09-977-406A-85

16	242	90.3	41	10	US-09-977-406A-84	Sequence 84, Appl
17	238	88.8	40	10	US-09-977-406A-83	Sequence 83, Appl
18	231	86.2	39	10	US-09-977-406A-82	Sequence 82, Appl
19	225	84.0	38	10	US-09-977-406A-81	Sequence 81, Appl
20	221.5	82.6	119	12	US-10-221-278-612	Sequence 612, Appl
21	221.5	82.1	119	15	US-10-291-172-612	Sequence 612, Appl
22	220	82.6	37	10	US-09-977-406A-80	Sequence 80, Appl
23	214	79.9	36	10	US-09-977-406A-79	Sequence 79, Appl
24	210	78.4	35	10	US-09-977-406A-78	Sequence 78, Appl
25	203	75.7	34	10	US-09-977-406A-77	Sequence 77, Appl
26	197	73.5	33	10	US-09-977-406A-76	Sequence 76, Appl
27	191	71.3	32	10	US-09-977-406A-75	Sequence 75, Appl
28	187	69.8	31	10	US-09-977-406A-74	Sequence 74, Appl
29	182	67.9	30	10	US-09-977-406A-73	Sequence 73, Appl
30	177	66.0	29	10	US-09-977-406A-72	Sequence 72, Appl
31	172	64.2	28	10	US-09-977-406A-71	Sequence 71, Appl
32	163	60.8	27	10	US-09-977-406A-70	Sequence 70, Appl
33	158	59.0	26	10	US-09-977-406A-69	Sequence 69, Appl
34	152	56.7	25	10	US-09-977-406A-68	Sequence 68, Appl
35	148	55.2	24	10	US-09-977-406A-67	Sequence 67, Appl
36	143	53.4	23	10	US-09-977-406A-66	Sequence 66, Appl
37	137	51.1	22	10	US-09-977-406A-65	Sequence 65, Appl
38	131	48.9	21	10	US-09-977-406A-64	Sequence 64, Appl
39	126	47.0	20	10	US-09-977-406A-63	Sequence 63, Appl
40	118	44.0	19	10	US-09-977-406A-62	Sequence 62, Appl
41	111	41.4	18	10	US-09-977-406A-61	Sequence 61, Appl
42	107	39.9	17	10	US-09-977-406A-60	Sequence 60, Appl
43	101	37.7	16	10	US-09-977-406A-59	Sequence 59, Appl
44	98	36.6	30	10	US-09-977-406A-90	Sequence 90, Appl
45	98	36.6	45	10	US-09-977-406A-91	Sequence 91, Appl

#### ALIGNMENTS

RESULT 1  
US-09-977-406A-88  
Sequence 88, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977, 406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 88  
LENGTH: 45  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide derived from rHSP94 sequence (polypeptide analog)  
US-09-977-406A-88

Query Match 100.0%; Score 268; DB 10; Length 45;  
Best Local Similarity 100.0%; Pred. No. 5.9e-27;  
Matches 45; Conservative 0; Mismatches 0; Indels 0;

QY 1 SCYFINEGVPGDSTRKMDLKNKHPINSEWQDNCETCTCYET 45  
Db 1 SCYFINEGVPGDSTRKMDLKNKHPINSEWQDNCETCTCYET 45

RESULT 2  
US-09-977-406A-1  
Sequence 1, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:

APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 94  
TYPE: PRT  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
AUTHORS: Ulvback, M., Lindstrom, C., Welber, H., Abrahamson, P.A., Lilja, H., and  
AUTHORS: Lundwall, A.  
TITLE: Molecular cloning of a small prostate protein, known as beta-  
TITLE: microsemnoprotein, PSP94 or beta-inhibin, and demonstration of transcripts  
TITLE: non-genital tissues.  
JOURNAL: Biochem. Biophys. Res Commun.  
VOLUME: 164  
ISSUE: 3  
PAGES: 1310-1315  
DATE: 1989  
DATABASE ACCESSION NUMBER: GI 131436  
DATABASE ENTRY DATE: 1988-08-01  
US-09-977-406A-1

Query Match 100.0%; Score 268; DB 10; Length 94;  
Best Local Similarity 100.0%; Pred. No. 1,3e-26;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCVFIPNEGVPDSTKCMDLKGKHPINSEWQTDNCECTCYET 45  
DB 1 SCVFIPNEGVPDSTKCMDLKGKHPINSEWQTDNCECTCYET 45

RESULT 3  
US-10-291-360-1  
Sequence 1, Application US/10291360  
Publication No. US20030119744A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PSP-94; Use for Treatment of Hypercalcemia and Bone metastasis  
FILE REFERENCE: 06508-051-US-02  
CURRENT APPLICATION NUMBER: US/10/291,360  
CURRENT FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: CA 2,361,736  
PRIOR FILING DATE: 2001-11-08  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 94  
TYPE: PRT  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
AUTHORS: Ulvback, M., Lindstrom, C., Welber, H., Abrahamson, P.A., Lilja, H., and  
AUTHORS: Lundwall, A.  
TITLE: Molecular cloning of a small prostate protein, known as beta-  
TITLE: microsemnoprotein, PSP94 or beta-inhibin, and demonstration of transcripts  
TITLE: non-genital tissues.  
JOURNAL: Biochem. Biophys. Res Commun.  
VOLUME: 164  
ISSUE: 3  
PAGES: 1310-1315  
DATE: 1989  
DATABASE ACCESSION NUMBER: GI 131436  
DATABASE ENTRY DATE: 1988-08-01  
US-10-291-360-1

Query Match 100.0%; Score 268; DB 14; Length 94;

Best Local Similarity 100.0%; Pred. No. 1,3e-26;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SCVFIPNEGVPDSTKCMDLKGKHPINSEWQTDNCECTCYET 45  
DB 1 SCVFIPNEGVPDSTKCMDLKGKHPINSEWQTDNCECTCYET 45

RESULT 4  
US-09-977-406A-2  
Sequence 2, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 102  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: recombinant human PSP94 (rHSP94) produced from yeast  
US-09-977-406A-2

Query Match 100.0%; Score 268; DB 10; Length 102;  
Best Local Similarity 100.0%; Pred. No. 1,5e-26;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCVFIPNEGVPDSTKCMDLKGKHPINSEWQTDNCECTCYET 45  
DB 9 SCVFIPNEGVPDSTKCMDLKGKHPINSEWQTDNCECTCYET 53

RESULT 5  
US-10-291-360-2  
Sequence 2, Application US/10291360  
Publication No. US20030119744A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PSP-94; Use for Treatment of Hypercalcemia and Bone metastasis  
FILE REFERENCE: 06508-051-US-02  
CURRENT APPLICATION NUMBER: US/10/291,360  
CURRENT FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: CA 2,361,736  
PRIOR FILING DATE: 2001-11-08  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 102  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: recombinant human PSP94 (rHSP94) produced from yeast  
US-10-291-360-2

Query Match 100.0%; Score 268; DB 14; Length 102;  
Best Local Similarity 100.0%; Pred. No. 1,5e-26;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCVFIPNEGVPDSTKCMDLKGKHPINSEWQTDNCECTCYET 45  
DB 9 SCVFIPNEGVPDSTKCMDLKGKHPINSEWQTDNCECTCYET 53

RESULT 6

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US-10-221-278-236
; Sequence 236, Application US/10221278
; Publication No. US20040034208A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20040034208A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US/10/221,278
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 236
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-221-278-236

Query Match      100.0%; Score 268; DB 12; Length 114;
Best Local Similarity 100.0%; Pred. No. 1,7e-26;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCVFIPNEGVPDSTRKCMDLKGKHPINSEWQDNCETCTCYET 45
Db 21 SCVFIPNEGVPDSTRKCMDLKGKHPINSEWQDNCETCTCYET 65

RESULT 7
US-10-012-896-1003
; Sequence 1003, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bascois, Carolea
; APPLICANT: Roy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121,427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
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US-10-205-823-271
; SEQ ID NO 1003
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-1003

Query Match      100.0%; Score 268; DB 13; Length 114;
Best Local Similarity 100.0%; Pred. No. 1,7e-26;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCVFIPNEGVPDSTRKCMDLKGKHPINSEWQDNCETCTCYET 45
Db 21 SCVFIPNEGVPDSTRKCMDLKGKHPINSEWQDNCETCTCYET 65

RESULT 8
US-10-205-823-271
; Sequence 271, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ganavarapu, Manjula
; APPLICANT: Gordatcheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Womsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; FILE REFERENCE: MRI-044
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 271
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-271

Query Match      100.0%; Score 268; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 1,7e-26;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCVFIPNEGVPDSTRKCMDLKGKHPINSEWQDNCETCTCYET 45
Db 21 SCVFIPNEGVPDSTRKCMDLKGKHPINSEWQDNCETCTCYET 65

RESULT 9
US-10-144-678A-1003
; Sequence 1003, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
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US-10-291-172-236
Sequence 236, Application US/10291172
Publication No. US20030228584A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-045
CURRENT APPLICATION NUMBER: US/10/291,172
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/693,267
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/665,363
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/616,847
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 752
SEQ ID NO 236
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-291-172-236

Query Match          100.0%; Score 268; DB 15; Length 114;
Best Local Similarity 100.0%; Pred. No. 1,7e-26;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SCYFIPNEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 45
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Db 21 SCYFIPNEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 65

RESULT 12
US-09-925-300-1027
Sequence 1027, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1027
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-300-1027

Query Match          100.0%; Score 268; DB 9; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.9e-26;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SCYFIPNEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 45
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Db 39 SCYFIPNEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 83

RESULT 13
US-09-977-406A-87
Sequence 87, Application US/09977406A
Publication No. US20030170220A1

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Mon Mar 22 13:39:31 2004

us-09-977-406a-88.rapb

Page 5

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; GENERAL INFORMATION:
; APPLICANT: PROCOYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 87
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-87

Query Match          98.5%; Score 264; DB 10; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.9e-26;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CYFIPNEGVPDSTRKCMCLKGNKHPINSEWQTDNCETCTCYET 45
DB 1 CYFIPNEGVPDSTRKCMCLKGNKHPINSEWQTDNCETCTCYET 44

RESULT 14
US-09-977-406A-86
; Sequence 86, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCOYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 86
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-86

Query Match          95.1%; Score 255; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.6e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YFTFNEGVPDSTRKCMCLKGNKHPINSEWQTDNCETCTCYET 45
DB 1 YFTFNEGVPDSTRKCMCLKGNKHPINSEWQTDNCETCTCYET 43

RESULT 15
US-09-977-406A-85
; Sequence 85, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCOYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 85
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-85
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; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 85
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-85

Query Match          92.5%; Score 248; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e-24;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 FIPNEGVPDSTRKCMCLKGNKHPINSEWQTDNCETCTCYET 42

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## OM protein - protein search, using sw model

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Title: US-09-977-406A-5  
Perfect score: 15  
Sequence: 1 EMQDNCETCTCYET 15

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Gapop 60.0 , Gapext 60.0

Searched: 1049977 seqs, 258955339 residues

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Minimum DB seq length: 0

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and is derived by analysis of the total score distribution.

## SUMMARIES

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2	15	100.0	15	US-10-291-360-5	Sequence 5, Appl1
3	15	100.0	16	US-09-977-406A-10	Sequence 10, Appl1
4	15	100.0	16	US-09-977-406A-59	Sequence 59, Appl1
5	15	100.0	17	US-09-977-406A-11	Sequence 11, Appl1
6	15	100.0	17	US-09-977-406A-60	Sequence 60, Appl1
7	15	100.0	18	US-09-977-406A-12	Sequence 12, Appl1
8	15	100.0	18	US-09-977-406A-61	Sequence 61, Appl1
9	15	100.0	19	US-09-977-406A-13	Sequence 13, Appl1
10	15	100.0	19	US-09-977-406A-62	Sequence 62, Appl1
11	15	100.0	20	US-09-977-406A-14	Sequence 14, Appl1
12	15	100.0	20	US-09-977-406A-63	Sequence 63, Appl1
13	15	100.0	21	US-09-977-406A-15	Sequence 15, Appl1
14	15	100.0	21	US-09-977-406A-64	Sequence 64, Appl1
15	15	100.0	22	US-09-977-406A-16	Sequence 16, Appl1

16	15	100.0	22	10	US-09-977-406A-65	Sequence 65, Appl1
17	15	100.0	23	10	US-09-977-406A-17	Sequence 17, Appl1
18	15	100.0	23	10	US-09-977-406A-66	Sequence 66, Appl1
19	15	100.0	24	10	US-09-977-406A-18	Sequence 18, Appl1
20	15	100.0	24	10	US-09-977-406A-67	Sequence 67, Appl1
21	15	100.0	25	10	US-09-977-406A-19	Sequence 19, Appl1
22	15	100.0	25	10	US-09-977-406A-68	Sequence 68, Appl1
23	15	100.0	26	10	US-09-977-406A-20	Sequence 20, Appl1
24	15	100.0	26	10	US-09-977-406A-69	Sequence 69, Appl1
25	15	100.0	27	10	US-09-977-406A-21	Sequence 21, Appl1
26	15	100.0	27	10	US-09-977-406A-70	Sequence 70, Appl1
27	15	100.0	28	10	US-09-977-406A-22	Sequence 22, Appl1
28	15	100.0	28	10	US-09-977-406A-71	Sequence 71, Appl1
29	15	100.0	29	10	US-09-977-406A-23	Sequence 23, Appl1
30	15	100.0	29	10	US-09-977-406A-72	Sequence 72, Appl1
31	15	100.0	30	10	US-09-977-406A-24	Sequence 24, Appl1
32	15	100.0	30	10	US-09-977-406A-73	Sequence 73, Appl1
33	15	100.0	30	10	US-09-977-406A-90	Sequence 90, Appl1
34	15	100.0	31	10	US-09-977-406A-25	Sequence 25, Appl1
35	15	100.0	31	10	US-09-977-406A-74	Sequence 74, Appl1
36	15	100.0	32	10	US-09-977-406A-26	Sequence 26, Appl1
37	15	100.0	32	10	US-09-977-406A-75	Sequence 75, Appl1
38	15	100.0	33	10	US-09-977-406A-27	Sequence 27, Appl1
39	15	100.0	33	10	US-09-977-406A-76	Sequence 76, Appl1
40	15	100.0	34	10	US-09-977-406A-28	Sequence 28, Appl1
41	15	100.0	34	10	US-09-977-406A-77	Sequence 77, Appl1
42	15	100.0	35	10	US-09-977-406A-29	Sequence 29, Appl1
43	15	100.0	35	10	US-09-977-406A-78	Sequence 78, Appl1
44	15	100.0	36	10	US-09-977-406A-30	Sequence 30, Appl1
45	15	100.0	36	10	US-09-977-406A-79	Sequence 79, Appl1

## ALIGNMENTS

RESULT 1  
US-09-977-406A-5  
; Sequence 5, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCYON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCK145 (polypeptide 31-45)  
US-09-977-406A-5  
Query Match 100.0%; Score 15; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EMQDNCETCTCYET 15  
Db 1 EMQDNCETCTCYET 15  
RESULT 2  
US-10-291-360-5  
; Sequence 5, Application US/10291360  
; Publication No. US20030119744A1  
; GENERAL INFORMATION:

APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis  
FILE REFERENCE: 06508-051-US-02  
CURRENT APPLICATION NUMBER: US/10/291,360  
CURRENT FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: CA 2,361,736  
PRIOR FILING DATE: 2001-11-08  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PCR3145 (polypeptide 31-45)  
US-10-291-360-5

Query Match 100.0%; Score 15; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYET 15  
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DB 1 EMQDNCETCTCYET 15

RESULT 3  
US-09-977-406A-10  
Sequence 10, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide derived from rHUPSP94 sequence (polypeptide analog)  
US-09-977-406A-10

Query Match 100.0%; Score 15; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.9e-10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYET 15  
|||||  
DB 1 EMQDNCETCTCYET 15

RESULT 4  
US-09-977-406A-59  
Sequence 59, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 59  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide derived from rHUPSP94 sequence (polypeptide analog)  
US-09-977-406A-59

Query Match 100.0%; Score 15; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.9e-10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYET 15  
|||||  
DB 2 EMQDNCETCTCYET 16

RESULT 5  
US-09-977-406A-11  
Sequence 11, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 11  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide derived from rHUPSP94 sequence (polypeptide analog)  
US-09-977-406A-11

Query Match 100.0%; Score 15; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2e-10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYET 15  
|||||  
DB 1 EMQDNCETCTCYET 15

RESULT 6  
US-09-977-406A-60  
Sequence 60, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 60  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-60

Query Match 100.0%; Score 15; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2e-10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 3 EWQDNCETCTCYET 17

RESULT 7  
US-09-977-406A-12  
Sequence 12, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:

APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 12  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-12

Query Match 100.0%; Score 15; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e-10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 1 EWQDNCETCTCYET 15

RESULT 8  
US-09-977-406A-61  
Sequence 61, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:

APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 61  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-61

Query Match 100.0%; Score 15; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e-10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 4 EWQDNCETCTCYET 18

RESULT 9  
US-09-977-406A-13  
Sequence 13, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:

APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 13  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-13

Query Match 100.0%; Score 15; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.2e-10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 1 EWQDNCETCTCYET 15

RESULT 10  
US-09-977-406A-62  
Sequence 62, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:

APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 62  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-62

Query Match 100.0%; Score 15; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.2e-10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYET 15  
DB 5 EWQDNCETCTCYET 19

RESULT 11  
US-09-977-406A-14

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/ Sequence 14, Application US/09977406A
/ Publication No. US20030170220A1
/ GENERAL INFORMATION:
/ APPLICANT: PROCYON BIOPHARMA INC.
/ TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
/ FILE REFERENCE: 06508-030-US-03
/ CURRENT FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: CA 2,321,256
/ PRIOR FILING DATE: 2000-10-16
/ PRIOR APPLICATION NUMBER: CA 2,355,334
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 92
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 14
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406A-14

Query Match      100.0%; Score 15; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2,3e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EMQTDNCETCTCYET 15
DB      1 EMQTDNCETCTCYET 15

RESULT 12
US-09-977-406A-63
/ Sequence 63, Application US/09977406A
/ Publication No. US20030170220A1
/ GENERAL INFORMATION:
/ APPLICANT: PROCYON BIOPHARMA INC.
/ TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
/ FILE REFERENCE: 06508-030-US-03
/ CURRENT FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: CA 2,321,256
/ PRIOR FILING DATE: 2000-10-16
/ PRIOR APPLICATION NUMBER: CA 2,355,334
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 92
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 63
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406A-63

Query Match      100.0%; Score 15; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2,3e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EMQTDNCETCTCYET 15
DB      6 EMQTDNCETCTCYET 20

RESULT 13
US-09-977-406A-15
/ Sequence 15, Application US/09977406A
/ Publication No. US20030170220A1
/ GENERAL INFORMATION:
/ APPLICANT: PROCYON BIOPHARMA INC.
/ TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
/ FILE REFERENCE: 06508-030-US-03
/ CURRENT FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: CA 2,355,334
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 92
/ SOFTWARE: PatentIn version 3.1
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/ CURRENT FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: CA 2,321,256
/ PRIOR FILING DATE: 2000-10-16
/ PRIOR APPLICATION NUMBER: CA 2,355,334
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 92
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 15
/ LENGTH: 21
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406A-15

Query Match      100.0%; Score 15; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 2,4e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EMQTDNCETCTCYET 15
DB      1 EMQTDNCETCTCYET 15

RESULT 14
US-09-977-406A-64
/ Sequence 64, Application US/09977406A
/ Publication No. US20030170220A1
/ GENERAL INFORMATION:
/ APPLICANT: PROCYON BIOPHARMA INC.
/ TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
/ FILE REFERENCE: 06508-030-US-03
/ CURRENT FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: CA 2,321,256
/ PRIOR FILING DATE: 2000-10-16
/ PRIOR APPLICATION NUMBER: CA 2,355,334
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 92
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 64
/ LENGTH: 21
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406A-64

Query Match      100.0%; Score 15; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 2,4e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EMQTDNCETCTCYET 15
DB      7 EMQTDNCETCTCYET 21

RESULT 15
US-09-977-406A-16
/ Sequence 16, Application US/09977406A
/ Publication No. US20030170220A1
/ GENERAL INFORMATION:
/ APPLICANT: PROCYON BIOPHARMA INC.
/ TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
/ FILE REFERENCE: 06508-030-US-03
/ CURRENT FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: CA 2,321,256
/ PRIOR FILING DATE: 2000-10-16
/ PRIOR APPLICATION NUMBER: CA 2,355,334
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 92
/ SOFTWARE: PatentIn version 3.1
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; SEQ ID NO: 16
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from RHUSP94 sequence (polypeptide analog)
US-09-977-406A-16

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Query Match      100.0%; Score 15; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 EMQTDNCETCTCYET 15
Db      1 EMQTDNCETCTCYET 15

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Job time : 12.2177 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2004, 06:07:38 ; Search time 52.129 Seconds  
(without alignments)  
317.925 Million cell updates/sec

Title: US-09-977-406A-58

Perfect score: 64  
Sequence: 1 EMOYDNCETCTCYETETISCC.....YIVVEKKPKTKCSVSEMI 64

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Gapop 60.0 , Gapext 60.0

Searched: 1049977 seqs, 258955339 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	64	100.0	64 10 US-09-977-406A-58	Sequence 58, Appl
2	64	100.0	94 10 US-09-977-406A-1	Sequence 1, Appl
3	64	100.0	94 14 US-10-291-360-1	Sequence 1, Appl
4	64	100.0	102 10 US-09-977-406A-2	Sequence 2, Appl
5	64	100.0	102 14 US-10-291-360-2	Sequence 2, Appl
6	64	100.0	114 12 US-10-221-878-236	Sequence 236, Appl
7	64	100.0	114 13 US-10-012-896-1003	Sequence 1003, Appl
8	64	100.0	114 14 US-10-205-823-271	Sequence 271, Appl
9	64	100.0	114 14 US-10-144-678A-1003	Sequence 1003, Appl
10	64	100.0	114 14 US-10-294-025-1003	Sequence 1003, Appl
11	64	100.0	114 15 US-10-291-172-236	Sequence 236, Appl
12	64	100.0	132 9 US-09-925-300-1027	Sequence 1027, Appl
13	63	98.4	63 10 US-09-977-406A-57	Sequence 57, Appl
14	62	96.9	62 10 US-09-977-406A-56	Sequence 56, Appl
15	61	95.3	61 10 US-09-977-406A-55	Sequence 55, Appl

16	60	93.8	60 10 US-09-977-406A-54	Sequence 54, Appl
17	59	92.2	59 10 US-09-977-406A-53	Sequence 53, Appl
18	58	90.6	58 10 US-09-977-406A-52	Sequence 52, Appl
19	57	89.1	57 10 US-09-977-406A-51	Sequence 51, Appl
20	56	87.5	56 10 US-09-977-406A-50	Sequence 50, Appl
21	55	85.9	55 10 US-09-977-406A-49	Sequence 49, Appl
22	54	84.4	54 10 US-09-977-406A-48	Sequence 48, Appl
23	53	82.8	53 10 US-09-977-406A-47	Sequence 47, Appl
24	52	81.2	52 10 US-09-977-406A-46	Sequence 46, Appl
25	51	79.7	51 10 US-09-977-406A-45	Sequence 45, Appl
26	50	78.1	50 10 US-09-977-406A-44	Sequence 44, Appl
27	49	76.6	49 10 US-09-977-406A-43	Sequence 43, Appl
28	48	75.0	48 10 US-09-977-406A-42	Sequence 42, Appl
29	47	73.4	47 10 US-09-977-406A-41	Sequence 41, Appl
30	46	71.9	46 10 US-09-977-406A-40	Sequence 40, Appl
31	45	70.3	45 10 US-09-977-406A-39	Sequence 39, Appl
32	44	68.8	44 10 US-09-977-406A-38	Sequence 38, Appl
33	43	67.2	43 10 US-09-977-406A-37	Sequence 37, Appl
34	42	65.6	42 10 US-09-977-406A-36	Sequence 36, Appl
35	41	64.1	41 10 US-09-977-406A-35	Sequence 35, Appl
36	40	62.5	40 10 US-09-977-406A-34	Sequence 34, Appl
37	39	60.9	39 10 US-09-977-406A-33	Sequence 33, Appl
38	38	59.4	38 10 US-09-977-406A-32	Sequence 32, Appl
39	37	57.8	37 10 US-09-977-406A-31	Sequence 31, Appl
40	36	56.2	36 10 US-09-977-406A-30	Sequence 30, Appl
41	35	54.7	35 10 US-09-977-406A-29	Sequence 29, Appl
42	34	53.1	34 10 US-09-977-406A-28	Sequence 28, Appl
43	33	51.6	33 10 US-09-977-406A-27	Sequence 27, Appl
44	32	50.0	32 10 US-09-977-406A-26	Sequence 26, Appl
45	31	48.4	31 10 US-09-977-406A-25	Sequence 25, Appl

## ALIGNMENTS

RESULT 1  
US-09-977-406A-58  
; Sequence 58, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCOON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03/09/977, 406A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 58  
; LENGTH: 64  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)  
US-09-977-406A-58

Query Match 100.0%; Score 64; DB 10; Length 64;  
Best Local Similarity 100.0%; Pred. No. 7.9e-59;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 EMOYDNCETCTCYETETISCTIVSTPVGDKNQCRIFFKEKCKTIIVVEKKPKTKCSVS 60

QY 61 EMI 64  
| | | | |  
DB 61 EMI 64

RESULT 2

US-09-977-406A-1  
; Sequence 1, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCYON PHARMACEUTICAL INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; PRIORITY FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 94  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; AUTHORS: Ulvback, M., Lindstrom, C., Welber, H., Abrahamson, P.A., Lilja, H., and  
; TITLE: Molecular cloning of a small prostate protein, known as beta-  
; TITLE: non-genital tissues.  
; JOURNAL: Biochem. Biophys. Res Commun.  
; VOLUME: 164  
; ISSUE: 3  
; PAGES: 1310-1315  
; DATE: 1989  
; DATABASE ACCESSION NUMBER: GI 131436  
; DATABASE ENTRY DATE: 1988-08-01  
US-09-977-406A-1  
Query Match 100.0%; Score 64; DB 10; Length 94;  
Best Local Similarity 100.0%; Pred. No. 1.1e-58;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 EMOTDNCETCTCYETETISCTTIVSTPVGYDKDNCQRIFKKEDCKYIVVEKDKPKTKCSVS 60  
DB 31 EMOTDNCETCTCYETETISCTTIVSTPVGYDKDNCQRIFKKEDCKYIVVEKDKPKTKCSVS 90  
CY 61 EMII 64  
DB 91 EMII 94  
RESULT 3  
US-10-291-360-1  
; Sequence 1, Application US/10291360  
; Publication No. US20030119744A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCYON BIOPHARMA INC.  
; TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis  
; FILE REFERENCE: 06508-051-US-02  
; CURRENT APPLICATION NUMBER: US/10/291,360  
; PRIORITY FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: CA 2,361,736  
; PRIOR FILING DATE: 2001-11-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 94  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; AUTHORS: Ulvback, M., Lindstrom, C., Welber, H., Abrahamson, P.A., Lilja, H., and  
; TITLE: Molecular cloning of a small prostate protein, known as beta-  
; TITLE: microsemoprotein, PSP94 or beta-inhibin, and demonstration of transcripts  
; JOURNAL: Biochem. Biophys. Res Commun.  
; VOLUME: 164

ISSUE: 3  
; PAGES: 1310-1315  
; DATE: 1989  
; DATABASE ACCESSION NUMBER: GI 131436  
; DATABASE ENTRY DATE: 1988-08-01  
US-10-291-360-1  
Query Match 100.0%; Score 64; DB 14; Length 94;  
Best Local Similarity 100.0%; Pred. No. 1.1e-58;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 EMOTDNCETCTCYETETISCTTIVSTPVGYDKDNCQRIFKKEDCKYIVVEKDKPKTKCSVS 60  
DB 31 EMOTDNCETCTCYETETISCTTIVSTPVGYDKDNCQRIFKKEDCKYIVVEKDKPKTKCSVS 90  
CY 61 EMII 64  
DB 91 EMII 94  
RESULT 4  
US-09-977-406A-2  
; Sequence 2, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCYON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; PRIORITY FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 102  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: recombinant human PSP94 (rHSP94) produced from yeast  
US-09-977-406A-2  
Query Match 100.0%; Score 64; DB 10; Length 102;  
Best Local Similarity 100.0%; Pred. No. 1.2e-58;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 EMOTDNCETCTCYETETISCTTIVSTPVGYDKDNCQRIFKKEDCKYIVVEKDKPKTKCSVS 60  
DB 39 EMOTDNCETCTCYETETISCTTIVSTPVGYDKDNCQRIFKKEDCKYIVVEKDKPKTKCSVS 98  
CY 61 EMII 64  
DB 99 EMII 102  
RESULT 5  
US-10-291-360-2  
; Sequence 2, Application US/10291360  
; Publication No. US20030119744A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCYON BIOPHARMA INC.  
; TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis  
; FILE REFERENCE: 06508-051-US-02  
; CURRENT APPLICATION NUMBER: US/10/291,360  
; PRIORITY FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: CA 2,361,736  
; PRIOR FILING DATE: 2001-11-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 102





PRIOR APPLICATION NUMBER: 60/362,158  
PRIOR FILING DATE: 2002-03-05  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 271  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-205-823-271

Query Match 100.0%; Score 64; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.3e-58;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWOTDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKTKCSVS 60  
DB 51 EWOTDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKTKCSVS 110  
QY 61 EWII 64  
DB 111 EWII 114

## RESULT 9

US-10-144-678A-1003  
Sequence 1003 Application US/10144678A  
Publication No. US20030157089A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yugu  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Reiter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A. W.  
APPLICANT: Hepler, William T.  
APPLICANT: Hurai, John  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Vinals y de Basols, Carlota  
APPLICANT: Foy, Teresa M.  
APPLICANT: Matanabe, Yoshihito  
APPLICANT: Deng, Ta

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C28  
CURRENT APPLICATION NUMBER: US/10/144,678A  
CURRENT FILING DATE: 2002-08-12  
NUMBER OF SEQ ID NOS: 1033  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1003  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-144-678A-1003

Query Match 100.0%; Score 64; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.3e-58;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWOTDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKTKCSVS 60  
DB 51 EWOTDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKTKCSVS 110

QY 61 EWII 64  
DB 111 EWII 114

## RESULT 10

US-10-294-025-1003  
Sequence 1003 Application US/10294025  
Publication No. US20030185830A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Stolk, John A.  
APPLICANT: Kalos, Michael D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C29  
CURRENT APPLICATION NUMBER: US/10/294,025  
CURRENT FILING DATE: 2002-11-12  
NUMBER OF SEQ ID NOS: 1038  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1003  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-294-025-1003

Query Match 100.0%; Score 64; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.3e-58;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWOTDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKTKCSVS 60  
DB 51 EWOTDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKTKCSVS 110  
QY 61 EWII 64  
DB 111 EWII 114

## RESULT 11

US-10-291-172-236  
Sequence 236 Application US/10291172  
Publication No. US20030228584A1  
GENERAL INFORMATION:  
APPLICANT: Hyseng, Inc  
TITLE OF INVENTION: No. US20030228584A1 Nucleic Acids and Polypeptides  
FILE REFERENCE: 21272-045  
CURRENT APPLICATION NUMBER: US/10/291,172  
CURRENT FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 09/693,267  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 09/665,363  
PRIOR FILING DATE: 2000-09-19  
PRIOR APPLICATION NUMBER: 09/616,847  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 09/596,193  
PRIOR FILING DATE: 2000-06-17  
PRIOR APPLICATION NUMBER: 09/574,454  
PRIOR FILING DATE: 2000-05-19  
PRIOR APPLICATION NUMBER: 09/519,705  
PRIOR FILING DATE: 2000-03-07  
NUMBER OF SEQ ID NOS: 752  
SEQ ID NO 236  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-291-172-236

Query Match 100.0%; Score 64; DB 15; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.3e-58;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWOTDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKTKCSVS 60

Db 51 EWQDNCETCTCYETEISCTLVSTPVGYDKNCQRIFFKEDCKYIVVEKKDPKKTCSVS 110  
QY 61 EMI 64  
111 EMI 114

RESULT 12  
US-09-925-300-1027  
; Sequence 1027, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen,  
; APPLICANT: Steve Ruben  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA101  
; CURRENT APPLICATION NUMBER: US/09/925,300  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05988  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 1027  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-300-1027

Query Match 100.0%; Score 64; DB 9; Length 132;  
Best Local Similarity 100.0%; Pred. No. 1.5e-58;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 69 EWQDNCETCTCYETEISCTLVSTPVGYDKNCQRIFFKEDCKYIVVEKKDPKKTCSVS 128  
QY 61 EMI 64  
111 EMI 114  
Db 129 EMI 132

RESULT 13  
US-09-977-406A-57  
; Sequence 57, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 57  
; LENGTH: 63  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)  
US-09-977-406A-57

Query Match 98.4%; Score 63; DB 10; Length 63;  
Best Local Similarity 100.0%; Pred. No. 8.4e-58;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 EWQDNCETCTCYETEISCTLVSTPVGYDKNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60  
QY 61 EMI 63  
111 EMI 63

RESULT 14  
US-09-977-406A-56  
; Sequence 56, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 56  
; LENGTH: 62  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)  
US-09-977-406A-56

Query Match 96.9%; Score 62; DB 10; Length 62;  
Best Local Similarity 100.0%; Pred. No. 9e-57;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EWQDNCETCTCYETEISCTLVSTPVGYDKNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60  
Db 1 EWQDNCETCTCYETEISCTLVSTPVGYDKNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60  
QY 61 EMI 62  
111 EMI 62  
Db 61 EMI 62

RESULT 15  
US-09-977-406A-55  
; Sequence 55, Application US/09977406A  
; Publication No. US20030170220A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCON BIOPHARMA INC.  
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
; FILE REFERENCE: 06508-030-US-03  
; CURRENT APPLICATION NUMBER: US/09/977,406A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: CA 2,321,256  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: CA 2,355,334  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 55  
; LENGTH: 61  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)  
US-09-977-406A-55

Query Match 95.3%; Score 61; DB 10; Length 61;  
Best Local Similarity 100.0%; Pred. No. 9.7e-56;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	EMQDNCERTCTCYETETISCTLIVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKKTCSVS	60
Qy	61	E 61	
Db	61	E 61	

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# OW protein - protein search, using sw model

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(without alignments)  
317.925 Million cell updates/sec

Title: US-09-977-406a-88

Perfect score: 45  
Sequence: 1 SCYFIPNEGVPQDSTRKCMDKGNKHPIINSEWQINDCETCTCYET 45

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Gapop 60.0 , Gapext 60.0

Searched: 1049977 seqs, 258955339 residues

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Minimum DB seq length: 0

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8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	45	100.0	45	10 US-09-977-406a-88
2	45	100.0	94	10 US-09-977-406a-1
3	45	100.0	94	14 US-10-291-360-1
4	45	100.0	102	10 US-09-977-406a-2
5	45	100.0	102	14 US-10-291-360-2
6	45	100.0	114	12 US-10-221-278-236
7	45	100.0	114	13 US-10-012-896-1003
8	45	100.0	114	14 US-10-205-823-271
9	45	100.0	114	14 US-10-144-678a-1003
10	45	100.0	114	14 US-10-294-025-1003
11	45	100.0	114	15 US-10-291-172-236
12	45	100.0	132	9 US-09-925-300-1027
13	45	97.8	44	10 US-09-977-406a-87
14	43	95.6	43	10 US-09-977-406a-86
15	42	93.3	42	10 US-09-977-406a-85

16	41	91.1	41	10 US-09-977-406a-84	Sequence 84, Appl
17	40	88.9	40	10 US-09-977-406a-83	Sequence 83, Appl
18	39	86.7	39	10 US-09-977-406a-82	Sequence 82, Appl
19	38	84.4	38	10 US-09-977-406a-81	Sequence 81, Appl
20	37	82.2	37	10 US-09-977-406a-80	Sequence 80, Appl
21	36	80.0	36	10 US-09-977-406a-79	Sequence 79, Appl
22	35	77.8	35	10 US-09-977-406a-78	Sequence 78, Appl
23	34	75.6	34	10 US-09-977-406a-77	Sequence 77, Appl
24	33	73.3	33	10 US-09-977-406a-76	Sequence 76, Appl
25	32	71.1	32	10 US-09-977-406a-75	Sequence 75, Appl
26	31	68.9	31	10 US-09-977-406a-74	Sequence 74, Appl
27	30	66.7	30	10 US-09-977-406a-73	Sequence 73, Appl
28	29	64.4	29	10 US-09-977-406a-72	Sequence 72, Appl
29	29	64.4	119	12 US-10-221-278-512	Sequence 72, App
30	29	64.4	119	15 US-10-291-172-612	Sequence 612, App
31	28	62.2	28	10 US-09-977-406a-71	Sequence 71, Appl
32	27	60.0	27	10 US-09-977-406a-70	Sequence 70, Appl
33	26	57.8	26	10 US-09-977-406a-69	Sequence 69, Appl
34	25	55.6	25	10 US-09-977-406a-68	Sequence 68, Appl
35	24	53.3	24	10 US-09-977-406a-67	Sequence 67, Appl
36	23	51.1	23	10 US-09-977-406a-66	Sequence 66, Appl
37	22	48.9	22	10 US-09-977-406a-65	Sequence 65, Appl
38	21	46.7	21	10 US-09-977-406a-64	Sequence 64, Appl
39	20	44.4	20	10 US-09-977-406a-63	Sequence 63, Appl
40	19	42.2	19	10 US-09-977-406a-62	Sequence 62, Appl
41	18	40.0	18	10 US-09-977-406a-61	Sequence 61, Appl
42	17	37.8	17	10 US-09-977-406a-60	Sequence 60, Appl
43	16	35.6	16	10 US-09-977-406a-59	Sequence 59, Appl
44	15	33.3	15	10 US-09-977-406a-58	Sequence 58, Appl
45	15	33.3	15	10 US-09-977-406a-57	Sequence 57, Appl

## ALIGNMENTS

```
US-09-977-406a-88
; Sequence 88, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406a-88

Query Match      100.0%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.5e-41;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 SCYFIPNEGVPQDSTRKCMDKGNKHPIINSEWQINDCETCTCYET 45
Db 1 SCYFIPNEGVPQDSTRKCMDKGNKHPIINSEWQINDCETCTCYET 45

RESULT 2
US-09-977-406a-1
; Sequence 1, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
```

APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 94  
TYPE: PRT  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
AUTHORS: Ulvback, M., Lindstrom, C., Welber, H., Abrahamson, P.A., Lilja, H., and  
AUTHORS: Lundwall, A.  
TITLE: Molecular cloning of a small prostate protein, known as beta-  
TITLE: microsemenoprotein, PSP94 or beta-inhibin, and demonstration of transcripts  
TITLE: non-genital tissues.  
JOURNAL: Biochem. Biophys. Res Commun.  
VOLUME: 164  
ISSUE: 3  
PAGES: 1310-1315  
DATE: 1989  
DATABASE ACCESSION NUMBER: GI 131436  
DATABASE ENTRY DATE: 1988-08-01  
US-09-977-406A-1

Query Match 100.0%; Score 45; DB 10; Length 94;  
Best Local Similarity 100.0%; Pred. No. 4,7e-41;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCVFIPNEGVPDSTKCMCLKGNKHPINSEWQTDNCECTCYET 45  
DB 1 SCVFIPNEGVPDSTKCMCLKGNKHPINSEWQTDNCECTCYET 45

RESULT 3  
US-10-291-360-1  
Sequence 1, Application US/10291360  
Publication No. US20030119744A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis  
FILE REFERENCE: 06508-051-US-02  
CURRENT APPLICATION NUMBER: US/10/291,360  
CURRENT FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: CA 2,361,736  
PRIOR FILING DATE: 2001-11-08  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 94  
TYPE: PRT  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
AUTHORS: Ulvback, M., Lindstrom, C., Welber, H., Abrahamson, P.A., Lilja, H., and  
AUTHORS: Lundwall, A.  
TITLE: Molecular cloning of a small prostate protein, known as beta-  
TITLE: microsemenoprotein, PSP94 or beta-inhibin, and demonstration of transcripts  
TITLE: non-genital tissues.  
JOURNAL: Biochem. Biophys. Res Commun.  
VOLUME: 164  
ISSUE: 3  
PAGES: 1310-1315  
DATE: 1989  
DATABASE ACCESSION NUMBER: GI 131436  
DATABASE ENTRY DATE: 1988-08-01  
US-10-291-360-1

Query Match 100.0%; Score 45; DB 14; Length 94;

Best Local Similarity 100.0%; Pred. No. 4,7e-41;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCVFIPNEGVPDSTKCMCLKGNKHPINSEWQTDNCECTCYET 45  
DB 1 SCVFIPNEGVPDSTKCMCLKGNKHPINSEWQTDNCECTCYET 45

RESULT 4  
US-09-977-406A-2  
Sequence 2, Application US/09977406A  
Publication No. US20030170220A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS  
FILE REFERENCE: 06508-030-US-03  
CURRENT APPLICATION NUMBER: US/09/977,406A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: CA 2,321,256  
PRIOR FILING DATE: 2000-10-16  
PRIOR APPLICATION NUMBER: CA 2,355,334  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 102  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: recombinant human PSP94 (rhPSP94) produced from yeast  
US-09-977-406A-2

Query Match 100.0%; Score 45; DB 10; Length 102;  
Best Local Similarity 100.0%; Pred. No. 5,1e-41;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCVFIPNEGVPDSTKCMCLKGNKHPINSEWQTDNCECTCYET 45  
DB 9 SCVFIPNEGVPDSTKCMCLKGNKHPINSEWQTDNCECTCYET 53

RESULT 5  
US-10-291-360-2  
Sequence 2, Application US/10291360  
Publication No. US20030119744A1  
GENERAL INFORMATION:  
APPLICANT: PROCYON BIOPHARMA INC.  
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis  
FILE REFERENCE: 06508-051-US-02  
CURRENT APPLICATION NUMBER: US/10/291,360  
CURRENT FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: CA 2,361,736  
PRIOR FILING DATE: 2001-11-08  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 102  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: recombinant human PSP94 (rhPSP94) produced from yeast  
US-10-291-360-2

Query Match 100.0%; Score 45; DB 14; Length 102;  
Best Local Similarity 100.0%; Pred. No. 5,1e-41;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCVFIPNEGVPDSTKCMCLKGNKHPINSEWQTDNCECTCYET 45  
DB 9 SCVFIPNEGVPDSTKCMCLKGNKHPINSEWQTDNCECTCYET 53

RESULT 6

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US-10-221-278-236
; Sequence 236, Application US/10221278
; Publication No. US20040034208A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20040034208A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/221,278
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 236
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-221-278-236

Query Match          100.0%; Score 45; DB 12; Length 114;
Best Local Similarity 100.0%; Pred. No. 5,6e-41;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWOTDNCETCTCYET 45
Db 21 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWOTDNCETCTCYET 65

RESULT 7
US-10-012-896-1003
; Sequence 1003, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugui
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Repler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121,427027
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 1003
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-1003

Query Match          100.0%; Score 45; DB 13; Length 114;
Best Local Similarity 100.0%; Pred. No. 5,6e-41;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWOTDNCETCTCYET 45
Db 21 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWOTDNCETCTCYET 65

RESULT 8
US-10-205-823-271
; Sequence 271, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; FILE REFERENCE: MRI-044
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 271
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-271

Query Match          100.0%; Score 45; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 5,6e-41;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWOTDNCETCTCYET 45
Db 21 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWOTDNCETCTCYET 65

RESULT 9
US-10-144-678A-1003
; Sequence 1003, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
```

APPLICANT: Jiang, Yugu  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Reiter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedrick, Thomas S.  
APPLICANT: Carter, Darick  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A. W.  
APPLICANT: Hepler, William T.  
APPLICANT: Huxal, John  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghon, Raymond L.  
APPLICANT: Vinals y de Bassols, Carola  
APPLICANT: Foy, Teresa W.  
APPLICANT: Watanabe, Yoshinhiro  
APPLICANT: Deng, Ya  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C28  
CURRENT APPLICATION NUMBER: US/10/144,678A  
CURRENT FILING DATE: 2002-08-12  
NUMBER OF SEQ ID NOS: 1033  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1003  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-144-678A-1003

Query Match 100.0%; Score 45; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 5.6e-41;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYFIPEGVPGDSTRKCMCLKGNKHPINSEWQTNCECTCYET 45  
Db 21 SCYFIPEGVPGDSTRKCMCLKGNKHPINSEWQTNCECTCYET 65  
RESULT 10  
US-10-294-025-1003  
Sequence 1003, Application US/10294025  
Publication No. US20030185830A1  
GENERAL INFORMATION:  
APPLICANT: Xi, Jiangchun  
APPLICANT: Stolk, John A.  
APPLICANT: Kalos, Michael D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C29  
CURRENT APPLICATION NUMBER: US/10/294,025  
CURRENT FILING DATE: 2002-11-12  
NUMBER OF SEQ ID NOS: 1038  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1003  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-294-025-1003

Query Match 100.0%; Score 45; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 5.6e-41;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYFIPEGVPGDSTRKCMCLKGNKHPINSEWQTNCECTCYET 45  
Db 21 SCYFIPEGVPGDSTRKCMCLKGNKHPINSEWQTNCECTCYET 65

RESULT 11

US-10-291-172-236  
Sequence 236, Application US/10291172  
Publication No. US20030228584A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc  
TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides  
FILE REFERENCE: 21272-045  
CURRENT APPLICATION NUMBER: US/10/291,172  
CURRENT FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 09/693,267  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 09/665,363  
PRIOR FILING DATE: 2000-09-19  
PRIOR APPLICATION NUMBER: 09/616,847  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: 09/596,193  
PRIOR FILING DATE: 2000-06-17  
PRIOR APPLICATION NUMBER: 09/574,454  
PRIOR FILING DATE: 2000-05-19  
PRIOR APPLICATION NUMBER: 09/519,705  
PRIOR FILING DATE: 2000-03-07  
NUMBER OF SEQ ID NOS: 752  
SEQ ID NO 236  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-291-172-236

Query Match 100.0%; Score 45; DB 15; Length 114;  
Best Local Similarity 100.0%; Pred. No. 5.6e-41;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYFIPEGVPGDSTRKCMCLKGNKHPINSEWQTNCECTCYET 45  
Db 21 SCYFIPEGVPGDSTRKCMCLKGNKHPINSEWQTNCECTCYET 65  
RESULT 12  
US-09-925-300-1027  
Sequence 1027, Application US/09925300  
Patent No. US20020151681A1  
GENERAL INFORMATION:  
APPLICANT: Craig Rosen,  
APPLICANT: Steve Ruben,  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA101  
CURRENT APPLICATION NUMBER: US/09/925,300  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05988  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1890  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1027  
LENGTH: 132  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-925-300-1027

Query Match 100.0%; Score 45; DB 9; Length 132;  
Best Local Similarity 100.0%; Pred. No. 6.4e-41;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYFIPEGVPGDSTRKCMCLKGNKHPINSEWQTNCECTCYET 45  
Db 39 SCYFIPEGVPGDSTRKCMCLKGNKHPINSEWQTNCECTCYET 83

RESULT 13  
US-09-977-406a-87  
Sequence 87, Application US/09977406A  
Publication No. US20030170220A1



```
; GENERAL INFORMATION:
; APPLICANT: PROCTON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-87

Query Match          97.8%; Score 44; DB 10; Length 44;
Best Local Similarity 100.0%; Pred. No. 3e-40;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  CYFIPNEGVPDSTRKCMCLKGNKHPIINSEWQTDNCETCTCYET 45
Db      1  CYFIPNEGVPDSTRKCMCLKGNKHPIINSEWQTDNCETCTCYET 44

RESULT 14
US-09-977-406A-86
; Sequence 86; Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCTON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-86

Query Match          95.6%; Score 43; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.5e-39;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  YFIPNEGVPDSTRKCMCLKGNKHPIINSEWQTDNCETCTCYET 45
Db      1  YFIPNEGVPDSTRKCMCLKGNKHPIINSEWQTDNCETCTCYET 43

RESULT 15
US-09-977-406A-85
; Sequence 85; Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCTON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
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; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-85

Query Match          93.3%; Score 42; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 4.1e-38;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4  FIPNEGVPDSTRKCMCLKGNKHPIINSEWQTDNCETCTCYET 45
Db      1  FIPNEGVPDSTRKCMCLKGNKHPIINSEWQTDNCETCTCYET 42

Search completed: March 18, 2004, 06:14:55
Job time : 36.6532 secs
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